SUMMARIES

5.1.4_p5_4578 Compugen Ltd. GenCore version Copyright (c) 1993 - 2003

protein search, using frame_plus_n2p model OM nucleic

Run on:

May 16, 2003, 12:14:56; Search time 113 Seconds (without alignments) 5044.656 Million cell updates/sec

US-10-008-355-1 3820 Title: Perfect score: Sequence:

1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa 2139

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

908470 seqs, 133250620 residues Searched: Total number of hits satisfying chosen parameters:

1816940

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

|: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT

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Re	Result No.	Score	Query Match	Length	DB	ΩI	cription
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J	c 19	132			20	AAY36845	2
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	22	130			23	AAU97883	Streptococcus.pneu
	23	13			20	AAW87504	i-methy
	24	127.5			18	AAW21725	Modified streptoki
J	c 25	127			20	AAY04998	Mycobacterium spec
٠	26	127			22	AAU38091	Streptococcus pneu
	27	12			22	AAB59827	Protein #4 encoded
	28	26.	т т		53	ABP27517	Streptococcus poly
	29	٠.			21	AAY95559	Caenorhabditis ele
	30	26.			21	AAY95556	Caenorhabditis ele
	31	17	٠		22	AAB27242	Human EXMAD-20 SEQ
	32	123.5	•		20	AAY43380	M. catarrhalis str
	33	22.	•	\sim	23	AA015221	Porphyromonas ging
	34	22			17	AAR88649	Neisseria meningit
	35	22.		\sim	18	AAW21723	Plasminogen-bindin
	36	22.	٠	81	18	AAW21728	Wild type plasmino
	37	'n.		œ	18	AAW21727	Streptokinase/malt
	38	22.		13	18	AAW21724	ified str
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ALIGNMENTS

AA015205 standard; Protein; 712 AA 05-SEP-2002 (first entry) AA015205; RESULT 1 AA015205

Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7).

Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis.

Porphyromonas gingivalis.

WO200238742-A2

16-MAY-2002.

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Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amiddlytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivals (e.g., gingivitis or periodontitis). The present amino acid sequence represents the porphyromonas gingivals (PDP-7) enzyme of the
                                                                                                                                                                                                           of
                                                                                                                                                                                                           identifying inhibitor
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the dipeptidylpeptidase for protecting an a
disease caused by Porphyromonas gingivalis
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                2001WO-US46782
                                                2000US-246827P
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                                                                                                                     Potempa JS,
                                                                                                                                                                                                                                                                            7; Fig 4; 65pp;
                                                                                                                                                 WPI; 2002-490075/52.
N-PSDB; AAL43635.
              08-NOV-2001;
                                                08-NOV-2000;
                                                                                                                     Travis J,
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                                                                                                                                                                                                                                                                            Claim
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Conservative: Mismatches: Indels: Length: Matches: Gaps: 3719.00 100.00% 100.00% 97.36% AĄ; Similarity: 712 Percent Similarity: Best Local Similarit Alignment Scores: Sequence Match: .. 9 Query

TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA 712 712 0 0 0 US-10-008-355-1 (1-2139) x AAO15205 (1-712) 41 21 121 181 241 121 61 301 101 361 81 g g Ω̈́D ò οy g ò g ò පු ò g ò õ

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               1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC
                       1621 TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                      Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage;
DPP-7 inhibitor identification; periodontal disease; gingivitis;
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide band between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the
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                                                                    Example 6; Fig 5; 65pp; English.
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The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23629 and AAB59831), tutI (AAF23630 and AAB59832), tutE (AAF23631 and AAB59834) and tutG (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. Toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of folluene and its analogs contained in liquid or solid waste source. The present sequence is a protein sequence for toluene degrading enzyme, TutD.
                                Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ATTCGCTCTACAGTTTCGACAAGCCGTCCATTG-----CCA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProLysProArgProThrCysArgProSerProGlyThrAlaArgArgValSerThrThr 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 TGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 TAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 CCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAA 124
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------CysGlyArgThrThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 TrpAsnValArgPheProSerMetAlaProAlaSerArgAlaProThrAlaLysSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAGAACCAACTCT
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                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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ThrArgAlaAlaThrProArgArgLysThrProCys----
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                                                                                                   Disclosure; Fig 5; 122pp; English
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174.00
34.00%
23.56%
4.55%
N-PSDB; AAF23625, AAF23627
                                                                                                                                                                                                                                                                                          1017 AA;
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Best Local Similarity:
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Qy	644	ACAACTGGATGTGGCCGC676
qq	300	gProSerProProSerSerSerAla
Οy	677	TCAGCGTATTCCGCGTGTATGCCGCTGTATGCCGCTGTGCCCGTGTGCCCGTGCCGGTGCCGGTGCCGGTGCTGC
Ωp	320	ArgArgArgCysAlaGlyPheSerSerAlaSerAlaThrAspSerAla1leArgArgSer 339
Qy	707	ACAACCGGCCGGAGTACAGCAAGGACAATAAACCCTATAAGCCGGTTTACTTCGCTG 766
20	2	
δλ Op	360	CCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCA 811
0	812	
go Op	380	LysLysProValargLysValalaAlaGlnSerSerArgPro 39
QY	851	GGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCA 910
Dp	400	SerCysTrpLysSerArgSerMetThrAlaThr
QY	911	AGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCA 961
Op	411	ThrdlyArgThrProThrCysAsnSerAlaArgArgProValIleSerArg 427
Qy	962	AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACC 1021
Dp	428	ArgSerProSerArgMetSer 438
δλ	1022	0 1
ΩΩ	439	AlaSerSerIleAsnMetArgSerThrSerValSerAlaProArgThrCysArgAla 457
Oy Op	1082	ACTGGATCCGTAAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGAAA 1141 Thiserserseralsercyaatgysteusser
ò	4	TTTATAAGGAAGGAG
g 9	7	GlyTrpThrProAlaProCysProSerSerProMetAlaGly 493
٥y	1169	GACTTATTGA
qq	494	ThrThrArg SerArgArgSerSerArgArgThrProSerTrp 507
Οy	1226	TTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCA 1282
QQ	508	
Qy	1283	AATCGCTTGACGACAAGTACAAAGACTACCTCGCTCGACCGTAAGGTGCTGCCCG 1342
QQ	516	ArgargasnThrProSerSerasnSeralaLysargargThrGlyLysValSerarg 535
ΟŸ	1343	CCATGCTCGATATTGTACGCCGCCGTATCCCTGCCG 1378
qq	536	
Qy	1379	ACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGA 1435
QQ	556	ValSerSerProAlaSerThrArgLysSerSerAlaAlaLysCys 570
Οy	1436	AGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCC 1492
QQ	571	AlaArgSerProThrThrLeuValValArgSerCysArgLeuValArgLeuSerAla 589
Οy	1493	ATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543
οg	290	CysThrTrpLysSerValArgAlaArgAlaProArgArgThrGlyAlaSerGly 607
οy	1544	AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603

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0y 1604 ATGCGATGGCG 0y 1604 ATGCGATGGCG 0b 619ThrTrp[0] 0y 1664 GTGAGA 0y 1664 GTGAGA 0y 1709 CCATGCGTATG 0b 654Cys 0y 1769 ACTATC 0y 1784 GCAGGGCGTA 0y 1784 GCAGGGCGTA 0y 1883 CCGAGACGGT 0y 1883 CCGAGACGGT 0y 1883 CCGAGACGGT 0y 1883 CCGAGACGGT 0y 1937 GTAACTCCGGT 0y 1937 GTAACTCGGT 0y 1937 GTAACTCGGT 0y 1937 GTAACTCGGT 0y 1937 GTAACTCGGT 0x AAB59826; 0x		AGGATCCTAAGGACGATGAGGAGTTGCGG ThrMetileLeuserCysalaPhebroalaThralaLeu TCCTGGACGTCTTCGGACGAAAACTATGGTCGCTATG III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	<pre>ndard; Protein; 1615 AA. (first entry) ncoded by TutD/E gene. adation; enzyme; waste degradation; TutE; TutD. atica. tallophilia. tallireducens. ulyticus. A2.</pre>	; 2000Wo-US14298. ; 99US-0323872. V OHIO. PW: 11080/05. 23627. comprising toluene degrading enzyme useful for biological forganic compounds, especially for degrading toluene or its Fig 12; 122pp; English.
Db 608 Qy 1604 Db 619 Qy 1664 Db 638 Qy 1709 Db 691 Qy 1784 Qy 1832 Db 729 Qy 1883 Db 749 Qy 1883 Db 749 Qy 1937 Db 749 Qy 1937 Db 749 Qy 1983 Db 749 Qy 1937 Db 749 Cos Thau Cos Thau Cos Accar Cos Accar Cos Accar Cos Cos Cos Cos Cos Cos Comp Cos Cos Cos Cos Cos Cos			standard; Pr ; 001 (first e #3 encoded by degradation; aromatica. nas maltophil r metalliredu tolulyticus.	CC-2000. IN-1999; 99US-(I-) UNIV OHIO. 119ano PW: 2001-041080/05. B; AAF23627. B; AAF23627. Ssition comprising the comprising of organic organic of organic orga
			RESULT 4 AAB59826 ID AAB59 AC AAB56 XX AC AAB56 DE Prote XX XX TO 10x XX TO 20x XX TO 30x XX TO 30x XX TO 30x XX TO 30x XX	

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The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23629 and AAB59831), tut1 (AAF23630 and AAB59832), tutF (AAF23631 and AAB59834). The tute (AAF23631 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase, toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of foluene and its analogs contained in liquid or solid waste source. The present sequence is a protein sequence encoded by toluene degrading enzyme gene, TutD/E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729 SerProArgSerThrThrGlyArgArgTrpSerSerProAlaArgArgSerAlaGlyArg 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         789 AlaSerArgThrArgCysArgArgAsnSerLeuProSerSerValThrArgSerSerAla 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 TCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGGATGGTTTCGTTTCTCGCACGA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 GCATCGTAGAGCCTTTCTATTCCAACGAATACTTCCTCATCGTCTACGATGTATTCA 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ATTCGCTCTACAGTTTCGACAAGCCGTCCATTG----CCA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 ATGCCGTGGTTATCT-----TCGGTGGCGGATGTACCG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 TGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TGCGTGAGCTCGGCTTTACGCTCCCGTTGG--------
                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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174.00
34.008
23.568
4.558
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                                                                                                                                                                           1615 AA;
                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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δy da	707 ACA ::: 938 Ser	ACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTG 766 ::: ::: SerthttatcSetAlaArcGsetAataArcaArcaAsstratacsetAlaSerthtalathr 957	qq	 1236 ArgAr
ò			Qy	1709 CCATG
g 6		ProThrThrGlySerThrCysCysAlaCysArgProAlaSer	qa	
oy da	812 TCGC :::	TCGGTTTCC	yo da	1769 ACTAT
60			Oy 4	
QQ	998 Ser	SerCysTrpLysSerArgSerMetThralaThr	2 2	1832
Qy		CAGGCTACCCGTATCA 961	qa Dp	1307 GlySe
Вр			٥٧	1883 CCGAG
ý d	962 AATA	AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACC 1021	qa	1327 AlaHi
ολ		ACGTGATAGGTCGTAAGCGTGCCAGGAAAGAGCATTCGCAG	Qy	
Dp	1037 Ala	::: ::: AlaSerSerIleAsnMetArgSerThrSerValSerAlaProArgThrCysArgAla 1055	<u>a</u>	134/ SerAi
Qγ	1082 ACT	ATGGCGATG	RESU AAB5 ID	RESULT 5 AAB59827 ID AAB59827 s
qq	1056 Thr	ThrSerSerAlaSerCysArgCysLeuSerCysProGlnSerThr 1071	XX AC	AAB59827;
ογ			XX	04-APR-20(
qq	1072 Thr	ThralaalaTrpasnSerGlyTrpThrProAlaProCysProSerSerProMetAlaGly 1091	XX	Protein #4
Oy Dp	1169 ACC 1092 Thr	ACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT 1225 	XXXX	Toluene de
οy	1226 TTG	TTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGGTATCCTCA 1282	s s s	Thauera an
g	1106	:::	\$ S \$	Azoarcus t
οy		AATGGCTTGACGACAAGTACAACTACCTCGCTCGACGTAAGGTGCTGCCCG 1342	N X	WO2000726
QQ	1114 Arg	ArgArgAsnThrProSerSerAsnSerAlaLysArgArgArgThrGlyLysValSerArg 1133	O X	07-DEC-20(
οy			PF	24-MAY-20(
qq	1134 Lys	LysCysalaSerThrSerSerGlyArgArgSerGlyAlaThrThrMetIleThrProThr 1153	PR XX	01-JUN-19
οy		TCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGA	PA XX	IU (-HOYU)
qq	>		PI	Coschigand
Oy Dp	1436	1436AGAAGTATGCAGCTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCC 1492 	DR DR	WPI; 2001 N-PSDB; AA
δλ	1493 ATG	1493 ATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543	T L d	Compositic treatment analogs
Dp	1188	rTrpLysSerValArgAlaArgAla	XX PS	Disclosure
oy c	1544 AAG	1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCGCTATTCAGGCCG 1603 1)	×SS	The preser
3			38	tutr (AAF)
Oy Dp	1604 ATG	ATGCGATGCCCAATGCCTATGCAAAGGCAAGGGTCTTTTCTTTGCCGGTTTGC 1663 ThtTrpGluprothratgatgGlyargArgArgCysCysAlaArgCysProArgCys 1235	888	toluene de toluene de compounds
ôy	1664 GTGAGA	3AGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCA 1708	<u> </u>	analogs co is a prote

(UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising tol treatment of organic compoanalogs. Disclosure; Fig 12; 122pp; The present invention relapproteins tuth (see AAF2362 tuth (AAF23631 and AAF5983) toluene degrading enzymes organical engagating engagat	AAB59827;	RESULT 5 AAB59827 ID AAB59827 standard, Protein; 1592 AA.	Qy 1937 GTAACTCCGGTAGCCCCGTAT 1957 Db 1347 SerArgProProLeuProTyr 1353	1327 AlaHisProlleSerSerShrSerLysSerArgThrSerHisSerArgGlyAlaAla 134
(UYOH-) UNIV	DT 04-APR-2001 (first entry) XX DE XX XX XX XX Toluene degradation; enzyme; waste degradation; TutE; TutD. XX OS Thauera aromatica. SS Acobacter metallireducens. SA Acoarcus tolulyticus. XX W0200072650-A2. XX PD 07-DEC-2000. XX PF 24-MAY-2000; 2000WO-US14298. XX PR 01-JUN-1999; 99US-0323872.	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872.	AAB59827 AAB59827 AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298.	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu 359827 AAB59827; 04-APR-2001 (first Protein #4 encoded b Toluene degradation; Thauera aromatica. Xanthomonas maltophi Geobacter metallired Azoarcus tolulyticus WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-
1007 CO COCC 1000 TO	04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Acoarcus tolulyticus. W0200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000W0-US14298.	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298.	AAB59827 AAB59827 AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298.	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu SULT 5 559827 AAB59827; 04-APR-2001 (first Protein #4 encoded b Toluene degradation; Thauera aromatica. Xanthomonas mallophi Geobacter metallired Azoarcus tolulyticus WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000W0-
01-JIIIV-1999: 990S-032387	04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000.	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000.	AAB59827 AAB59827 AAB59827 AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000.	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu 1347 SerArgProProLeu 1348 S9827 AAB59827; 04-APR-2001 (first Protein #4 encoded b Toluene degradation; Thauera aromatica. Xanthomonas maltophi Geobacter metallired Azoarcus tolulyticus WO200072650-A2.
24-MAY-2000; 2000WO-US14	04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2.	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2.	AAB59827 AAB59827 AAB59827; AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2.	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu 1347 SerArgProProLeu 159827 AAB59827, 04-APR-2001 (first Protein #4 encoded b Toluene degradation; Thauera aromatica. Xanthomonas maltophi Geobacter metallired Azoarcus tolulyticus
07-DEC-2000. 24-MAY-2000; 2000WO-US14 01-JIIN-1999; 99US-0323	04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus.	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus.	AAB59827 AAB59827 AAB59827; AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus.	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu SULT 5 559827 AAB59827; AAB59827; 04-APR-2001 (first Protein #4 encoded b Toluene degradation; Thauera aromatica. Xanthomonas maltophi Geobacter metallired Azoarcus tolulyticus
WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14	04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE;	AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE;	S59827 AAB59827 standard; Protein; 1592 AA. AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene. Toluene degradation; enzyme; waste degradation; TutE;	1937 GTAACTCCGGTAGCC 1347 SerArgProProLeu SULT 5 359827 AAB59827; 04-APR-2001 (first Protein #4 encoded b Toluene degradation;
Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducen Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14	04-APR-2001 (first entry) Protein #4 encoded by TutD/E	AABS9827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E	UULT 5 859827 AAB59827 standard; Protein; 1592 AAB59827; 04-APR-2001 (first entry) Protein #4 encoded by TutD/E gene	1937 GTAACTCCGGTAGCC
Toluene degradation; enzyme; waste degradation; TutE; Thauera aromatica Xanthomonas maltophilia. Santhomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. W0200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000W0-US14298.	#0%:47 1000 and 4.40	AAB59827;	UULT 5 559827 AAB59827 standard; Protein; 1592 AAB59827;	1937 GTAACTCCGGTAGCC
1883 CCGAGAACGGTCACTTCCTTTCCTATCGACACGACMTCACGG 193 1327 AlaHisProlleSerSerSerSerThrSerLysSerArgThrSerHisSerArgClyAlaAla 134 1327 AlaHisProlleSerSerSerSerThrSerLysSerArgThrSerHisSerArgClyAlaAla 134 1337 GTAACTCCGGTAGCCCGTT 1957 111	1883 CCGAGAACGGTCCATATCGTTTCCTATCGAACGACATCACGGGCG 193 1327 AlaHisProlleSerSerSerThrSerLysSerArgThrSerHisSerArgGlyAlaAla 134 1937 GTAACTCCGGTAGCCCCGTAT 1957 1937 GTAACTCCGGTAGCCCCGTAT 1957 111	1883 CCGAGAACGGTCAGCTCCATATCGATCGAACAACGACTCACGGGGGGGG	1883 CCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCG 193 1327 AlaHisProlleSerSerThrSerLysSerArgThrSerHisSerArgGlyAlaAla 134	EGT BUSHBUSHADEROADSAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1307 GlySerThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArgIleSer 132 1883 CCGAGAACGGTCAGCTCCATATCGTTTCCTATCGAACACGACTCACGGGCG 193 1327 AlaHisProIleSerSerSerThrSerLySserArgThrSerHisSerArgGlyAlaAla 134 1937 GTAACTCCGGTAGCCCGTAT 1957 1147 SerArgProProLeuProTyr 1353 1347 SerArgProProLeuProTyr 1353 1347 SerArgProProLeuProTyr 1353 AAB59827 AAB59827 AAB59827 Thauera aromatica Toluene degradation; enzyme; waste degradation; TutE; TutD. Thauera aromatica Xanthomonas maltophilia. Geobacter metallireducens. Acoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298.	1307 GlySerThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArgIleSer 132 1883 CCGAGAACGGTCAGCTCCTATCGTTTCCAACGACACGAC	1307 GlyserThrPheArgProMetGlyArgThrProSerSerProValArgAsnArgIleSer 132 1883 CCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACGACATCACGGGCG 193 1327 AlaHisProIleSerSerSerThrSerLySSerArgThrSerHisSerArgGlyAlaAla 134 1937 GTAACTCCGGTAGCCCGTAT 1957 1347 SerArgProProLeuProTyr 1353	1307 GlyserThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArg1leSer 132 1883 CCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACGACATCACGGGCG 193 1327 AlaHisProlleSerSerSerThrSerLySSerArgThrSerHisSerArgGlyAlaAla 134	1307 GlySerThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArglleSer 132
1832TACAGGAGAATATCCTGACCTTTCCGCACCAAAACTATGCTGGTATG 188 1307 GlySerThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArgIleSer 132 1883 CCGAGAACGGTCACTATCGCTTTCCTATCGAACACACACA	1832TACAGGAGAATATCCTCGACCTTTCGCACCAAAACTATGGTCGCTATG 188 1307 GlySerThrPheArgProMetGlyArgThrProSerSerProvalArgAsnArgIleSer 132 1883 CCGAGAACGGTCCATATCGTTTCTATCGAACAACGACATCACGG 193 1327 AlaHisProlleSerSerFarrorTTCTATCGACACGACATCACGGTGCG 193 1327 AlaHisProlleSerSerFarrorTTSerHisSerHisSerArgGlyAlaAla 134 1937 GTAACTCCGGTAGCCCGTAT 1957 111	1832TACAGGAGAATATCCTCGACCTTTCCGCACCAAAACTATGGTCGCTATG 188 1307 GlySerThrPheArgProMetGlyArgThrProSerSerProValArgAsnArg1leSer 132 1883 CCGAGAACGGTCAGCTCCATATCGAACACACACACACAGGGCG 193 1327 AlaHisProIleSerSerThrSerLysSerArgThrSerHisSerArgGlyAlaAla 134 1937 GTAACTCCGGTAGCCCGTAT 1957 1147 SerArgProProLeuProTyr 1353	1832TACAGGAGAATATCCTCGACCTTCCGCACCAAAACTATGGTCGCTATG 188 :: ::: :::	1832TACAGGAGAATATCCTCGACCTTCGGCACCAAAAACTATGGTCGGTATG 188 ::: ::: :::
1784 GCAAGGGCTATTGGAGAAGCAGGATCCTAAGAGCGATTGCG	1784 GCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTGCCG	1784 GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTGCCG	1784 GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCG	1784 GCAAGGGGGTATTGGAGAAGCAGGATCCTAAGAGGGATGAGTTTGCCG 183
1269 IlelieSerIleMetPheSerSerMetSerSeralaargMetLysCysalaLeuhigSer 128 1784 GCAAGGGCTATTGGAGAAGGAGGATCCTAAGACGAGTTTGCCG	1269 IlelleserIlemetPheserSerMetSerSerAlaArgMetLysCysAlaionin 1289 1181 1281 1	1269 IlelleSerIleMetPheserSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1784 GCAAGGGCGTATTGGAGGATCCTAAGAGCGTGATGACTTTGCCG	1269 IleIleSerIleMetPheserSerMetSerSerAlaArgMetLysCysAlaEuArgrer 128 1784 GCAAGGGCGTATTGGAGAAGGGATGACTTGCCG	1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1784 GCAAGGGCGTATTGGAGAAGGGATCGATGAGTTGCCG
1769 ACTATC	1769 ACTATCATACGACGG 178	1769 ACTATCATACGACAG 178 1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1784 GCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCATGAGTTTGCCG	1769 ACTATCATACGACAG 178 1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1784 GCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGGAGGATGAGTTGCCG	1769 ACTATCATACGACAG 178 1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1269 IleIleSerIleMetPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 128 1784 GCAAGGGGTATTGGAGAAGCAGGATCCTAAGAGGATGAGTTTGCCG
1709 CCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGTGCTGTAA 176 1252CysAlaProberTailself 1/11 1 1 1 1 1 1 1 1	1709 CCATGCGTATGAGCTCCATCAAGGGATATGAACCGCAGGACGTGCTGGTACA 176	1709 CCATGCGTATGAGCTCCATCAAGGGATATGAACCGCAGGACGTGCTGGTACA 176 1109 CCATGCGTATGAGCTACCGCTCCATCAAGGGATATGAACCGCAGGAGCGTGCTGGTACA 176 1109 ACTATC	1709 CCATGCGTATGGGTACAGGGATATGAACCGCAGGACGTGCTGGTACA 176	1709 CCATGCGTATGGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCTGGTACA 176
1236 Arghillinis: 1236 Arghillinis: 1236 Arghillinis: 1252				

XX SQ	Sequence 1592 AA;	oy 4	GCACCTTACGGTCGAGGGAGGTAGTCTTTGTACTTGTCGTCAAGCGATTTGAGGA
Aligno Pred. Score Percer Best I Query DB:	Alignment Scores: 3.74e-05 Length: 1592 Pred. No.: 154.50 Matches: 140 Score: 28.05% Conservative: 46 Best Local Similarity: 21.12% Mismatches: 172 Ouery Match: 22 Gaps: 365	oy oy	1276TACCGGCATGAGGAT
us-		qq	AlaThrAspIleHisSerGlyArgTyrCysTrpProArgThrAlaSerSerArgAlaAla
Qy	2080 AGAGAACGTAGCGGATGTCCACGCTGATTGTGCGCTGCAGATCGGGTTCGAACGTGGTGT 2021	Qy	SerGlyAlaSerAlaLysArgThrArgLeuArgArgArgSerCysProValArgSerPro
Qy Db	2020 CACCACTCATAGCTTCCCATGCAAAGCAAGGACGGATCAGACGGCCGTTCTTAT 1961	Qy Dp	1204 CGAAGA
Qy	CGAATACGGGGCTACCGGAGTTACCGCCGTGATGT	Qy Db	1177 TCTCACGGTTGGCCTTCCTTAT
6 G	TGTTCGATAGGA	Qy	1147
Qy	4 8 7	Qy Db	1117 CATAGACAGCACTCTTGCCGTTCTTACGGATCCAGTCTGCGAATGCTCTTT 1067
8 8	TATTCTCCTGTACGGCAAACTCATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCT	Oy Dp	1066 CCTCGGCAC
3 & 2	TGCCTG TGC	Qy	1027 GACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAGCATACTTGCTGG 968
oy da	1780 TCGTATGATAGTTGTACCAGGCACCGTCCTGCGGTTCATATCCCTTGATGGAGCCGTAGC 1721 888 TrbAlaSerGlyCysProarallaArg	Qy Db	967 CATATTTGATACGGGTAGCCTGATCTGCGCTCA:TGGCTTCCTTCCAGA 920
QY DP	TCATACGCATGGTGAAGTTGGCATCGCCAGAG	Qy	919 TGCCTTGCTTGATACCGCGAACTTCGATACGAGGATTGTTCTCGTTTTCGATACGATCTT 860 11 178
Qy	STCCGGGGTACATCTCACGCAAACGCAAAGAAAAGACGCTTCCTCAATGG	Qy Dp	859 CCACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCCGG
y g	CATAGGCATTGGCCATCGCCTGAATAGCGCGAGCAGCAGCTATTACGCTCTTGG	Qy Db	820
2	AAAGCTCTACTGCGGATCTTTCTCGATAGCCTTGGCAAACTTTTCCTTGTCCATGGACT	Qy	784
6 64 E	4 TGAGCATGGCATGGAACTTGTCGCTATAAGGAACCACACTCTTGTCGAATACGAAGT 1	Qy	760AGTAAACGGCCTTATAGGGTTTATTGTCCT 731 ::::: ::: ::
Oy Dp	CTGCATACTTCTTCGTCGCCTTTGAATTTCTTGTCGATTACATTCTTGAATATCGG ThrCvsThrAlaArdvsG1v	Qy Db	730TGCTGTATTCGGCCGCCGGTTGTCGGCACGGCATACACGCGGAATACGC 680 :::1
Qy Db	CGTACAATATCGAGCATGCGGGCA ::: :::	oy oy	679 TGAAGTCGCCGTGTGACGCGCCACATCCAGTTGT

 Db 1302 Arg	::: ArgMetArg 1304	Oy	1924
RESULT 6		qa	221 CysProArgAr
AABSSGI/ ID AABSSG17 XX	standard; Protein; 999 AA.	٥y	1909 AAGCGATATGG
		අ _ධ .	241 ArgArgSerPr
DT 04-APR-2001	001 (first entry)	ΟY	1849 CGAGGATATTC
TutD	protein #8.	Dp	261 ArgPheArgGl
Toluene	degradation; enzyme; waste degradation; TutD.	ΟY	1792 CGCCCTTGC
	Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens.	do yo	273 ArgargCysTr 1783CTGTCGTA
	Azoarcus tolulyticus.	qq	Д
	650-A2.	Qy	1726 CGTAGCTCATA
XX XX PF 24-MAY-2000:	000. 000. 2000m0-ffs14298	qq	306 ArgGlySer
		Qy	1687GAGCACGT
	HO	qa .	325 GlyArgArgVa
•	. Ma ou	QY	1630 CAATGGCATAG
	20,080,100	qa	341
	WF1; ZOUI U4100V/U3. N-PSDB; AAF23625, AAF23627.	Qy	1570 TCTTGGAAAGC
	Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its analogs	da .	342
AA PS Disclosu VV	Disclosure; Fig 5; 122pp; English.	qq	347 TrpThr
	The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23639 and AAB59831), tutl (AAF23630 and AAB59832), tutf (AAF23631 and AAB59833) and tutG (AAF23632 and AAB59834). The	QY	1453 CGAAGTCTGCP ::: 363 ArgAlaThrCy
CC toluene	degrading enzymes are homologues of pyruvate formate lyase. The degrading enzymes are useful for biological treatment of organic	o vo	1393 TATCGGGGAGC
	contained in liquid or solid waste source. The present sequence	G 90	
CC is a pro	otein sequence for toluene degrading enzyme, Tutb.	QY	
SQ Sequence	999 AA;	QQ	
Alignment Scores Pred. No.: Score:	: 3.37e-05 Length: 153.50 Matches:	Qy	1282 TGAGGATP
Percent Similarity: Best Local Similarity	28.278 : 21.508	ġ _O	ArgGlySe
Query Match: DB:	Indels: Gaps:	δŏ	1261
US-10-008-355-1	-1 (1-2139) x AAB59817 (1-999)	a :	430 GLYCYSALATE
Oy 2080 AGA	AGAGAACGTAGCGGATGTCCACGCTGATTGTGCGCTGCAGATCGGGTTCGAACTCGAATT 2021	ž ž	ASO MisalsSerGl
Db 173 Arg	ArgcysArgAspAlaCysGluArgArgCysArgAlaArgCys 184	ò	
2020		qo	
185	pArgSerArgAlaSer	Qy	1183 AAGTCATCTC
Oy 1966 TCT Db 205 Ard	1966 TCTTATCGAATACGGGCTACCGGAGTTACCGCCGTGATGT	QQ	::: 490 ArgProSerSe

9. Y	1924	
an	zzi cyskroargargargargcysseritegryalds	riovai 240
oy O	1909 AAGCGATATGGAGCTGACCGTTCTCGGCATAGCG ::: ::: 241 AraArgSerProValAsnSerSerLvsArgAlaH	ACCATAGTTTTGGTGCGGAAGAGGT 1850 SArqArqCysThrAlaArqArqGly 260
, ò	1849 CGAGGATATTCTCCTGTACGGCAAACTCATCGCT	TCCTGCTTCTCCAATA 17
Dp	261	272
Οy	Qy 1792 CGCCCTTGC	1784
qq	Db 273 ArgArgCysTrpArgTrpProArgProArgArgCysAr	gCysSerArgArgTrpGlyArg 292
Qy	Qy 1783CTGTCGTATGATAGTTGTACCAGGCACCGTCCTGCGGTTCAT.	GTTCATATCCCTTGATGGAGC 1727
Db	293	TrpArg 305
οy	Qy 1726 CGTAGCTCATACGCATGGTGAAGTTGGCATCGCTCGGCA	1688
qq	306	AlaSerProLysArgThrCys 324
ογ	1687GAGCACGTCCGGGGTACATCTCACGCAAAC	CGGCAAAGAAAAGACGCTTGCCCTTCT 1631
qq .	325 GlyArgArgVal	CysPr
Qy	1630 CAATGCCATAGGCATTGGCC	ATCGCATCGCCTGAATAGCGCGAGCAGCAGCTATTACGC 1571
qq	Db 341	341
Qy	Qy 1570 TCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTT	TGGCAAACTTTTCCTTGTCCA 1511
qq	Db 342	SerSerProlleArg 346
0y	1510 rgGaCTTGAGCATGGCATGGAACTTGTCGCT	GGAACCACACTCTTGTCGAATA 1454
qq	Db 347 TrpThrGlyArgCysArgTrpArg	: III gArgProLeuGlyCysSerPro 362
QY	1453 CGAAGTCTGCATA	TGTCGATTACATTCTTGAATA 1394
qq	363 ArgAlaThrCysThrAlaArg	371
ΟŸ	1393	ATATCGAGCATGGCGG 1340
QQ	Db 372ArgAspGlyCysSerAlaPhePheGlyAsnProLeuHisArgSerLeuArg	::: ::: HisArgSerLeuArgGlyPro 390
οy	Qy 1339GCAGCACCTTACGGTCGAGGGGGGGGGGTAGTCTTGTACTTGTCGTCAGG	TGTACTTGTCGTCAAGCGATT 1283
QQ	391	ThrThrArgArgCysAlaVal 409
ΟŸ	1282 TGAGGA1	1262
qΩ	410 ArgGlyser	gArgProHisLysProProLys 429
Qγ	1261CAGGATTTGTAGCCAATGCGTTG	∢ .
qq	430 GlyCysAlaThrAspIleHisSerGlyArg	pProArgThrAlaSerSerArg 449
Qγ	Qy 1219	OTCG
Dp	Db 450 AlaAlaSerGlyAlaSerAlaLysArgThrArgLeuA	gArgArgSerCysProvalArg 469
oγ	1210 TAC	GCGTCTCGCTCAAAT 1.184
Op	470 SerProArgA	rAlaCysGlySerSerSerArg 489
oy (QY 1183 AAGTCATCACGGTTGGCCTTGGCTCCTTAT-	1148
ć		TOTOCOTCOLI I DOCUCE I VALO

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0y 1 Db 1	147 510 123	
,	530 ProalaserThrProCysArgArgArgArgArgArgArgTyrG1ySerArgArg	
Qy 1 Db	072 CTCTTTCCTCGGCAC	
Qy 1 Db	033 GAGCGAGACCCCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAGCATACT 974 ::: 568 ProGlnArgGlyThr 572	
٥y	3 IGCTGGCATATTTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCT 92	
q ^0	573 Cys	
7 A	5	
ΟŸ	ACCCCAAGAAGTGAGGTAGCGATCCGTAC	
qq	587 SerArgProHisLeuProLeuArgArgCysLysGluArgCysProPheArgCysSer 606	
ΟŸ	TCGTCAGO	
οp	607 ProAlaSerProProThrAlaSerProThrTrpProAlaSerSerGlySerProCysGly 626	
ζο i	4	
QQ O	627 AlaSerGıyAlaSerThrProAlaSerAlaSerTrpAlaHisSerArgPheArgSerSer 646	
QY Dp	760TGTCCT 731 :::::::::::::::::::::::::::::::::::	
ōλ	730TGCTGTATTCGCCCGGCCGGTTGTCGCACCGGCATACACGCGGA 686	
qq	:::	
Qy	GTGACGCGGCCACATC	
QQ	687 CysargGluThrargLeuCysGluSerArgHisAlaSerCysTrpArgGlyAspProVal 706	
Qy Db	643 CCGTATCGCCTCCGA 629 ::: 707 ProAsnArgMetArg 711	
366	T 7 702 ABG66702 standard; Protein; 1296 AA.	
	ABG66/02; 30-aug-2002 (first outro)	
	polypeptide #37.	
	<pre>luman; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; eripheral nervous system disease; amyotrophic lateral sclerosis; tendon</pre>	; uc
K K K K K K K K K K K K K K K K K K K	myerous cert usorder; Iymphoid cell disorder; platetet disorder; bone cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infectio allergic condition; thrombolysis; thrombosis; coaquiation disorder; fungal infection	e; s; on;
	Homo sapiens.	

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disease, ischemmiatory conductors such as alternites, without and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral brain tissue, and are useful for the treatment of central and peripheral contains system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, and amyotrophic lateral cartivity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue regeneration of bone, cartilage, tendon, ligament and/or nerve tissue corresponded to the sequences of the invention are also useful for gut disease. The sequences of the invention are also useful for gut correction or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autorimmune disorders e.g. multiple sclerosis and myssthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG6666-ABG66758 represent human coagulation disorders. Sequences ABG6666-ABG66758 represent human coagulation and coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 CAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCA 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| ::: ||||::: ||||::: 572 ProSerThrAspMetIleThrSerHisThrAsnLeuThrArg---SerSerProLeu 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 TCCGCGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAAGGACAATAAACCCT 745
                                                                                                                                                                                                                              Wang D;
                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing
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Gaps:
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Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 604-607; 672pp; English.
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153.50
33.76%
21.46%
                                                                                                30-NOV-2001; 2001WO-US47004.
                                                                                                                                          30-NOV-2000; 2000US-0028952
                                                                                                                                                                                                                              Tang YT, Goodrich RW,
Yamazaki V, Ujwal ML,
                                                                                                                                                                                                                                                                                         WPI; 2002-508509/54.
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                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                               N-PSDB; ABK94926
                 WO200244340-A2.
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ž	746		784
q	611	ThrserProThrSerThrValLysGlySerThrThrSerIleArgTyrSerThrSerMet	630
٨	785	ACAAGGCTGTGACCATATGCCATGACCATCGGTT	817
ą	631	 ThrGlyThrLeuSerMetGluThrSerLeuProProThrSerSerSerLeuProThrThr	650
<u>~</u>	818		850
ą	651	GluThrAlaThrMetThrProThrThrThrLeuIleThrThrThrProAsnThrThrSer	670
χ	851		883
ą	671		069
λ	884	ATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAA	943
ð	691		710
Σ	944	ATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGA	1003
ď	711		728
۸.	1004	ATTCGATCGGTATGAACCGCGGTCTCGGTCTTGACGTGATAGGTCGTAAGCGTG	1060
ð	729		746
٠.	1061	CGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGA	1096
ā	747	ThrAspIleSerThrLeuProThrArgThrHisIleIleSerSerSerProSerIleGln	766
ξ, q	1097 767	ACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAGGAAG :::	1156 786
~	1157		1216
ą	787	 ThrLeuArg11eThrG1uAsnThrProI1eSerSerPheSerThrSerI1eVal	804
<u>></u> 4	1217	TGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCGGGTA	1276
Q	802		816
ې. ق	1277	TCCTCAAATCGCTTGACGACAAGTACAAAG :::::	1306 836
2	1307		3.56
. a	837	ThraspSerSerThrSerThrLeuHisThrLeuThrProSerThrAlaLeuSerThrIle	856
<u>></u> .	1367	GTATCC	1378
Q	857	ValSerThrSerGlnValProIleProSerThrHisSerSerThrLeuGlnThrThrPro	876
<u>~</u>	1379		1411
q	877	SerThrProSerLeuGlnThrSerLeuThrSerThrSerGluPheThrThrGluSerPhe	968
<u>></u> 4	1412	ACAAGAATTCAAAGGGGACACGAAGAAGTATGCAGACTTCGTATTCGACAGAGTGTGG	1471
2	60	THE ALGORITHMS STATES AND THE SELFIES	0 T A
<u>م</u> م	1472	TTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAA	1522 935
<u>></u>	1523		1554
ą	935	::: alpheSerThrThrIleHisSerValProSerSerProTvrIlePheSerThrGluAsnV	955

οy	1555 -		1588
QO	955 a	lGlySerAlaSerIleThrGlyPhe	975
ογ	1589 G	GGGCTATTCAGGCCGATGCGATGGCCAATGCCTATGAGAAGGGCAAGCGTCTTT	1648
QQ	975 er	rSerThrSerSerSerLeuThrThrAlaLeuThrGluIleThrPro-PheSerTyrIle	994
Qy Db	1649 TC + 995 Se	TCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATG	1699
δy	00	TGAGCTACGGCTCCA	73
qq	1 1015 Pi	 ProThrAspProCysValGluMetAspProSerThrGluAlaThrSerProProThrThr	1034
Qy	1732 -		1732
QQ	1035 Pi	roLeuThrValPheProPheThrThrGluMetValThrCysProThrSerIleSerIle	1054
Qy	1732		1732
QQ	1055 Gl	${\tt lnThrThrLeuThrThrMetAspThrSerSerMetMetProGluSerGluSerSer}$	1074
δλ	733	TCAAGGGATATGAACCGCAGGACGGTGCTGGTACAACTATCATA	
QO	1075 I.	leSerProAsnAlaSerSerThrGlyThrGlyThrValProThrAsnThrValPhe	1094
92	1778 CC	CGACAGGCCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGG	1837
2 6	8 6	GAATATICTICGACCTCTTTCCCCACCAAAACTATGGTCGCTATGCCGGGAAGGGTC	1894
g 2	101	ThrSerGluThrTrpLeuSerAsnSerSerVallleProLeuProGlyVal	11
Qy	1895 AC	GCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGGGGGG	1954
QQ	1120 Se		1133
Qy	1955 TA	TATTCGATAAGAACGGCCGTCTGATCGGTCTTTCGATGGCAACTGGGAAGCTATGA	2014
Dp	1134 T	hrlleLeuargThrSerSerLysSerThrHisProSerProProThrThrArg	1151
Qy	2015 G	GTGGTGACATCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACG	2074
QQ	1152	ThrSerGluThrProValAlaThrThrGlnThrProThrThr	1165
Qy	2075 T	TTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCCAAGAGC 2125	
qq	1166 Le	euThrSerArgArgThrThrArgIleThrSerGlnMetThrThrGlnSer 1182	
RES ABG ID	RESULT 8 ABG66756 ID ABG6675	56 standard; Protein; 1296 AA.	
X S X	1995	26;	
V L X	30-AUG-3	-2002 (first entry)	
S E	Human novel	novel polypeptide #91.	
X X X	Human;	inflammatory condition; shock; sepsis; immune response;	
K K K	periphe	would meating, central mervous system disease, macmacopure eral nervous system disease; amyotrophic lateral scherosis; d cell disorder; lymphoid cell disorder; platelet disorder;	tendon; bone;
XXX	cartile bone de	age: ligament; nerve tissue; ulcer; osteoporosis; osteoarthr agenerative disorder; periodontal disease; reperfusion infur throsie: liver fibrosis: autoimmune disorder, barterial info	itis; Y;
K K	allerg: fungal	allergic condition; thrombolysis; thrombosis; coagulation disorder; fungal infection.	
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                                                                                                              Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -
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                                                                          Asundi V,
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                                                                                                                                       Claim 10; Page 669-671; 672pp; English.
                                                                         Liu C, Zhou
Drmanac RT;
                                    30-NOV-2001; 2001WO-US47004
                                                 2000US-0028952
                                                                         odrich RW,
Ujwal ML,
                                                                                           WPI; 2002-508509/54.
                                                                         Goodrich
                                                             (HYSE-) HYSEQ INC
                                                                                                  N-PSDB; ABK94980
           WO200244340-A2.
Homo sapiens.
                                                30-NOV-2000;
                                                                              Yamazaki V,
                        06-JUN-2002
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polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of mysloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of cisease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coaqulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention. invention relates to human novel polynucleotides and associated

1296 AA; Sequence

685 CAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCA 565 :::||| ||||| |||::::: 539 LysThrThrLeuThrSerLeuLysThrThrAlaSerArgProThrAlaAsnSerThrLeu |||| | ProSerThrAspMetIleThrSerHisThrThrAsnLeuThrArg---SerSerProLeu 686 TCCGCGTGTATGCCGGTGCCGACAACCGGCCGGAGTACAGCAAGGACAATAAAACCCT TCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTA AGTICGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTAT 1296 150 86 251 212 Conservative: Mismatches: Matches: ength: Indels: US-10-008-355-1 (1-2139) x ABG66756 (1-1296) Gaps: SerSerLeuThrSerSer-----4.05e-05 153.50 33.76% 21.46% 4.02% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: 999 559 626 Dp Db qq δy ò ò

1411 1217 TGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTA 1276 1472 TTC------CTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAA 1522 .004 ATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTG--- 1060 ACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAGGAAG 1156 1157 GAGCCAAGGCCAACCGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGG 1216 ACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTAFTCGACAAGAGTGTGG 1471 670 691 AlaileThrSerHisPheThrThrSerGluThrAlaValThrProThrProValThrPro 710 ----SerValGlyThrSerThrSerLeuThrThrThrAspPheProSerIlePro 746 747 ThrAspileSerThrLeuProThrArgThrHisIleIleSerSerSerProSerIleGln 766 LeuThrSerAlaThrGlyThrGlnThrSerProAlaProThrThrValThrPheGlySer 836 ValSerThrSerGlnValProlleProSerThrHisSerSerThrLeuGlnThrThrPro 876 -------TTTACTTCGCTGCCGTATCCATGCAAGGCT 784 ||| :::||| ||| 591 LeuAlaThrLeuProThrThrThrTyrPro 611 ThrSerProThrSerThrValLysGlySerThrThrSerIleArgTyrSerThrSerMet ----TGACCATCGGTT |||::: | ThrGlyThrLeuSerMetGluThrSerLeuProProThrSerSerSerLeuProThrThr -- GGGGTGTGGAAGATCGTATCGAAAACGAGAACA 671 HisSerThrProSerPheThrSerSerThrIleTyrSerThrValSerThrSerThrThr 944 ATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGA 711 SerSerLeuSer---ThrAspIleProThrThrSerLeuArgThrLeuThrProSer--------CCGAGGAAAGAGCAT-----TCGCAGACTGGATCCGTAAGA SerThrGluThrSerSerLeuValGlyThrThrSerProThrMetSerThrValArgMet --GlnThrProProVal ACTACCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC ||| ::: ||| |ThrAspSerSerThrSerThrLeuHisThrLeuThrProSerThrAlaLeuSerThrIle ----ACAAGCTCCCCGATATATTCAAGAATGTAATCG ThrargGlySerThrSerThr --- AsnAlaIleLeuThrSerPheSerThrIleIleTrp 787 ThrLeuArglleThrGluAsnThrProlleSerSerPheSerThrSerIleVal----818 TCCCGGGCAGTACGGATCGCTACCTCACTTCTT--------------ACGACTATGCCA----1523 AGTTTGCCAAGGCTATCGAGAAAGATCCGGCA------ValileProGluThrProThr---1277 TCCTCAAATCGCTTGACGACAAGTACA------CICCCG--746 ATAAGCCCG--785 ACAAGGCTG--GTATCC----1097 817 837 1367 857 877 1412 897 916 1307 729 767 805 851 1061 1379 Dp q g g QY Db Q οy g ΩŽ Op δλ q Ω Db δ qq δλ 9 à g ò a ò q Ω ò δy q οŽ δ οy δy ρy

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935 alPheSerThrIleHisSerValProSerSerProTyrIlePheSerThrGluAsnV 955
                                                                                                                                                                                                                                                                                                                                                                                      --- GTAGAGCTTTCCAAGAGCGTAATAGCTGCTC
                                                                                                                    975 erSerThrSerSerSerLeuThrThrAlaLeuThrGluIleThrPro-PheSerTyrIle
                                                                                                                                                 TCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTG------CTCTGCCGAGCGATG
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| 134 ThrIleLeuArgThrSerSerLysSerThrHisProSerProProThrThrArg
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05-DEC-1996.

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The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzhenier's or Huntingdon's disease) or acute transactic injuries. Transgenic cells and organisms transfected with UNC-53 cDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the chances can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the change of the UNC-53 protein can be used to identify proteins which are active in the signal transduction pathway that can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TTTACCAACCACAGTGC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 GGATACGGTGCTATC---CAGAGCCAAAGCACGGTGGATCACGACTATCTGCGGGTGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 TTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAG 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysArgLeuAlaLysIleThrSerAsnLeuAspGly---LeuGluThrCysLeuAspTyr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuLysAsnLeuGlyLeuAsp-----CysSerLysLeuThrLysThrAspIleAsp 96
                                                                                                                                                                                                                                                                                                                                        8A and 7A of Caenorhabditis elegans are new
                                                                                                                                                                                                                                                Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful promote neuronal regeneration, revascularisation or wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerLysGlySerLeuSerLysSerIleArgAspIleSerAsnAspPheArgAspTyrArg
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84
211
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Matches:
Conservative:
Mismatches:
                                                                                                                                                            Vandekerckhove J;
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148.50
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20.91%
3.89%
                96WO-EP02311
                                                  95GB-0010944
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                                                                                                    (STRI/) STRINGHAM E.
(VAND/) VANDEKERCKHOVE J.
                                                                                                                                                                                                                                                                                                                                         protein variants
                                                                                                                                                            Stringham
                                                                                                                                                                                              WPI; 1997-034369/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                N-PSDB; AAT71314
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              31-MAY-1996;
                                                  31-MAY-1995;
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                                                                                       (BOGA/)
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                                                                                                                                                                                                                                                                                                                                        UNC-53
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1572 CGTAATAGCTGCTCGC 1590

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οy	628	ITCGGAGGCGATACGGACACTGGATGTGGCCGCGTCACACGGCGACTTCAGCGTATTC 687	a
qq	136	oProAlaValSerLys141	Δ ,
op Op	688	CGCGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGACAATAAACCCTAT 747 :::	x K H X
Qy Dp	748	AAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATG 807	«×¤×
Qy Db	808	ACCATCGGTTTCCCGGCCAGTACGGTCGCTCACTCTTGGGGTGTGGAAGATCGT 867 ::: ::: ::: ::	
Qy	868	ATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGC	××o×
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Qy Db	1111 310	GTCTATGGCGATGTATTGTCTCTCGAAAAGGCTTATAAGGAAGG	₩×00
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QY	1231 343		0000
QY Db	1291 354	GACGACAAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTGCCCGCCATGCTC 1350 :::::: sProProThrSerLySLeuCysThrProLy 373	0000
Qy	1351 373	GATATTGTACGCGGCGTATCCCTGCCGACAGCTCCCCGATATATTCAAGATGTAATC 1410 :::	xson at
Qy	1411	GACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAA 1463 	r o c u
Qy Db	1464	GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCTCAAGTCCATGGACAAGGA 1520	00 0
Qy Db	1521		0 0

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UNC-53 protein variants 8A and 7A of Caenorhabditis elegans are new. The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute traumatic injuries. Transgenic cells and organisms transfected with UNC-53 sobA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the CDNA sequences can be used to identify homologues of the C. elegans are active in the signal transduction pathway that can be used as mentioned above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...-TITACCAACCACTGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful to promote neuronal regeneration, revascularisation or wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNC-53; neuronal regeneration; revascularisation; wound healing; neurodegenerative disease; Alzheimer's disease; Huntingdon's; peripheral neuropathies; metastasis inhibition; cancer.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 111-116; 278pp; English.
                                                                                                                                                           C. elegans UNC-53 protein variant 7A.
                                                                AAW20057 standard; Protein; 1583 AA.
 452
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                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                STRINGHAM E. VANDEKERCKHOVE J.
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446 rIleValThrAlaIleArg
                                                                                                                                                                                                                                                         Caenorhabditis elegans
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(VAND/)
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943 GATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAG 1002
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271 GGATACGGTGCTATC---CAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGGT 327
                                                                                                                                                 188 CGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAG 447
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                                                                       328 TTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTG
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LysArgLeuAlaLysIleThrSerAsnLeuAspGly---LeuGluThrCysLeuAspTyr
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                   GACGACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCGCCATGCTC 1350
                                                                                                       GATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATC 1410
                                                                                                                                                                            1411 GACAAGAAATTCAAAGGCGACACGAAGAAG-----TATGCAGACTTCGTATTCGACAA 1463
                                                                                                                                                                                                                                                1464 GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAG---TCCATGGACAAGGA 1520
                                                                                                                                                                                                                                                                                                                      1521 AAAGTTTGCCAAGGCTATCGAGAAGATCCGGCA------GTAGAGCTTTCCAAGAG 1571
                                                                                                                                                                                                                                                                                                                                           -- ProvalLysSerGlyLeuLy
                                                                                                                                        ----LysThrAspAlaProllelleSerGlnGlnAspSe
                                                                                                                                                                                                  354 sProProThrSerLysLeuGlySerAlaThrSerMetSerLysLeuCysThrPro---Ly
                                                                                                                                                                                                                                                                                   406 nSerThrSerProThrSerSerSerThrGluGlySerLeuSerMetHisSerThrSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 36734; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #6366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG06375 standard; Protein; 2570 AA.
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2000US-0649167
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                                                                                                                                            373 sValSerTyrArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                            446 rIlevalThralaIleArg
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 343 rLysIleAlaAla-
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequence of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. 1890 SerLeuThrAsnTyrAlaThrSerLeuAsnThrProValSerTyrProProTrpThrPro 1909 1930 GluIleSerThrProLysThrSerPro---ProProThrSerGlnMetValGluPhe--- 1947 ---ProValLeuGlyThrArgMetThrSerSerAsnThrGlnProLeuLeuMetThrSer 1966 1967 TrpAsnileProThrAlaGluGlySerGlnPheProIleSerThrThrIleAsnValPro 1986 956 GTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTA 1015 1016 TGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCAT 1075 TCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTC 1135 TCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGA 1195 491 CCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACA 550 1987 ThrserAsnGluMetGluThrGluThrLeuHisLeuValProGlyProLeu---SerThr 611 CCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGG ---GCAAGGACAATAAACCCTATAAGCCCGTTTAACTTCGCTGCCGTATCCATGCAAGGCT ---LeuVal 1910 SerSerAlaThrLeuProSerLeuThrSerPheValTyrSerProHisSerThrGluAla 785 ACAAGGCTGACG-----ACTATGCCATGACCATCGGTTTCCCGGCAGTACGGATCGCT ACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAG 899 TTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGGG----CAGATCAGGCTACCC 551 ACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTC 2570 133 81 195 191 29 Length: Matches: Conservative: 1877 SerAsnThrArgLysMetThrSerLeuLeuGluLysThr----Mismatches: Indels: 1864 ProThrLysAsnValLysThrThrThrAsnCysPheSer (1-2570)US-10-008-355-1 (1-2139) x ABG06375 0.000223 148.00 35.67% 22.17% 3.87% SerGlnThrGly-----2570 AA; 2006 PheThrAla ----Best Local Similarity: Percent Similarity: Alignment Scores: Sequence Query Match: DB: 839 2009 2015 671 728 1948 1076 1136 1889 g qq Ω g Qy a ò 000000000000000x8 ò pp g qq qq δ Q ò QQ ο̈́ 9 δ ò ŏ δy òγ

2070 ThrThrLeuProSerIleLeu-2026 MetSerGlyIle---2115 1796 2261 2037 1367 1487 2096 1661 1721 1307 1427 2079 2222 g qq g qq Ор ŏ g οÿ qq δ Op ōλ Db δλ qq δλ q ò q Óγ g δy d à Db ò q δ QQ ò g QΫ́ ÓΥ SerLysAspValMetAlaMetSerSerIlePro-----

2307 AGTICCATGCCATGCTCAAGT --- CCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543 hrSerSerThrValGluValSerLysSerThrPheLeuThrSerAspMetIleSerAlaH 2135 1196 CGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAA 1255 GTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAATTCAAAG 1426 GCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGCTTCCTTATAGCGACA 1486 1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCCGCGCTATTCAGGCCG ------ACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGC 2241 AsnArgIleProThrAlaSerSerProSerThrLeuIleIleProLysProThrLeuAsp TCGATAAGAACGCCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTG ProLeu-----IleSerThrGlyValThrTyrPro --CCTGGTACAACTATCATACGACAGGCCAAGGCCGTAT SerLeu---LeuAsnIleMetThrThrThrSer----ThrValProGlyAlaSerPhe 2018 GTGACATCGAGT---ŢCGAACCCGATCTGCAGC---GCACAATCAGCGTGGACATCCGCT TGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCG-----TCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTAT ------LeuProAsnHisGlyLeuSer 2155 ThrileProThrProThrLeuGlyGlyIleThrThrGlyPheProThrSerLeuProMet ATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGT------ACAAAG GluAsnProSerLeuSerThrSerLeuArgAlaIleThrSerThrLeuAlaAspValLys ACTACCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC isProPheThrAsnLeu-ThrThrLeuProSerAlaThrMetSerThrIleLeuThrArg TGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAAGTTCACCATGCGTATGA ---GlualaSerSerArgThrThrIleThrAlaAsnProArgThrValSerHisProSer 2072 ACGITCITCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGG 2125 GCTACGGCTCCATCAAGG-----GATATGAACCGCAGGACGGTG----SerPheSerArgLysThrMetSerProSerThrThrAsp-----HisThrPheGluLysMetThrThrSerValThrPro-----ATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTC-

RESULT 12 ABP27518

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719 SerLeuHisGluHisIleAlaAsnLeuAlaGlySerProAlaIleLysLysGlyIleLeu 738
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509 AsnGluGluAsnGluAspIleLeuGluAspIleValLeuThrLeuThrLeuPheGlu--- 627
                                            163 TACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACC
                                                                                                                               223 GGTATCACAGTGTCCGATCAGGGCCTG----ATCTTTACCAACCACCACTGCGGATAC
                                                                                                                                                                            -----LeuPheAspAspLysValMetLysGlnLeuLysArgArgArgTyrThrGlyTrp
                                                                                                                                                                                                                                                                    660 GlyArgLeuSerArgLySLeuIleAsnGlyIleArgAspLysGlnSerGlyLysThrIle
                                                                                                                                                                                                                                                                                                              304 GATCACGACTATCTGCGC---GATGGTTTCGTTTCTCGC--------
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                                                                                   -----AspArgGluMetileGluGluArgLeuLysThrTyrAlaHis-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have entihacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a Streptococcus ample. (I) is used to detect of a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to detect streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity characterinty.
                                                                                                                                                                                                                     Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antlinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein
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Matches:
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                                                                                                                                                                            Streptococcus polypeptide SEQ ID NO 4212.
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                                         ABP27518 standard; Protein; 1368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3578; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-008-355-1 (1-2139) x ABP27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2000; 2000GB-0026333
                                                                                                                               (first entry)
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31.74%
19.49%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN68149
                                                                                                                                                                                                                                                                                                                                                     WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                               02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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Pettelin H;
                                                                                   ABP27518;
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---GTGAAGTATCTGCGC 390

964 TATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGC 1023

------AspAsnLeuThrLysAlaGluArgGly-----

897 Phe-----

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AATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTC 162

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· 6	907		
ογ	1075	TTCGCAGACTGGATC	
a à	1104	/ ileinriyshisvalaladınilebewaspSerArgMetAsnThrLysTyrAspGluAsn 946	
e e	947	AspLysLeulleArgGluValLysVallleThrLeuLysSerLysLeuValSerAspPhe	
ογ	1104		
Dp	196	7 ArgLysAspPheGlnPheTyrLysValArgGluIleAsnAsnTyrHisHisAlaHisAsp 986	
O.Y Db	1105		
οy	1144	GCTTATAAGGAAGGA	· · ·
qq	1007	GluPheValTyrGlyAspTyrLysValTyrAspValArgLysMetIle	• .
Oy Db	1171	CGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCTACC	
Qy Db	1231	CAGTITGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCG 1287 	
οy	1288		
qq	1067	GlyGluThrGlyGlu	
Qγ	1330		
QQ	1085	5 LysValLeuSerMetProGlnValAsnileValLysLysThrGluValGlnThrGlyGly 1104	
op ox	1369	9	
Οy	1402	AATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGAC	
QQ	1120		
٥y	1462	2 AAGAGTGGTTCCTTATAGCGACAAGTTCCATGCC	
qq	1136	SerProThrValAla	
Qy Db	1498	8 ATGCTCAAGTCC	<u>.</u>
Οy	1531		
QQ	1176	LysAsnProlleAspPheLeuGluAlaLysGlyT	
Οy	1555		
QQ	1196	6 IleLysLeuProLysTyr 1201	
o y	1615	AATGCCAATGCCATTGAGAAGGGCAAGGTCTTTTCTTTGCCGGTTTGCGTGAGATGTAC	
20	1707	serbeurneslubeusluasnslyargbysargmetbeualaseralaslyslubeusln	
S S	1675	CCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGC	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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| 11|||| 1337 | 1318 LeuGlyalaProAlaAlaPheLysTyrPheAspThrIleAspArgLysArgTyrThr 1337
--GCCTGGTACAAC 1770
                                                                                                                                   1771 TATCATACGACAGGCCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCC 1830
                                                                                                                                                                       1278 LysargValIleLeuAlaAspAlaAsnLeuAspLysValLeuSerAlaTyrAsnLysHis 1297
                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 36210; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1885 GAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGC 1935
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1723 TACGGCTCCATCAAGGGATATGAACCGCAGGACGGT--
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Alignme	Scores:	qq	640
Pred. No.: Score:	0.000739 Length: 141.50 Matches:	ΟŸ	1003 AAT
Percent Best Lo	Conservative:	qq	656 rGl
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3	GTGAGGAGCTTCGGGATTCCGGGGTCTTTCCGTGAAGTATCTGCG	δy	1342 GCC
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	GOLINILISOOCI LIIL III III ALII VALIIII LIII LIII LI	δy	1582 GĊT
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Oy 6 Db 5	622 GGTAAGTTCGGAGGCGATACGGATACTGGATGTGGCCGGCGTCACACGGGCGAC 675 	qq	838 eTh
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	GAATACAGGAAGAATAAAACCCTATAAAAGCCCTTTTACTTAC	Οy	1762 TGG
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	TO A TRACE A B G G CT A C A C CT C A C CT C A C CT C A C CT C	Qy	1822 GAG
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serThrThrTh 656	AGCGTGC	hrGluLysPr 676	CTATGGCGAT 1122	FTGAGATGACT 1182	serSer 703	AGGTGGTTCGTTTTGCA 1230	hrProThrTh 721	12	serSerThrGl 741	AGGTGCTGCCC 1341	hrThrThrLe 761	-	leThrSer 780	CGTATTCGAC 1461	NaProAsnTh 798	15	hrGlnSerTh 815	CGTAATAGCT 1581	828	GAAGGCAAG 1641	luLysProIl 838	GAGCGATGCC 1701	alAlaSerSe 858	GGACGGTGCC 1761	sSerThrGluAs 877	18	hrSerAla	1	sThrThrGlnAs 908	CGAAC 19	lnGluAlaTh 927	CTGATC 19	hrGluSerSe 947	CGAACCCGAT 2040
oThrSerThrThrSerLysLeuS	rcttgacgtgataggtcgta	nrAlaAlaThrThrSerTh	CGTAAGAACGGCAAGAGTGCTGT : rValSerThrThr	AGGAGCCAAGGCCAACC	erSerProLysProThrSe	AGGTGGT	ysProSerThrArgThrThr	rgctcatgccggtatcc; 	nrThrThrProLeuArg:	ACTACCTCCCCTCGCTCGACGTAAGGTGCTGCCC	отһгтһгтһгтһгРгоGlпРготһгтһгтһгтһгтһгСе	GCCGCCGTTCCCTGCCGACACCTCCCCGATATATTCA	ırThrThrGluLysPro	SAAGAAGTATGCAGACT	LoLysThrThrSerThrAl	rgccatgctcaagtcca?	lnLysGluThrThrProThrGlnSerTh	AGTAGAGCTTTCCAAGA(ırAsnAsn	CAATGCCTATGCCATTG	ProGluProThrSerThrGluLy	SCCCGGACGTGCTCTGCC		CAAGGGATATGAACCGC	sProThrThrGluLy	ATTGGAGAAGCAGGATCC	AsnSerValLysT	CCGCACCA	serGluProThrLy	rcagctccatatcgctttcctat	euLysThrSerThrGlnGl	GTATTCGAT :::	leThrThrLysLysAlaThrGl	SAGTGGTGACATCGAGT7 :::::
sThrThrAspileProThrS	CGGTATGAACCGCGGTCTCGCTCGTCT	sThrThrThrThrHisLysPheThrAl	GAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGCA :::	CTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGAT	::: ::: -ThrLysLysSerThrGluS6	AGCGAGACGCTCTTCGGTGGTACCG-	hrGlyLysProThrThrProLy	CACTITGCCAACGCAITGGCIACAAATCCTGATGCICAIGCCGGTATCCTCAAATCGCTT	ThrThrGlnIleThrT	AAGACTACCTC	GlnProProThrThrTh	GCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGGCACAAGCTCCCCGATATATTCAAG	LysThrSerThrThrThrTh	AATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAAGTCTTCGTATTCGAC	erProLysProThrThrThrGlnLy	IJ	LysValAlaIleThrThrGln	AAAGTITGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCT	ePheThrArgLysThrThrThrAsnAsn	ATTCAGGCCGATGCGATGCCTATGCCATTGAGAAGGCCAAG	[d	CGTCTTTTCTTTGCCGGTTTGCGTGAGGTGTACCCCGGACGACGAT	ProLysProSerThrThrThrP	AACTICACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGTGC	ThrIleSerSerProLys	ACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGAF		ATCCT	rSerThrGlnArgAlaThrSerThrT	GCCGAGAACGG	ProLysProThrThrL	AACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGAT	LysValSerThrValThrI]	GGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGAT :::::::: :::
	AATTCGATCGGTA	rGlnLysThrThr	GAGGAAAGAGCAT ::: oLysThrThrThr	GTATTGTCTTCTC		TATTTGAGCGAGA	ThrGly	CAGTTTGCCAACG	rThrLysValThr	GACGACAAGTACAAAG	uThrThrSerThrGlnProPr	GCCATGCTCGATA	uThrValThrProLysThr	AATGTAATCGACA	SerPro	GTGT	rThr	AAGTTTGCCAAGG	rSerThrThrIle	в стветсвеветл	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CÉTCTTTTTTT	eThrSerThrThrProLy	AACTTCACCATGC	rThrGluLysThrThr	TGGTACAACTATC	nProThrThr	TGCCGT	uThrSerSerThr	AAAACTATG	nIleThrThrThrThr	AACGACATCACGG	rThrSerThrGln	GGTCTTGCTTTCG :::
640	1003	959	1063	1123	069	1183	704	m	721	1291	741	1342	761	1402	781	1462	798	1522	815	1582	829	1642	838	1702	828	1762	//8	1822	888	1865	806	2	927	1981
qq	δy	qq	Qy	οy	qq	Qy	qq	ΟÝ	qq	δλ	qq	δò	QQ	δy	Db	Qy	QQ	δý	qq	Οy	QQ	Qy	QQ	Qy	qq	δo 7	QΩ	δý	οp	Οy	qq	Qy	q	٥y

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           In AAX87940. This DNA fragment comprises a Stul-Stul fragment of M. tuberculosis genomic DNA and contains an insertion sequence-like element and repetitive sequences. The DNA fragment is useful as a probe, especially for detecting or identifying M. tuberculosis in clinical isolates and body fluids e.g. sputum, cerebrospinal fluid, pleural fluid, urine, gastric lavage, bronchial lavage, pericardial or Lymph node aspirate (all claimed). It is also useful for restriction fragment length polymorphism analysis of M. tuberculosis of tuberculosis and M. tuberculosis infection.
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ò	1669TCTCACGCAAACCGGCAAAGAAAAGACGCTTGCCCTTCTCAATGGCATAGGCAT 1616	Qy 679 TGAAGTCGCCCGTGTGACGCC	TGACGC
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ολ	ATGGACTTGAGCATGGCA	499	
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ô	TCTGCATACTTCGTGTCGCCTTTGAATTTCTTGTCGATTACATTGTTGA	Qy 454 GCTCCATCTCGTCAGTGATAC	GTGATA
. a		Db 358 Asn	
ò	ATATATCGGGGAGCTTGTCGGCAGGGATACGCCGGCGTACAATATCGAGCATGGCGGCA	Qy 394 TCTTGCGCAGATACTTCACGC	TTCACC
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3 6		Db 378 GlyArgSerTyrArgTrp	gTrp-
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÷ ÷		Db 386 ThrLysSerGlyArgSerGlr	'gSerG
a a		Qy 226 TACCGGTACATCCGCCACCG	CCACC
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οy	1156 CTTCCTTATAAGCCTTTTCGAGAGAGACAATACATCGCCCATAGACAGCACTCTTGCCGT 1097		
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ò t	ATCCAGTCTGCGAATGCTCTTTCCTCGGCACGCTTACGACCTATCACGT	1705 standard;	Proteir
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οy	859 CCACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCAT 800	XX PD 27-SEP-2001.	
qq	275 275	AX PF 23-MAR-2001; 2001WO-US092	:60Sn-(
Οy	799 AGTCGTCAGCCTTGTAGCCTTGCATGGATACGGCAGCGAAGTAAACGGGCTTATAGGGTT 740	AA 23-MAR-2000; 2000US-191637	3-1916
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidas, therapeutics and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 GlnLeuGluGluValLeuValValValLeuGlnTrpAspLeuValSerValLeuIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 AlaAlaArgGlnHisHisSerValGlyHisAlaAlaMetGlyLeuArgLeuIleGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 SerHisAlaAlaAspHisArgIleValAla------SerGluLeuGlyAsn
                                                                                                                                           ID NO 11907; 21pp + Sequence Listing; English
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151
109
264
222
36
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Matches:
Conservative:
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34.85%
20.24%
3.49%
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               WPI; 2001-656860/75.
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Best Local Similarity:
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                                  N-PSDB; ABL05808
                                                                                                                                             Disclosure; SEQ
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DB:
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:::||| ||| 164 LeuGlySerAsnGluAspLeuHisAsn-----

Qy Db	1545 TTTCTCGATAGCCTTGGCAAACTTT	TCCTTGTCCATGGACTTGAGCATGGCATGGAACTT 1486
Qy	1485 GTCGCTATAAGGAACCACACACTTG ::: 187 GluGlvLeuvalv	TCGAATACGAAGTCTGCATACTTCTTCGTGTCGCC 1426 ::: alGluthrLeuLeuAlaGlvLeuAspHisTleAla 202
Οy	1425 TTTGAATTTCTTGTCGATTACATTC	
qq	203 GlySerLeuValValGlyV	lyvalGlnArgIleGlyGlySerLeuAsn 222
Qy	1377 GGCAG 223 GlyGlyLeuHisIleAspGlyIleAl	AGGGATACGCCGGCGTACAATATCGAGCATGGCGGG 1339
Qy	1338 CAGCACCT	1 12
qa ,	243 GlnThrPheGlyHisValAspG	yvalileLeuLeu 262
Qy Dp	1296 GTCGTCAAGCGATTT	GAGGATACCGGCATGAGCATC 1261 ::: roValValAlaAspAsnGlyLeuValTyr 282
Qy	1260 AGGATTTGTAGCCAATGCGTTGGCAAACTGT	AAAACG.
qq	283 LeuvalGluAspAr	HisAr
Qy	1200 GAGCGTCTCGCTCA	<pre>rGGCTCCTTCCTTATAAGCCTT 11 :::::::: </pre>
qq	296 HisGluLysAlaArgGluAlaLeuVal1	eMetVa
ΟŊ	1140 TTCGAGAGAGACAATACATCGCCATAC	GGATCCAGTC 10
g	313 ValHisAsnGluAlaValGlnLeuValI	GluLeuLeuValHisAlaVa
δō	1080 TGCGAATGCTCTTTCCTCGGCACGCTTACG	TATCACGTCAAGACGAGACGCG 10
gg	333	ValAl
λō da	QY 1020 GTTCATACCGATCGAATTCTTCCAATAGTTAGG	GCACTCTGAGCATACTTGCTGGCATATTT 961 ::::: :::::::::::::::::::::::::::
2	960 GATACGGGT	AGATGCCTTGCTTGATACCGCG 90
g d	35	#GAIGCCTIGAIACCGCG 30 ::: uAspValLeuVal 37
Qy	900 AACTTCGATACGA	ATACGATCTTCCACACCCCAAGAAGTGAG 841
qq	373	::: ::: ::: ValValLeuValValGluAlaValValIleLeuPro 384
Οy	840 GTAGCGATCCGTACTGCCCGGGAAACCGATG	STCATGGCATAGTÜGTCAGCCTTG
qq	385 ValProLeu	lyTyrA]
QY	780 TIGCATGGATACGGC	AGGGTTTATIGTCC
QQ	393	::
Qy	720 GGCCGGCCGGTT	SANGTCGCCCGT
qa	403	 alGluSerGlyHisLeuAlaGluIleVal 417
δλ		-ACGCGGCCACATCCAGTTGTCCGTATCGCCTCCGAACTT 625
qq	418 GlyGlnThrLeuGlnValPr	16
Qy	624 ACCTACAGAGCTGGGAGG	AGCAAATACCATACGAACGTCCTTGAÄTACATCGTAGACGAT 565
qq	Db 438 Thr	AlaThrIleLeuValLysAsp 445

564 GAGGAAGTATTCGTTGTAGAA 11.1 446 MEtLeuleualaalaLeuargi 504 ATTTCTTTTTGCCAGTTC 416	564 GAGGAAGTATTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGTTGGTTCTCGTCTGC 505 ::::	ATTTCTTTTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGCGCTCCATCTC 445	GTCAGTGATACCCTTGAGCTGTCCTTCTGTCCGTTACCTTCACGATCTTGCGCAG 385 	ATACTTCACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACC 325 ::::: ValValHisLeu 502	ATCGCGCAGATAGTCGTGATCCAC	GATAGCACCGTATCCGCAGTGGTGGTTGGTAAAGATCAGGCCCTGATCGGACAC 232 :::	TGTGATACCGGTACATCCGCCACCGAAGATAACCACGGCATTGGCAATGGACGGCTTGTC 172	 GAGCTCACGCATTCGATCCAGATTCTCCTGATTGAGTTCGTTGAGGAGCCACAT 82 	
	564 GAGGAAGTATTCGTTGTTGGA/ ::: 446 MetLeuLeualaalaLeuArgE						231 TGTGATACCGGTACATCCGCC/ 111 540HisileileThrGluGln		81 GCCTTTGTCGGCTTTGGC 64 ::: 599 HisVallleGlyGluGly 604

Search completed: May 16, 2003, 12:28:32 Job time : 165 secs

Sun May 25 15:40:16 2003

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Sequence 33, Appl Sequence 14, Appl Sequence 14, Appl Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 31, Appli Sequence 21, Appli Sequence 22, Appli Sequence 24, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 28, Appli Sequence 28, Appli Sequence 29, Appli

3.0 846 2 3.0 846 4 3.0 885 1	112 2.9 652 1 112 2.9 652 3	20 111.5 2.9 1014 4 21 111 2.9 1114 4 22 110 2.9 1027 4	24 109 2.9 15/7 2 24 106 2.9 15/7 2 25 104 2.7 888 4 39 26 103.5 2.7 562 4	28 102.5 2.7 333 2 03-08-816-105A-1 29 102.5 2.7 833 4 05-05-1105A-1 30 102.5 2.7 833 4 05-05-14-302-3 31 102.5 2.7 838 4 05-09-154-302-3 31 102.5 2.7 1938 4 05-09-14-302-2 32 102.5 2.6 3898 2 05-08-876-991-2	33 102.5 2.6 3898 2 34 102 2.7 413 4	102 2.6 11/2 1 102 2.7 1940 2 103 3 7 1946 4	101.5 2.7 1940 4 101.5 2.7 747 1 101.5 2.7 3025 6	101 2.6 43.1 10.5-08.40.7.42.2. 101 2.6 772 4 US-09-134-078-28 100.5 2.6 371 4 US-09-199-637A-295 100.5 2.6 638 1 US-08-12-241-6 100 2.6 571 6 520.0183-17	45 100 2.6 668 1 US-08-445-050-9 a_1.2311		HPLICANT: HAPLICANT: TITLE OF II: FILE REFERI CURRENT APP PRIOR APPLI. PRIOR FILII			FEATURE: NAME/RES: UNSURE LOCATION: (4)	···.	Appli ;	
GenCore version 5.1.4_p5_4578 · Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model	Run on: May 16, 2003, 12:23:56 ; Search time 30.5 Seconds (without alignments) 4126.927 Million cell updates/sec	Title: Perfect score: 3820 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 21	Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Searched: 262574 segs, 29422922 residues	Total number of hits satisfying chosen parameters: 525148	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL-frame-12p.model -DEV-x1p -Q-/cgn2_1/USPTO_spool/USI0008355/runat_16052003_110339_9386/app_quer: -DB-Issued Patents AA -OFMIN-fastan -SUFFIX-n2p.rai -MIRMATCH-0 1 -1.00	-LOOPEXT-0 -UNITS-bits -START-1 -END1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST-45 -DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFWT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USER-US10008355_@CGN_1 1_33 _@runat_1605203_110339_9386 -NCPU-6 -ICPU-3 -NO_XLEXX -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -LONGLOG -DEY_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7	Database : Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.	. SUMMARIES	Result Query No. Score Match Length DB ID Description	138 3.5 430 4 US-09-156-836B-2 Sequence 130 3.4 883 2 US-08-953-492-2 Sequence 129 3.3 430 3 US-08-997-897-2 Sequence 127.5 3.3 1194 2 US-08-488-940-18 Sequence	123.5 3.2 713 4 US-09-059-584-53 Sequence 122.5 3.2 800 2 US-08-488-940-4 Sequence 122.5 3.2 813 2 US-08-488-940-3 Sequence	

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amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino	amino amino	7.39e-05 138.00 23.61% 19.50%
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Qγ	1960	CGAATACGGGCTACCGGAGTTACCGC	ACCGGAGTTACCGC	:	-CCGTGATGTCGTTCGATAGGAAAG	1907
Dp	10	ArgArgArgSerLe	uArgCysValArgGl	*	aArgCysLeuTrpGly***	58
Qy	1906	CGATATGGAGCTGA	ACCGTTCTCGGCATAG	CGACCATAGTTTTG	GTGCGGAAGAGGTCGA	1847
qq	, 30	IleGlySerGlyAs	spArgGluIleAspGl	.yGlu	IleGlySerGlyAspArgGluIleAspGlyGluSerGlyPro	4.3
Qy	1846	GGATATICICCTG1	GGATATICICCTGTACGGCAAACTCATCGCTCTTAGGAT	CCT	GCTTCTCCAATACGCCCT	1787
qq	44	GlyTyrArgProPr	coProArgSerHis-	-	-Cys***SerArgPro	57
δλ	1786	TGCCTGTCG	TATGATAGTTGTACCAGGCACC	CAGGCACCGTCCTGCGGTT	TCATATCC	1733
Op	28	ч	gArgTyr***ArgCysArgAs	gAsp***ArgSerArgCy	gCys	73
ΟY	1732	TGGAGCCGTAGCTC	CATACGCATGGTGAAGTTGGCATCGCTCGGCAGAGCAC	TTGGCATCGCTCGGC	AGAGCACGTCCGGGGT	1.673
QQ	74	rog	oGlyTyrSerCysArgTy	yrTrpCys	HisProArg***	68
Qy	1672	CA				1670
QQ	90	SerCysArgCysTr	sTrpCysTyrArgArg**	*SerArgArgCysCy	sSerCysProCysCys	109
Qy	1669	TCTCACGCAAA	CCGGCAAAGAAAAGA	CGCTTGCCCTTCTCA	ATGGCATAGGCAT	1616
qq	110	III ArgSerProCys**	 SerProCys***SerArgArgArg***GlyCysProCysCysSerCysGlnHis	*GlyCysProCysCy	sserCysGlnHis***	129
Qy	1615			;	TGGCCATCGCATCGGCCTGAATAGCGC	1589
qq	130	GlyCysArgTyrCysAr	sArgTyrProGlySerAr	::: :rArgTyrProSerSerArg	 	145
Qy	1588	GAGCAGCAGCTATT	ACGCTCTTGGAAAGC	TCTACTGCCGGATCT	ATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGG	1529
Dp	146			CysProSerLeuArg	uArgCys	151
Qy	1528	AACT			-TGGACTTGAGCATGGCATGGA	1490
qq	152	argargèheargCysProar	g***Ar	sGlnArgTy	SProAsn***ThrGly	171
δλ	1489	ACTTGT		:	ACCACACTCTTGTCGA	1457
qq	172	 ArgCysCysArgCy	sProSerSerSerArg	*	:::11 *GlnTyr***SerProAlaGlyCysArg	191
Qy	1456	ATACGAAGTCTGCA	VTACTTCTTCGTGTCG	CCTTTGAATTTCTTG	TCGATTACATTCTTGA	1397
qq	192	Ar	gThrAlaArgCysAr	.gCysCy	ArgThrAlaArgCysArgCysCys	199
δ.	1396	ATATATCGGGGAGC	TTGTCGGCAGGGATA	CGCCGGCGTACAATA	ATCGGGGAGCTTGTCGGCAGGATACGCCGGCGTACAATATCGAGCATGGCGGCA	1337
qq	200		scys		-ArgCysTrpArgThr	206
οy	1336	GCACCTTACGGTCG	CGAGCGAGGGAGGTAG	TCTTTGTACTTGTCG	TCAAGCGATTTGAGGA	1277
qq	207			gCysCysCysAr	ArgCysCysCysArg	212
٥y	1276	TACCGGCATGAGCA	ATCAGGATTTGTAGCC	CAGGATTTGTAGCCAATGCGTTGGCAAACTGTGCAAAACGAAC	TGTGCAAAACGAACCA	1217
qo	213			CysTrpGlnSe	rLeuGly***SerArg	221
Oy	1216	CTCGGTACCAC	AGAGCG	TCTCGCTCAAATAAGTCATCTCACGGTTGGCCTTGGCT	CGGTTGGCCTC	1157
QQ	222	ProArg	1	rArgArgCysSerAr	b	231
٥y	1156	CTTCCTTATAAGCC	TTTTCGAGAGAGAC	AATACATCGCCATAG	CCTTATAAGCCTTTCGAGAGAAGACAATACATCGCCATAGACAGCACTCTTGCGGT	1097
qq	232			ArgArgPheGl	ArgargPheGlnAsnArgCysCysArg	240

	SerArgGlyPheArgIleArgCysCysSerPhePro252	; Patent No
1039 CAAGACGA	CAAGACGAGCGAGGCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAG 980	
!	.:: ::: GlyPheArgAsnArg	
979 CATACTTG	CATACTTGCTGCAGCATATTTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCTTC	
LeuArgCysPheHis	spheHis	
rcccrrcc	GAGGATTGTTCT	
859 CCACACCC	CCACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCAT 800	
275	275	
799 AGTCGTCA	AGTCGTCAGCCTTGTAGCCTTGCATGGATACGGCGAAGTAAACGGGCTTATAGGGTT 740	
275	275	
739 TATTGTCC	TGCTGTATTCGGCCGGCC	
276CysPro		
679 TGAAGTCG	AGTTGTCCG	•• ••
287	::: CysGlnGlyCys***SerHisArgArgPheArgCysArgGluCysCys 302	** ** '
619 CAGAGCTG	CAGAGCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGA 560	
302	305	
	AATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTGTGCATTTT	
	ArgCysArgGluCysSerArgArgProGly 3	••••
499 CTT	497	••••
318 LeuProGl	LeuProGlyArgAsp***ArgProValGlyHisArgLysIleProThrCysCysPheArg 337	
496	TTTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGAC 455	
338 Cys***Ar	Cys***ArgSerProArgSerArgProAlaLeu***TrpProProGlySerCys***Thr 357	· · · · ·
454 GCTCCATC	GCTCCATCTCGTCAGTGATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGA 395	506-80-80
358 Asn		Pred. No.:
394 TCTTGCGC	TCTTGCGCAGATACTTCACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAG 335	Score: Percent Sim
111 362 CysCysPr	 CysCysProSer***SerArgPro1leProAlaArgProArgLeuPro 377	Best Local Query Match
334 AAACGAAA	AAACGAAACCATCGCGCAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGT 275	DB
	:::::: GlyargSerTyrargTrp 385	US-10-008
274 ATCCGCAG	ATCCGCAGTGGTGTGGTAAAGATCAGGCCCTGATCGGACACTGTGA 227	Qy —
386 ThrLysse	::: . ThrLysSerGlyArgSerGlnAsnCySTrpHisArgSerSerGlySerArgThr 403	අය ්
226 TACCGGTA	ΑŢ	09
 404ArgTyr	 rargHisArgCys***ArgIleProThrThrAlaHisTrpSerSer** 421	qa ———
172 CGAAAC 167	291	QV
	423	qa
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		609	45 669	54 729 57	789
	8883 	els: 176 s: 24 (1-883) -AAGGACGTTCGTATGGTATTTGCTCCT	erlleVallleProPro	GGCCGCCGAATACAGC	CCATGCAAGGCTACAAG
8953492 orah beth L vals Beecham Corporation Road Windows Version 2.0 708/953,492 97 7844,064 97 07991.8 96 N:	Length: Matches: Conservative: Mismatches:	Indels: Gaps: -953-492-2 (1-883)	 InLysAlaLysProTyrS GCGATACGGACAACTGGA	ATGCCGGTGCCGACAACC	TTTACTTCGCTGCCGTAT
cation US/0 [50] Why, James Worski, Deb	TION INFORMATIO 610-270-4478 10-270-5090 SEQ ID NO: 2: ACTERISTICS: Acid a maino acids a cid cid si single linear i protein protein protein 130.00 130.00 120.688	3.40% 2 22139) x US-08		ProAsnValThrGlyLysLeu HisLeu GGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAACCGGCCGG	AAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAG
Sequence 2, Application Patent No. 5849555 GENERAL INFORMATION: APPLICANT: Jaworski, APPLICANT: Wang, MINDRESSEE: SmithKl STREET: 709 Swedel, STATE: PA COWPRY: LAMP OF PLUS STATE: PA COMPUTER READABLE FOR MEDIUM TYPE: DISKE COMPUTER: IBM COMPUTER: TBM COMPUTER:		Query Match: DB: US-10-008-355-1 (1- OY 574 GATGTATTC	111111 26 AspvalF 610 CCCAGCT	46 ProAsnv 670 GGCGACT 111 55 Gly	730 AAGGACA
	IN I	Que OB: US-	Db	qa Ao	δλ

Page 4

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ACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGC 1818
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|YrProProArgPheAsnAspThrPheLeuGlnTrpMetGluAsnValHisAsp 402
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MAR, DEEPAK
MAR, DEEPAK
ILVASTAVA, BRAHM SHANKER
BI UO11469-7
CATTON NUMBER: US/08/997,897C
G DATE: 1997-12-24
ID NOS: 7
ENTIN VET. 2.0
                                                                                                                                  TTTGCCGTACAGGAGAATATCCTCGAC 1851
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rpThrGlnAspGluAspValLeuAsp 445
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; LOCATION: (159)	Db 74 TrpCysHisP	TrpCysHisProGlyTyrSerCysArgTyrTrpCysHisProArg*** 89
; FEATURE: ; NAME/KEY: UNSURE	Qy 1672 ACA	1
	90	::: SerCysArgCysTrpCysTyrArgArg***SerArgArgCysCysSerCysProCysCys 109
NAME/KEY: UNSURE COCATION: (182)	Qy 1669TCTCACG	TCTCACGCAAACGCAAAGAAAGACGCTTGCCCTTCTCAATGGCATAGGCAT 1616
NAME/KEY: UNSURE	Db 110 ArgSerProCy	ArgSerProCys***SerArgArgArg***GlyCysProCysCysSerCysGlnH1s** 129
	Oy 1615 Db 130 GlyCysArgT	GlyCysArgTyrCysArgTyrProGlySerArgTyrProSerSefArg145
FATURE: NAME/KEY: UNSURE LOCATION: (259) FEATURE:	Qy 1588 GAGCAGCAGC	GAGCAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGG 1529
; NAME/KEY: UNSURE ; LOCATION: (269)	Т	CTS
; FEATURE: ; LOAGITON: (291)	::: Db 152 ArgArgPheA	::: ArgargPheArgCysProArg***ArgCysGlnArgTyrTrpCy3ProAsn***ThrGly 171
 Z	OY 1489 ACTTGT 11	ACTTGT
; FFALION: (339)		ATACGAAGTCTGCATACTTCTTCGTGTCGCCTTTGAATTTCTTGTCGATTACATTCTTGA 1397
FEATURE: NAME/KEY: UNSURE 1.0CENTON . 1340.	192	
	Db 200	ATAIAICGGGGGAGGGATACGCCGGCGTACAATATCATCAGATGATGAGGAGTAGGGGGGA 1337
CATION: (330) FEATURE: NAME: TOCATION: (346)	Qy 1336 GCACCTTACG	GCACCTTACGGTCGAGGGAGGGAGGTCTTTGTACTTGTCGTCAAGCGATTTGAGGA 1277
	1276	ACCA A BOOM A BO
; LOCATION: (410) ; FEATURE (410) , NAME VEFF. INSTIDE	213	
: LOCATION: (421) US-08-997-897-2	Qy 1216 CCTCGGTACC. Db 222 ProArg	CCTCGGTACCACCGAAGAGCGTCTCGCTCAAATAAGTCATCTCACGGTTGGCCTTGGCTC 1157 ::: :::
ent Scores: 0.000589 Length:	1156	AGCACTCTTGCCGT
Score: 129.00 Matches: 132 Percent Similarity: 23.46\$ Conservive: 28 Best Local Similarity: 19.35\$ Mismarches: 170	232	:::
3.26% Indels: 3 Gaps: 6007-807-2 (1-420)	Qy 1096 TCTTACGGAT 	TCTTACGGATCCAGTCTGCGAATGCTCTTTCCTCGGCACGCTTACGACCTATCACGT 1040
OY 1960 CGAATACGGGGCTACCGGAGTTACCGCCCGTCATGTTCGATAGGAAG 1907	Qy 1039 CAAGACGAGC	CAAGACGAGCGAGACCGCGGTTCATACCGAATTCTTCCAAfAGTTAGCACTCTGAG 980
10 ArgargargSerLeuArgCysValArgGln***ProSerAlaArgCysLeuTrpGly***	979	ATTIGATACGGGTAGCCTGATCGCGCTCATGGCTTCCAGA
Qy 1906 CGATATGGAGCTGACCGTTCTCGGCATAGCACCATAGTTTTTGGTGCGGAAGAGGTCGA 1847 "Db 30 lleGlySerGlyAspArqGlulleAspGlvClu	261	
AGGATCCTGCTTCTCCAATACGCCCT	Qy 919 TGCCTTGCTT Db 266	TGCCTTGCTTGATACCGGAACTTCGATACGAGGATTGTTCTCGTTTCGATACGATCTT 860
1786 TGCCTGTCGTATGATAGTTGTACCAGGCACCGTCGGGGTTCATATCCTTGA	QY 859 CCACACCCCA	CCACACCCCCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCAT 800
58 Cysarglysargargry***ArgCysargasp***ArgSerargCys 73	275	
ACGTCCGGGGT	QY 799 AGTCGTCAGC Db 275	AGTCGTCAGCCTTGTAGCCTTGCATGGATACGGCAGCGAAGTAAACGGGCTTATAGGGTT 740

139 TAPTGTCCTTGCTGTATTCGGCCGGCCGGCATACACGCGGATACCC 680 276CysacgAcgygshediyavsacidiycyskacy
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680 ValAspValAspThrAsnGluLeuLySSerGluGlnLeuLeuThrAlaSerGluArg 699
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|751 LysArgPro------GluGlyGluAsnAlaSerTyrHis--------761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCG------GGTCTTTCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495
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133
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMUNICATION INPORMATION:
TELEPHONE: 617/542-8906
TELEFA: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
ELENGTH: 1194 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                          TRANDEDNESS: not relevant
TOPOLOGY: linear
AOLECULE TYPE: protein
488-940-18
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00188
127.50
35.05%
20.09%
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.ocal Similarity:
Match:
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13 13 13 13 13 13 13 13	762 829 ACG 779 Tyr		TACAACTATCATACGACGAAGGGCGTATTG TyrasnasnLeuaspalaPheGlyIleMetaspTyrThrLeuThrGlyLys
The contraction of the contrac	889 CGTATC	930 QY B17	GAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTC
Margament Marg		984 QY 837 Db	CGCACCAAAACTATGGTCGCTATGCCGAAACGGTCAGTATC
	985AGTGCT <i>I</i> 838 SerProLysSerLys	1035 QY 857 Db	906 GCTTTC ::: 63 AlaTyr
### SETTION 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 ### POPICIONE 1.0 1.0 1.0 1.0 1.0 1.0 ### POPICION 1.0 1.0 ### POPICION 1.0 1.0 ### POPICION 1.0 1.0	1036 CTTGACGTGATAGGT +::::: 858 AlaAspLeuLeu	1095 RES US- 1 S 874 ; P	5 059-584-9 ence 53, nt No. 64
######################################	1096 AAC 875 AsnAspAspTyrPhe	1128	Lisa E ers, Anthony ss, Robin E
AGENTECTTTTCCACCCATTCCACCCATTC 1248	1129 TCTTCTCTCGAAAA(::: 895 GlyLysValTyrPh	1188	Loosmore, Sneena M. Du, Run-Pan Yang, Yan-Ping Klein, Michel H
STREET: 6ft Floor, 330 University Avenue	1189 AGCGAGACGCTCTT 	TTTGCCAACGCATTG 1248	Transferrin Receptor Genes of Moraxell 60 53: IcBurney
### AGENTACCTCCCCTCCTCCTCGACCGTAAGGTG 1335 COMPTTER READBLE FORM: ### MEDIUM TYPE: Floopy disk ### MEDIUM TYPE: Floopy TYPE: Floopy disk ### MEDIUM TYPE: Floopy TYPE: Floopy Type ### MED	1249 GCTACAAATCCTGA 929LysProll		6th Floor, Coronto Ontario Canada
	1303	1335	ZIP: MSG IRR. COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
International content of the conte	1336 CTGCCCGCCATGCT ::	1395	DOS/MS-DOS lease #1.0, Version #1 : S/09/059,584
FILING DATE: 03-JAN-1997 FILING DATE: 03-JAN-1997	1396 TTCAAGAATGTAAT .::::::::: 983 AlaGinSerileLe	1455 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	199 US
REGISTRATION NUMBER: 1938-794 REFERENCE/DOCKET NUMBER: 1038-794 REFERENCE/DOCKET NUMBER: 1038-79	1456 TTCGACAAGAGTGT ' :: 999 ArgAspSerSerIl	1515 ;	
CCGATGCCAATGCC	1516 AAGGAAAAGTTTGC . ::: 1019 GlnGluPheThrTy	1575	REGISTRATION NUMBER: 24973 REFERENCE/DOCKET NUMBER: 1038-794 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
TYPE: amino acid	1576 ATAGCTGCTGCTCG(1039 GlyLeuAsnGluGl)	1632 · ; 1058 · ;	TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 713 amino acids
CTCTGCGGAGCGATGCCAACTTCACC	1633 AAGGGCAAG :: 1059 LysGlyGluLysPro	CCGGT 1659 leLys 1078 ·	TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear)9-059-584-53
AGGGATATGAACCGCAGGACGGTGCCTGG 1764 Percent Similarity: 31.34% Conservative:	1660 TTGCGTGAGATGTAO :::::: 1079 TyrValAspValAs	1710 ·· erGlu 1098	nment Scores: 0.00313 Length: . No.: 123.50 Matches:
	1711 ATGCGTATGAGCTACGGCTCCATCA ::: ::: 1099 ArgAsnLeuaspPheargAspLeu-	AGGGATATGAACCSCAGGACGGTGCCTGG 1764 ::: ::: TyrAspProArgAspLysAlaLysLeuLeu 1116	119.37% Conservative: 19.37% Mismatches: 3.23% Indels: 4 Gaps:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 TyrGlyHisSerGluPheAspValAsnPheAlaAspLysLysIleLysGlyLysLeu 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AspileHisGlyAsnArgPheArgGlySerAla------ThrAla 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 ileSerAsnGlnLeuSerGlyThrAlaValThrAlaLysGluArgTyrLysIleGluAla 381
                                                                            156 IleProPheAspLysAsnLeuIleGluTyrLeuLysLysSerSerGluValValSerLys 175
                                                                                                                                                             176 PheGluAlaGlnLysGlyGlyIleGluAsnAsnThrArgLeuThrHisLysAspLeuSer 195
                                                                                                                                                                                                     475 GTATGCCAAGAACTGGCCAAAAAAGAAATGCAGACGAGAACCAACTCTGCATCGTAGAG 534
                                                                                                                                                                                                                                                                                                                                                                GACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGAC 645
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                                        355 CTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAG 414
                                                                                                                      415 GTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAG 474
                                                                                                                                                                                                                            212 ThrGlnPheAlaGlnGluLysTyrLysGluLeuIleGluAsnAlaHisAspLysLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AsnArgAspLeuGluTyrValLysSerGlyPheAsnTyr-----
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265 TyrTyrGlyAlaLeuTyrTyrLysGlySerGluThrAlaLysGluLeuProGlnThrSer
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US-10-008-355-1 (1-2139) x US-09-059-584-53 (1-713)
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1429 GACACGAAGAAGTATGCAGAC---TTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC 1485
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                                                                     CTCCCCTCGCTCGACCGTAAGGTGCTGCCCCCATGCTCGATATTGTACGCCGGCGTATC 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 LeuMetValAsnAspGluValIleValLysThrTyrGlyLysAsnPheGluTyrLeuLys 548
                                                                                                                                                                                                                                                                                                                                                                                                                   549 PheGlyGluLeuSerValGlyAspSerHisSerValPheLeuGlnGlyGluArgThrAla 568
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433 ThraspaspasnLysLeuPheGlyValPheGlyAlaLysArgAspLysValGluLysThr 452
                                                                                                                                                                                                                                                                                        ----GlyThrPheAsnAsnThrAsnLysAlaThrThrPheThrPro 475
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; Patent No. 5854049
; GENERAL INFORMATION:
    APPLICANT: Reed, Guy L.
    TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
; UNMBER OF SEQUENCES: 20
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREE: MA
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                                                                                                                                              GlualaileLeuAspAlaTyrAlaLeu---------
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			264 196	324	375	435	495	501	285	558 305	609	648	342
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: Patentin Release #1.0, Version #1.30 GURENATION OWNER: 05-00-00-00-00-00-00-00-00-00-00-00-00-0	ment Scores: 0.00432 Length: 800 No.: 122.50 Matches: 130 mt Similarity: 33.98* Conservative: 99 Local Similarity: 19.29* Mismatches: 254 Match: 3.21* Indels: 191 atch: 2.34* Gaps: 35	-355-1 (1-2139) x US-08-488-940-4 (1-800)	GGTATCACAGTGTCCGATCAGGCCTG	CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGAT	GGTTTCGTTTCTCGCACGATGGGTGAGGATCCGATTCCGGGTCTTTCC ::: ::: ASNASPIlePheArgThrIleLeuProMetAspGInGluPheThrTyrarg	GTGAAGTATCTGGGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT	ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA ::: :: :::	AAAGAA	_	AATGCAGACGAGAACCAACTCTGCATGGAGCCTTTCTATTCCAACAAGAATAC :::	TTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT		• ⊟
COMPUTER MEDIUM COMPUTE OPERATI SOFTWAN APPLICY APPLICY ANDE: NAME: REGISTI REFERE TELECOMM TELECOMM TELECOMM TELECOMM TELECOMM TELECO	ment No.: nt Si Local Matc	-008	223	265 197	325	376	436	496	266	502	559	610	324 649
IN IN	Alignment S. Pred. No.: Score: Percent Sim Best Local Query Match DB:	US-10	Qy	Qy	Oy Db	Oy Dp	QY Dp	ογ	QQ	Qy Db	oy Db	δλ	oy Oy

10	1642	-SD OB:	UB: US-10-008-355-1 (1-2139) x US-08-488-940-3 (1-813)
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### CONTRINCT CONTRINCT CONTRICT CONTR	GCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATC	qa	
###	spLeu	da Db	CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGAT
Comparison Com	::: ::: TyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGly	Oy	GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCC
### CANADAGAMANACTATCCTCCACCTCTTCCCCCACCANANACTATGGT 1875	771TATCATACGACAGGCGTATTGGAGAGCAGGATCCTAAGAGCGAT 1821 	da .	ASNASPILEPheArgThrII:: ASNASPILEPheArgThrIII::: GTGAAGTATCTGCGCAAGATCGTGAAGGTAAAGGACAAGGTAGAAGGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGGTAGAAGA
	ATGGT	qa ·	
### Trigon US/OB4488940	ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGly 756	Qy	ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA
tion Us/08488940 N: Ouy L. Ouy L. Ouy L. Ouy L. Out : PLASMIN-RESISTANT STREPTOKINASE EBS 20 DDRESS: 20 DDRESS: 21 DDRESS: 22 DDRESS: 22 DDRESS: 24 DDRESS: 25 DDRESS: 26 DDRESS: 27 DDRESS: 28 DDRESS: 28 DDRESS: 29 DDRESS: 20 D	876 CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTC 1911 ::: 757 LysArgProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 770	Db Qy	LeudsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLys AAAGAA
tion Us/08488940 N: With Michael Street Oxidar Street Compatible Street Compatible Street Compatible Street No. 00438 Length: Oxidate Street Oxidate	2,040	q _Q	 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr
National Care of the Page 13.00 of the Page 13.0	or 100 3.7 Application US/08488940 Sequence 3, Application US/08488940 Patent No. 58834049	Qy	AATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATAC
ON THASMIN-RESISTANT STREPTOKINASE DEFENSE: ENTREPTOKINASE BY & RICHARGON P.C. EN	SNERAL INFORMATION: APDITTANT: Reed Guy L	qa	ValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArg
## Short Street	VENTION:	λο το	TTCTCATCATCTACGATGTATTCAAGGACGTTCGTATGGTCTTCTTCTTCTTCTTCTTCTTTCT
Define E FORM: Floppy disk Comparation EVEL PORTY Floppy disk Comparation EWEL PORTY ENTER Elease #1.0, Version #1.30 O9-JUN DATA: D9-JUN D9-JUN DATA: D9-JUN DA	chardson Street	org Ko	CCCAGCTCTGTAGGTAAGTTCGGAGGCGATAAGGAGAAC
## Properties	CITY: Boston STATE: MA COUNTRY: ICA	qa	::::::: ::::::: ::::::
Pioppy disk PC compatible EM:	: 02110-2804 TER READABLE FORM:	Qy	#GGATGTGGCCGCGTCACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGAC
ERI: PC-DOS/MS-DOS entin Release #1.0, Version #1.30 LON DATA: MBER: US/08/488,940 09-JUN 1995 1514 NFORMATION: Janis K. NFORMATION: AINFORMATION: AINFOR	IUM TYPE: Floppy disk PUTER: IBM PC compatible	qa	AsnHisAspAspThrAsnArgIleIleThrValTyrMetGly
MBER: US/08/488,940 09-310v-1995 15.14 NFORMATION: Janis R. NAMBER: 34,819 ET NUMBER: 05433/009001 NINFORMATION: 542-5070 542-5070 542-5070 542-6906 543-6906 543-6	DOS 11.0, Version #1	QQ	AACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCC
WFORMATION: Janis K. N INFORMATION: N INFORMATI	APPLICATION NUMBER: US/OB/488,940 FILING DATE: 09-JUN-1995 CTACETPTAMION: G14	Qy	GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGT
### Part	CENSSITION: JI. ATTORNEY/AGENT INFORMATION: NAME: Fracer Invice F	qa	ds4
N INFORMATION: N/542-5070 542-6070 542-6070 542-6070 542-6070 542-6070 679 5110 No: 3: 1100 acids 1100 a	REGISTRATION NUMBER: 34,819 REFERENCE/DOCKET NUMBER: 05433/009001	Oy	ACGGATCGCTACCTCACTTCTTGG
542-8906 52 ID NO: 3: ERISTICS: info acids info acids not relevant ar protein 0.00438	OMMUNICATION INFORMATION: EPHONE: 617/542-5070	qa	LysAspArgTyrThrGluGluGluArgGluValTyrSerTyrLeuArgTyrThrGlyThr
### SETS	TELEFAX: 617/542-8906 TELEX: 200154 RMATION FOR SEQ ID NO: 3:	Qy	GGTGTGGAAGATCGTATCGAAAACGACAATCCTCGTATC
0.00438 Length: 813 Oy 122.50 Matches: 130 Oy 33.98% Conservative: 99 19.29% Mismatches: 254	ds.	Qy	GAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC
0.00438 Length: 813 Oy Oy Matches: 130 Oy Oy 33.98% Conservative: 99 Ob 19.29% Mismatches: 254	acid : not relevan	qu	
0.00438 Length: 813 Qy 122.50 Matches: 130 Qy 33.98% Conservative: 99 19.29% Mismatches: 254 Db	1	Qy	CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGG
0.00438 Length: 813 OY 122.50 Matches: 130 S3.98% Conservative: 99 Db 19.29% Mismatches: 254	,	qq	445 ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAla 464
53.56 Conservative: 99 DD	122.50 Matches	δ i	1000 AAGAATTCGATCGATCACCCCGTCTCGCTCACGTGATAGGTCGTAGACGT 1059
	19.29% Conservative:	an -	<pre>4bb ThraspserGlyAlaMetserHisLysLeuCiuLysAlaAspLeuLeuLysAla 482</pre>

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                                                                                                                            1153 GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212
                                                                                                                                                                                                   .213 GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCC 1272
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522 AspGlySer---ValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 540
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-----LysProileGlnAsnGln 553
                                                                                                                                                                                                                                                                                                                                                                        666 ThrAspLeulleSerGluLysTyrTyrValLeuLysLysGlyGluLysProTyrAspPro
                                                                                          502 AspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLys
                                                                                                                                                                                                                                                                                                              554 Ala-----LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 HisProGly-----TyrThrIleTyrGluArgAspSerSerIleValThrHis
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; Patent No. 5854049
; Patent INFORMATION:
APPLICANT: Reed, Guy L.
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558 GlyAspThrileThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAshLysAsn 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCG------GGTCTTTCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SerGly 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 LeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLys 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATAC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: ||| |||:::||| ||| 657 ValAspValAspThrAsnGluLeuLySSerGluGlnLeuLeuThrAlaSerGluArg 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ATCTTTACCAACCAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGGT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 AsnAspIlePheArgThrIle-----LeuProMetAspGlnGluPheThrTyrArg 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1181
130
99
254
191
35
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisproGlyTyrThrIleTyrGluArgAspSerSerIle-----
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612 ValLysAsnArgGluGlnAlaTyrArgIleAsnLysLys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-008-355-1 (1-2139) x US-08-488-940-2 (1-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8006
                                                                                                                                                                                                                                                                                    GGTATCACAGTGTCCGATCAGGGCCTG----
                                                              Richardson P.C.
                                                                                                                                                                                                                                     IBM PC compatible
                                                              ADDRESSEE: Fish & Richardso STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1181 amino acids
                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00589
122.50
33.98%
19.29%
3.21%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 09-JUN
                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AAAGAA----
                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-488-940-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  578
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٥y	559TICCTCATCGTCTACGATGTATICAAGGACGTICGTATGTGTATTGCTCCT 609	HOLTER STATE OF THE STATE OF TH	. 0
QQ	proArgAspLysAlaLys	* 6 6	i è
ΟŸ	610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGATACGGACAAC 648	QY. 1540 GAGAAGATCCGGG :::::: 1014 Assard[]uG]na]	<u> </u>
Dp	705AsnasnLeuaspalaPheGlylleMetaspTyrThrLeuThrGlyLysValGluasp 723	1600	יט ווע
ογ	TGGATGTGGCCGCGTCACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGAC	1034	eSe
g		Оу 1642	i
Š S	709 AACCGGCCGGATACAGCAATAAACCCTATAAGCCCGTTTACTTGGCTGCC 768	_ Db 1054 PheAspArgSerHi	rHi
ò	AAGGCTACAAGGCTGACGACGACGATGACCATGACCATGGCTTTCCCGGGCAGT	Qy 1684 GCTCTGCCGAGCG	790
g q		1074	rG]
δý	CCTCACTTC	1735 AAGG	AC.
QQ		1094Ty	pPı
οy	853 GGTGTGGAAGATCGTATCGAAAACGAGAACATCCTCGTATC	1771	72 - E
qq	773 ProIleProAspAsnProAsnAspLysAsnAsnSerGlnLeuValValSerValAlaGly 792	1833	1 2
٥y	895 GAAGTTCGCGGTATCAAGCAAGCCATCTGGAAGCCATGAGCGCAGATCAGGCTACC 954	QY 1022 GAGIIIGCCGIACA 	: : : : : - : :
qq	793 ThrValGludlyThrAsnGlnAspileSerLeuLySPhePheGluIleAspLeuThrSer 812	1211	5 6
oy Ob	955 CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGG 999	UY 18/0 CGCTATICG ::: Db 1138 LysArgProGluGl	ng]
δ	AAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGT	RESULT 9 US-08-488-940-1	
qq	833 ThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeuLysAla 850	; Sequence 1, Application; Patent No. 5854049	17
δ	GCCGAGGAAGGATTCGCAGACTGGATCCGTAAGAAC	; APPLICANT: Reed, C ; TITLE OF INVENTION:	NO.
g	851 IleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIle 869	NUMBER OF SEQUENCES	CES
Oy Dp	1099GGCAAGAGTGCTGTCTATGGGGATGTATGTCTTCTCTCGAAAAGGCTTATAAG 1152 	ADDRESSEE: Fish STREET: 225 Frar CITY: Boston	sh rar
٥٧	1153 GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212	63 6	
QQ	:: ::: 890 AspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 908	; ZIP: UZIIU-2804 ; COMPUTER READABLE F . MEDIUM MYDE: E1	о Б. Б.
ΟY	1213 GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCC 1272	COMPUTER: FAC COMPUTER: IBM PC COMPUTER: COMPUTER:	7 Z E
g	LysProlleGlnAsnGln	; SOFTWARE: Patent ; CURRENT APPLICATION	ent
Š S	1273 GGTATCCTCAAATCGCTTGACGACAAGTAC	; APPLICATION NUMBE; FILING DATE: 09-	MBE 09-
3 3		ATTORNEY/AGENT IN	NFC
g 4	1303 AAAAATAACTICCTCCTTG-TG-TG-TG-TG-TG-TG-TG-TG-TG-TG-TG-TG-	; NAME: Fraser, Ja ; REGISTRATION NUME ; REFERENCE/DOCKET	J. UME ET
ογ	1360 CGCCGGCGTATCCCTGCCGACAGCTCCCCGGATATATTCAAGAATGTAATCGACAAGAAA 1419	; TELECOMMUNICATION I ; TELEPHONE: 617/5	Z 5.
QQ	958 GlyAspThrIleThrSerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 977	TELEFAX: 01/342 TELEX: 200154 TELEX: 200154	7 0
οy	TTCAAAGGCGACACGAAGAA	; SEQUENCE CHARACTERI ; LENGTH: 1194 ami	ERI
qa i	978 HisbroGlyTyrThrIleTyrGluArgAspSerSerIleValThrHis 993	ino ac ESS:	ció
ò	1480 AGCGACAAGTTCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATC 1539	; TOPOLOGY: linear	ear

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| ::::::|||
aTyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn 1033
                                                                                                                        ::
erGluLysTyrTyrValLeuLysLysGlyGluLysPrOTyrAspPro 1053
                                           SAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 1599
                                                                                                       CAATGCC---TATGCCATTGAGAAGGGCAAG------ 1641
                                                                                                                                                               ----CGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGT 1683
                                                                                                                                                                                     ::::!!!!!
SLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGlu 1073
                                                                                                                                                                                                                                               GCAGGACGGTGCC-----TGGTACAAC------1770
                                                                                                                                                                                                                                                                                                                                                                 GGAGAATATCCTCGACCTCTTCCGC-----ACCAAAACTATGGT 1875
                                                                                                                                                                                                                          ATGCCAACTTCACC-----ATGCGTATGAGCTACGGCTCCATC 1734
                                                                                                                                                                                                                                                                                                       TACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGAT 1821
                                                                                                                                                                                                                                                                                                                                                                                                                            3uy L.: PLASMIN-RESISTANT STREPTOKINASE
S: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGAGAACGGTCAGCTCCATATCGCTTTC 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORM:
Lioppy disk
Compatible
RH: PC-DOS/MS-DOS
nntIn Release #1.0, Version #1.30
MBER: US/08/488,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514
Janis K.
Janis K.
MBER: 34,819
T NUMBER: 05433/009001
TINFORMATION:
7542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESS:
& Richardson P.C.
nklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on US/08488940
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ISTICS:
ino acids
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; us-08	MOLECULE TYPE: protein -488-940-1	
Alignmer Pred. Nc Score: Percent Best Loc Query Ma	No.: 0.00594 Length: 1194 No.: 122.50 Matches: 130 it Similarity: 33.98% Conservative: 99 Local Similarity: 19.29% Mismatches: 254 Match: 2 Gaps: 35	,, ,,
US-10	-008-355-1 (1-2139) x US-08-488-940-1 (1-1194)	
Qy Db	223 GGTATCACAGTGTCCGATCAGGGCCTGATCTTTACCAACCAC 264	
Qy	265 CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGTGGATCACGACTATCTGCGCGAT 324	
da .	CGATTCCGGGTCTTTCC 375	
Qy Dp	CGTGAAGGTAACGGACAGGTAGAAGGACAGCTCAAGGGT 435	• •
Qy	AGCTCAGGAGGTATGCCAAGACTGGCCAAA 495 	• •
Qy		
Qy	502AATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATAC 558 .:: ::: Db 680 ValAspValAspThrAsnGluLeuLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArg 699	
Qy .	559TTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT 609 1	
Qy	CGGACAAC 648 ::::: alGluAsp 736	
oy Dp	649 TGGATGTGGCCGCTCACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGAC 708 1	
ΟΥ Db	GCTGCC 768	
Qγ	OY 769 GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGT 828 Db	
9 0 0	765ASP 765	
g qg	LysAspArgTyrThrGluGluGluArgGluValTyrSerTyrLeuArgTyrThrGlyThr 785	
QV	853 GGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC	
Qy Db	895 GAAGTTCGCGGTATCAAGCAAGGCAATCTGGAAGCCATGAGCGCAGATCAGGCTACC 954	
	,	

٥y	955	JAAATATGCCAGCAAGTATGCTCAGAGTGCTAAC	6
qq	826	::: ::: ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAla 845	
QY	ō.	0.5	
q n	840	ThraspserGlyAlametserHisLysLeuGluLysAlaAspLeuLeuLysAla 863	
δÿ	ō.	109	86
q	864	IleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIle 882	2
ΟY	1099	GCCAAGAGIGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAG 1152	
qq	883	AspPhealaSerAspalaThrIleThrAspArgAsnGlyLysValTyrPhealaAspLys 902	2
Qy	1153	GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212	112
q	903	AspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 921	-
Qy	1213	GCATTGGCTACAAATCCTGATGCTCATGCC 127	:72
qq	922	LysProlleGln	14
Qy	1273	130	102
qq	935	AlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp 952	25
Qγ	1303	AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTA 1359	.59.
qq	953	AspaspheargProGlyLeuLysAspThrLysLeuLeuLysThrLusThrLeuAlalle 970	0,
Qγ	1360	CGCCGGCGTATCCCTGCCGACAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAA 1419	119
ΩD	971	GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 990	0
Qy	1420	TICAAAGGCACACGAAGAAGTAIGCAGACTICGIATICGACAAGAGIGIGGIICCTIAI 147	641
qq	991	100	900
Óλ	1480	AGGGACAAGTTCCATGCCATGCCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATC 153	
q	1007	AspasnaspilePheargThrileLeuProMetAspGlnGluPheThrTyrargValLys 102	. 920
Qy	1540	GAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 159	669
qq	1027	104	946
Qy	1600	GCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAG 164	541
qq	1047	.euileSerGluLysTyrTyrValLeuLysLysGlyGluLysProTyrAspPro 106	990
Οy	1642	168	583
QQ	1067	PheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGlu 108	980
ΟŸ	1684	ATGCGTATGAGCTACGGCTCCATC 173	134
QQ	1087	110	
Qy	1735	AAGGGATATGAACCGCAGGACGGTGCCTGGTACAAC	07.0
q	1107	TyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGly 112	
Qy	1771	TATCATACGACAGGCAAGGCCGTATTGGAGAAGCAGGATCCTAAGAGCGAT 182	321
qq	1125	ileMetAspTyrThrLeuThrGlyLys113	133
Qy	1822	GAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGT 187	375
QQ	1134	paspThrasnargileIleThrValTyrMetGly 115	
QY	1876	CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTC 1911	

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571 GlyAspThrileThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::: ||||||:::
608 AsnAspilePheArgThrIle------LeuProMetAspGlnGluPheThrTyrArg 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: :::|||:::
LeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLys 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGGAT 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCG------GGTCTTTCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 ValLysAsnArgGluGlnAlaTyrArgIleAsnLysLys------SerGly 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 ATCACTGACGAGGTTGGGGCTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ATCTTTACCAACCAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 HisProGlyTyrThrIleTyrGluArgAspSerSerIle------ValThrHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1194
130
99
254
191
35
                                                                                         Sequence 17, Application US/08488940
Patent No. 5854049
GENERAL INFORMATION:
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-008-355-1 (1-2139) x US-08-488-940-17 (1-1194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/488,940
ELING DATE: 09-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 GGTATCACAGTGTCCGATCAGGGCCTG------
                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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33.98%
19.29%
3.21%
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Best Local Similarity:
Query Match:
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                                                      RESULT 10
US-08-488-940-17
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ζ	4 40	TOC
qa	099	 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr 679
Qy	502	NGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGA
qa	680	::: ::: ValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuT
QY	559	
qq	700	AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAl
Οy		CCCAGCTCTGTAGGTAAGTTCGGA
qq	718	AsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLy
Qy	649	TGGATGTGGCCGCGTCACACGGG
qa	737	eIleThr
QY	709	
qa	751	LysArgProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 764
Ωy	169	GTATCCATGCAAGGCTACAAG
qq	765	765 765 765 765 765 765 765 765 765 765
Qy	829	ACGGATCGCTACCT
qq	166	
QY	853	GGTGTGGAAGATCGT
a a	786	
Qy	895	GAAGTTCGCGGTATCAAGCAAGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTAC
qq	806	ThrValGluGlyThrAsnGlnAspIleSerLeuLySPhePheG
QY	955	CGTATCAAATATGC
qq	826	ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysS
ΟŊ	1000	AAGAATTCGATCGGTATGAACCGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGT 1059
qq	846	
Qy	1060	GCCGAGGAAAGAGCATTCGCAGACTG
qq	864	IleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIle 882
Qy	1099	STCTATGG
qq	. 883	AspPhe
Qy	1153	GAA
qq	903	AspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 921
QY	1213	GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATC
qq	922	
δy	1273	GGTAT
qq	935	AlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp 952
Qy	1303	AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTA 1359
qa	953	AspAspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaile 970

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1596 AATAGCGCGAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGAT 1537
                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                      US-09-036-987A-3
                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                 TYPE:
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1360 CGCCGCCGTATCCCTGCCGACAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAAA 1419
                                                                                                                1006
                                                                                                                                                                        1540 GAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 1599
                                                                                                                                                                                                                                                                 1027 AsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn 1046
                                                                                                                                                                                                                                                                                                                          -----CGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGT 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1087 LeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeu 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1822 GAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC-----ACCAAAACTATGGT 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1134 ------ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGly 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1684 GCTCTGCCGAGCGATGCCAACTTCACC-----ATGCGTATGAGCTACGGCTCCATC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGly 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TATCATACGACAGGCAAGGGCGTATTGGAGGAGGAGCAGGATCCTAAGAGCGAT 1821
                         971 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn
                                                                         1420 TTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTAT
                                                                                                          HisProGly-----TyrThrIleTyrGluArgAspSerSerIleValThrHis
                                                                                                                                                1480 AGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATC
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1067 PheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGlu
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                                                                                                                                                                                                                                                                                                    1600 GCCGATGCGATGGCCAATGCC---TATGCCATTGAGAAGGGCAAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1151 LysArgProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1876 CGC----TATGCCGAGAACGGTCAGCTCCATATCGCTTTC 1911
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1125 IleMetAspTyrThrLeuThrGlyLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes FOI
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09036987A Patent No. 6143526
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-09-036-987A-3
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1516 ArgAlaAlaSerValProIleValPheLeuThrAlaTyrTyrAlaLeuValAspLeuAla 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1713 CATGGTGAAGTTGGCATCGCTCGGCAGAGCACGTCCGGGGTACATCTCACGCAAACCGGC 1654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1974 ACGGCCGTTCTTATCGAATAC-----GGGGCTACCGGAGTTACCGCCCGTGATGTCGTT 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2139 TTAGATCAACTTCAGCTCTTGGATGAGACGGGGGCACTGACCCCGATTTGTCAATCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2079 GAGAACGTAGCGGATGTCCACGCT------GATTGTGCGCCTGCAGATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1435 ValArgIleAlaMetArgAlaAlaGlyValAsnPheArgAspAlaLeuIleAlaLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1467 AlaGlyValValValGluThrGlyProGlyValThrGlyLeuAlaProGlyAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCGATAGGAAAGCGATATGGAGCTGACCGTTCTCGGCATAGCGACAAAGTTTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1496 ProLeuAlaValAlaAspHisArgMetValThrArgIleProAlaGlyTrpSerPheAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1821: ------ATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCTTGCCTGTCGTATG
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-008-355-1 (1-2139) x US-09-036-987A-3 (1-2152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
      US/09/036,987A
                                                                                                              NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,61
TELECOMMUNICATION INFORMATION:
TELEFHONE: (317)337-4816
TELEFAX: (317)337-4816
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/0:
FILING DATE: 09-WAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                   2152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119.00
30.96%
19.10%
3.01%
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MOLECULE TYPE: protein
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		Db 1941 Alak
qa	1612 AsnSerLeuAlaGlyGlu	
ΟŊ	1536 AGC	66/
Q	::: 1621 AlaSerLeuArgMetLeuProArgGlyGlyArgPheLeuGluLeuGlyLysThrAspVal 1640	_
Qy	1507 1507	
qq	1641 ArgAspProValGluValAlaAspAlaHisProGlyValSerTyrGlnAlaPheAspThr 1660	1969
ò	1506 CTTGAGCATGGCATGGAACTTGTCGCTATAAGGAACCACACTCTTGTCGAATACGAA 1450	Qy 675 GTCG
qq	::: LeuPheGlu 16	1970
ò	1449 GTCTGCATACTT	Qy 615 GCTG
q		6
ò	1416 CTTGTCGATTACATTCTTGAATATATCGGGGAGCTTGTCGGCAGGGATACGCCGGCG 1360	Qy 555 TTCC
· 8		Db 1985 LeuA
ò	TAPO ANTONO DE CONTRACADO DE C	Qy 495 TTTC
i a	TrpAssAlaAlaGlvThrValLeuValThrGlvGlvThrGlvAlaLeuGlvAlaGluVal 174	Db ' 2005 ValA
ò	128	Qy 435
; 음		Db 2025 Gly ¹
ò	GAGGATACCGGCATGAGCATTTGTAGCCAATGCGTTGGC	Oy 378 CACG
· 6		Db 2045 AsnC
3 ;	TEANT AND THE TE	Qy 318 CAGA
<u> </u>		Db 2049
a d	Ser LeuctintacysAspval	Qy 258 GGTA
à i	AGICATCICACGGTIGGCCTTGGCTCTTTCTTTTTTTTTT	Db 2062 Thre
ga .		Qy 198 CACG
δλ	ATCGCCATAGACAGCACTCTTGCCGTTCTTACGGATCCAGTCTGCGGAATGCTCTTTCCTC	Db 2077
යු	1807 ThralavalvalHisAlaAlaGlyvalLeuAspAspGlyvalSerGlu 1822	Oy 147
Οy	1062 GGCACGCTTACGACCTATCACGTC	0
qq	1823SerLeuThrValGluArgLeuAspGlnValLeuArgProLysValAspGlyAlaArg 1841	114
οy	1035 ACGAGCGAGACCGCGGTTCATACCGAATGGAATTCTTCCAATAGTTAGCACTCTGAGCATA 976	2112
q	1842 AsnLeuLeuGluLeulleAspProAspValAlaLeuValLeuPheSerSerValSerGly 1861	9 (
Qy	CCA	US-09-370-700-
qq	1862 ValLeuGlySerGlyGlyGlnGlyAsnTyrAlaAlaAlaAsnSerPheLeuAspAla 1880	; Sequence 3, ; Patent No. 6
Qy	915 TTGCTTGATACCGCGAACTTCGATACGAGGATTGTTCTC 877	APPLICANT:
qq	1181 LeuAlaGlnGlnArgGlnSerArgGlyLeuProThrArgSerLeuAlaTrpGlyProTrp 1900	; APPLICANT: ; APPLICANT:
δō.	877	; APPLICANT: ; APPLICANT:
qq	1901 AlaGluHisGlyMetAlaSerThrLeuArgGluAlaGluGlnAspArgLeuAlaArgSer 1920	APPLICANT: APPLICANT: APPLICANT:
٥y	876	FILE REFERE
QΩ	1921 GlyLeuLeuProIleSerThrGluGluGlyLeuSerGlnPheAspAlaAlaCysGlyGly 1940	CURRENT FIL
οy	852 CCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCATAGTC 796	: EARLIER FIL

ΩΩ	1941	AlaHisThrValValAlaProValArgPheSerArgLeuSerAspGlyAsnAlaIleLys	1960
QY	795	CCTTGTAGCCTTGCATGGATACGGCAGCGAAGTAAAACGGGCTTP	736
qq	1961	::: PheSerVal	1969
Qy	735	GTCCTTGCTGTATTCGGCCGGCTGTTGTCGGCACCGGCATACACGCGGAATACGCTGAA	919
qq	1969		1969
Qγ	675	GTCGCCCCTGTGACGCGCCACATCCAGTTGTCCGTATCGCCTCCGAACTTACCTACAGA	616
ΩD	1970		1978
Qy	615	GCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAAGTA	556
qa	1979	AlaAspAlaGluSer	1984
Qγ	555	TTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTGCATTTTCTTT	496
qa	1985	LeuArgLysArgLeuGlyArgLeuProAspAlaGluGlnHisArgIleLeuLeuAspLeu	2004
Οy	495	TTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTTGCGCAGACGCTCCATCTCGTCAGTGAT	436
qu	2002	ValArgMetHisValAlaAlaValLeuGlyPheAlaGlySerGlnGlulleThrAlaAsp	2024
Οy	435	ACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT	379
QC	2025	GlyThrPheLysValLeuGlyPheAspSerLeuThrValValGluLeuArgAsnArgIle	2044
Qy	378	CACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACCATCGCG	319
qq	204.5	AsnGlyAlaThr	2048
٥y	318	CAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGTATCCGCAGTGGTGGTT	259
qa	2049		2061
ογ	258	GGTAAAGATCAGGCCCTGATCGGACACTGTGATACCGGTACATCCGCCACCGAAGATAAC	199
QQ	2062	ThrProAspAlaLeuAlaAlaHisLeuValThrAlaLeuSerAla	2076
Qy	198	CACGCCATTGCCAATGGACGGCTTGTCGAAACTGTAGAGCGAATCCAACGG	148
qa	2077		2091
Οy	147	GAGCGTAAAGCCGAGCTCAGGTTCGATCCAG	115
qa	2092	AsnLeuProThrLeuAlaArgAspGluAlaThrArgAlaGlnIleThrThrArgLeuGln	2111
٥y	114	ATTCTCCTG 106	
qa	2112	AlaileLeu 2114	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	SULT 12 -09-370 Sequence Sequence Sequence Sequence APPLICE AP	SSULT 12 5-09-370-700-3 Sequence 3, Application US/09370700 Betant No. 6274350 GENERAL INFORMATION: APPLICANT: Baltz, Richard H APPLICANT: Baltz, Richard H APPLICANT: APPLICANT: Treadway, Patti J APPLICANT: Treadway, Patti J APPLICANT: Treadway, Patti J APPLICANT: Waldron, Clive TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide FILE REFERENCE: 50489 DIVI CURRENT APPLICATION NUMBER: US/09/370,700 CURRENT APPLICATION NUMBER: US/09/370,700 EARLIER APPLICATION NUMBER: US 09/36987 EARLIER FILING DATE: 1998-03-09 NUMBER OF SEQ ID NOS: 39	

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1454
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1621 AlaSerLeuArgMetLeuProArgGlyGlyArgPheLeuGluLeuGlyLysThrAspVal 1640
                                                                                                                                                                                                                                                            2139 TIAGATCAACTTCAGCTCTTGGATGAGACGGGGGCACTGACCCCATTTGTCAATCATGAA 2080
                                                                                                                                                                                                                                                                                2079 GAGAACGTAGCGGATGTCCACGCT------GATTGTGCGCTGCAGATCGGG 2035
                                                                                                                                                                                                                                                                                                                                                                                    2034 TTCGAACTCGATGTCACCACTCATAGCTTCCCAGTTGCCATCGAAAGCAAGACCGATCAG 1975
                                                                                                                                                                                                                                                                                                                                                                                                                1455 Met------TyrProGlyValAlaSerLeuGlySerGluGly 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1974 ACGCCCGTTCTTATCGAATAC-----GGGGCTACCGGAGTTACCGCCCGTGATGTCGTT 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1920 GTTCGATAGGAAAGCGATATGGAGCTGACCGTTCTCGGCATAGCGACCATAGTTTTTGGT 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1821 ------ATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCTTGCCTGTCGTATG 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1773 ATAGTTGTACCAGGCACCGTCCTGCGGTTCATATCCCTTGATGGAGCCGTAGCTCATACG 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1713 CATGGTGAAGTTGGCATCGCTCGGCAGAGCACGTCCGGGGTACATCTCACGCAAACCGGC 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1574 AspLysTrpGlnAlaValGluLeuSerArgGluHisLeuAlaSerSerArgThrCysAsp 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1653 ---AAAGAAAAAGACGCTTGCCCTTCTCAATGGCATAGGCATTGGCCATCGCATCGGCCTG 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1594 PheGluGinGinPheLeuGiyAlaThrGlyGlyArgGlyValAsp-----ValValLeu 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATAGCGCGAGCAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGAT 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1467 AlaGlyValValValGluThrGlyProGlyValThrGlyLeuAlaProGlyAsp-----
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161
100
274
308
33
                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                           ; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-3
                                                                                                                      0.0213
119.00
30.96%
19.10%
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2152
TYPE: PRT
                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                           Alignment Scores
                                                                                                                                                                                    Query Match:
DB:
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Qy Db	1506	CTTGTCGCTAT ::: ArgileGlyGl
Qy	1449	GTCTGCATACTT
QQ	1681	늰
Qy.	4 1	ATTACATT CTTGAATATATGGGGGAGCTTGTCGGCAGGGATACGCGGCG 136
QQ	0	isLeuSerGInAlaArgHisValGlyLysLeuValLeuThrMetProProVal 172
Oy	1359	ACAAT
QQ	1721	AlaAlaGlyThrVal
QY	1338	CAGCACCTTACGGTCGAGCGAGGGAGGTAGTCTTGTACTTGTCGTCAAGCGATTT 1282
qq	1741	- 50
QY	1281	GAGGATACCGGCATGAGCATCAGGATTTGTAGCCAATGCGTTGGC 1237
qa	1761	
ογ	1236	CGCTCAAAT
qq	1781	rLeuGlnAlaCysAspValAlaAspArgGluThrLeuAlaLysVal 1
οy	1182	GGCTCC
Dp	1797	
Qy	1122	GCCGTTCTTACGGATCCAGTCTGCGAA
qa	1807	
Qy	1062	CACGCTTACGACCTATCACGTC
Dβ	1823	gProLysValAspGlyAl
QY	1035	ACGAGGGAGACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAGCATA 976
QQ	1842	AsnLeuLeuGluLeulleAspProAspValAlaLeuValLeuPheSerSerValSerGly 1861
Qy	975	CTTGCTGGCATATTTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCTTC
qq	1862	ValleuGlySerGlyGlyGlnGlyAsnTyrAlaAlaAlaAsnSerPheLeuAspAla 1880
QY	915	TTGCTTGATACCGCGAACTTCGATACGAGGATTGTTCTC
Db	1881	LeualaGlnGlnArgGlnSerArgGlyLeuProThrArgSerLeuAlaTrpGlyProTrp 1900
Qγ	877	877
QΩ	1901	aGluHisGlyMet
Οy	876	GTTTCGATACG
QQ	1921	GlyLeuLeuProIleSerThrGluGluGlyLeuSerGlnPheAspAlaAlaCySGlyGly 1940
οy	852	CCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCATAGTC 796
qq	1941	.:.
Qy	795	CATGGAT
q _Q	1961	PheSerVal 1969
Qy	735	TGCTGTATTCGGCCGGCCGG
qq	1969	1969
Qy	675	GTCGCCGTGTGACGCGGCCACATCCAGTTGTCC

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2048
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                                                                                                     2092 AsnLeuProThrLeuAlaArgAspGluAlaThrArgAlaGlnIleThrThrArgLeuGln 2111
                                                                                                                                                                                                                                                                                                             --- ACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT 379
                                                                                                                                                                                                                                                                                                                                                                                               CACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACCATCGCG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTAAAGATCAGGCCCTGATCGGACACTGTGATACCGGTACATCCGCCACCGAAGATAAC 199
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                                                                                                                                            555 ITCGITGTIGGAATAGAAAGGCICTACGAIGCAGAGIIGGIICCICGICIGCAITITICTII
                                                                                                                                                                                     1985 LeuArgLysArgLeuGlyArgLeuProAspAlaGluGlnHisArgIleLeuLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                    2025 GlyThrPheLysValLeuGlyPheAspSerLeuThrValValGluLeuArgAsnArgIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 -----GAGCGTAAAGCCGAGCTCACGCATCGATCCAG
                                                          615 GCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAAGTA
                                                                                                                                                                                                                             TTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGACGCTCCATCTCGTCAGTGAT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STATE: California
COUNTRY: United States of America
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Patent No. 5962643
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 5962643e1
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 43
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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APPLICATION NUMBER: US
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ADDRESSEE: Pretty, S
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2112 AlaIleLeu 2114
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996 TTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGA 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --CCAACGCATTGGCTACAAATCCTGATGCTCA 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TATGGCGATGTATTGTCTTTCTCTCGAAAAGGCTTATAGGA 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   762 CGCTGCCGTATCCATGCAAGGC----TACAAGGCTGACGACTATGCCATGACCATCGG 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 eAlaProAsnAspGlyGluCysHisLeuSerProLysGlyGluTyrThrHisSerThrLe 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 uGlnAspTyrProSerIleSer-----GlnIleAsnGlnLysValLysAspAsnAla11 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          936 GAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTA 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 eAsnIleIlePheAlaValThrAlaSerGlnLeuSerValTyrGluLysLeuValGluHi 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------AsnAspSerSerAsnValVa 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 GGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: ::: 315 ValPheSerThrAspAla-GlyPheHisTyrAlaGlyAspGlyLysLeuGlyGlyValII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 TITCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GlyAsnLeuAsp-----AlaProGluGlyGlyPheAspAlaIleMetGlnAlaIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702 TGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1269 TGCCGGTATCCTCAAATCGCTTG------------
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119
66
201
211
26
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                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                      US-10-008-355-1 (1-2139) x US-07-728-215-33 (1-846)
                                                                                                                                                                                                                                                                                                                Indels:
Gaps:
 8717
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELERAX: (619) 535-849
INFORMATION FOR SEQ ID NO: 33:
                                                                                                           LENGTH: 846 amino acids
TYPE: AMINO ACID:
STRANDEDNESS: single
                                                                                                                                                                                                                                          0.0227
115.50
30.99%
19.93%
3.02%
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                 single
                                                                                                                                                                  linear
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Best Local Similarity:
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                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                   US-07-728-215-33
                                                                                                                                                                                                                                                                                                                  Query Match:
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ERAL INFORMATION:

ογ	1291 1291	GENE
QQ	507 ysGluAsnProGlySerIleGlyTyrGlnValGlnAlaAsnSerCysSerGlyHisGlyT 527	A A P
ΟY	1292ACGA 1295	IL
qq	527 hrSerMetCysGlyIleCysAsnCysAspAspSerTyrPheGlyAsnLysCysGluCysS 547	OO
δŏ	CAAGTACAAAGACTACCTCC	
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Qy Dp	1323 CGACCGTAAGGTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAA 1382	8
٥y	1383 GCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATT 1421	
qq		CO
δŏ	CAAAGGCGACACGAAGTATCCAGA :::	
g	GluArgAsnArgAsnGlnLeuCysSerGlyProAspHisGlyThrCysGluCysGlyArg	PR
oy D	1449 CTTCGTATTCGACAAGACTGTGGTTCCTTATAGCGACAAGTTCCA 1493 ::::::::::::::::::::::::::::::::::::	; AT'
Qy	1494 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGC 1553	
qq		H
οy	1554 AGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCGCGCTATTCAGGCCGATGCGAT 1610	INFO
qq	660GlyThrCysGluCys 664	,
Qy	1611 GGCCAATGCCTATGCCATTGAGAAGGGGCAAGCGTTTTCTTTGTTTG	
QQ	665 GlyValCysLysCysThrValAsnAspGlnGlyArgPheSerGlyArgHisCysGluLys 684), MO
oy Op	1671 GTACCCCGGACGTGCTCTGCCGAG	Alignme Pred. N
ô	1707 CACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGC 1760	Score:
qq	ThrGln	Best Lo Query M
Qy	1761 CTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGA 1820	DB:
qq	722 PheValProValGlyValGluLys-ValGluIleAspGluThrLysAspGluGlnMetCy 741	
۲۵ - و۲	1821 TGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTA 1880	
, 8	TGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACAACTACAACTAACT	. 0y 7
ga Ga		Dp 3
Οy	1927ATCACGGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCG 1973	Qy 7
qq		
οy	1974 TCTGATCGGTCTTCGATGGCAACTGGGAAGCTATGAGT 2016	ν. Αυ
qa	790 -LeuValGlyLeuAlalleLeuLeuLeuTrpLysLeuLeuThr 803	
RESU US-C	RESULT 14 US-08-938-085A-33	
 R	Sequence 33, Application US/08938085A Patent No. 6339148	6 40

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282 GlyAsnLeuAsp-----AlaProGluGlyGlyPheAspAlaIleMetGlnAlaIleAla 299
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APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
ITILE OF INVEWTION: A No. 6339148el Integrin Beta Subunit and Uses
ITILE OF INVENTION: Thereof
IUMBER OF SEQUENCES: 62
:ORRESSPONDENCE ADDRESS:
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                                                                                                    ...ureSSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
SURMATION FOR SEQ ID NO: 33:
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Gaps:
                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vers CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A FILLING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     5: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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115.50
30.99%
19.93%
3.02%
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MEDIUM TYPE: Floppy
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ZIP: 94111-3834
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CORRESPONDENCE ADDRESS:
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APPLICANT: HERSKOWITZ
APPLICANT: LI, JOACHI
APPLICANT: GAVIN, Kim
TITLE OF INVENTION: O
NUMBER OF SEQUENCES:
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SOFTWARE: PatentI
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                 996 TTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAA 1055
                                                                                                                                                            1056 GCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTC-- 1113
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                                                                                                                                                                                                                                                        1114 -------TATGGCGATGTATTGTCTTCTCTCGAAAGGCTTATAAGGA 1154
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::: | | | | | :: : :: 372 eAsnIlellePheAlaValThrAlaSerGlnLeuSerValTyrGluLysLeuValGluHi 392
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                                                                                                                                                                                                             ----- AsnAspSerSerAsnValVa 409
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erAlaThrAspLeuThrSerLysPheAlaAsnAspThrSerCysArgAlaAspSerThrS
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TGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGAC------- 1926
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rSerGluGlnGlyGluLeuHisValTyrAlaGlnGluAsnLysGluCysProAlaLysVa 775
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685 CysPro---ThrCysSerGlyArgCysGlnGluLeuLysAspCysValGlnCysGlnMet 703
                                                                                                               TyrLysThrGlyGluLeuLys----AsnGlyAspAspCysAlaArgAsnCysThrGln 721
                                                      1707 CACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGC--
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GAVIN, Kimberly
FENTION: ORIGIN OF REPLICATION COMPLEX GENES
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                                                                                                                                                                                                                                                                                                                                                   741 sLysPhePheAspGluAspAspCysLysPheMetPhe-------
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REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08484105
Patent No. 5589341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAURENSON, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
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BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 494-8700
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 885 amino acids
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FOSS, Margit
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MEDIUM TYPE: Floppy
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PCAC 111	CAACCACCACTG	. да 	
eHi:	LeuserAlaTyrWetIleHisGluValArgLeuAsnThrSerAsnTyrVal 84	Qy	
ıTyr	Cognication 281 :::	qq	
TAT-	-TATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGGGA 323	Qy	
eTyr.	GlnLeuAspGlyGluPheTyrGluThrAsnLySGluLySGlyAspLyS-PhePheGluGl 124	3 8	
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FGAAC		0y	
InPhe	eTyrLeuArgAspLeuGlnPheValAlaAsn	3 8	
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CCAACAAC	-GTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGA 587 :: :: eGluGluUxslleArGerSerAsnProLvsValSerLeuGluUxrIeuarak 214	yo da	
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ACAA	CGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATC 813	Oy	159
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qq	332	roLeuGlnProSerAlaValHis
Qy	066	CTCGCTCGTCTTGACGTGAT
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Qy	1050	CGTAAGCGTCCCGACGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAA 1
qq	360	SerLysArgTyrLysAsnProLy 3
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QCI	7	AlaAlaAspPheAspAsnTyrLeuProAlaArgGluAsnGluPheAlaSerIleTyrLe 45
δλ	œ	TCGCTT1
qq	452	SerLeuTyrSerAlaIleGluAlaGlyThrSerThrSerIleTyrIleAlaGlyThrPr 47
Qy	1291	GACGACAGIA
Dβ	472	reuThrValArgGluValValLySAspLeuMetThrSerAlaAs 49
Qy	1326	SCCCGCCATG
QQ	492	GlnLysGluLeuProArgPheGlnTyrIleGluIleAsnGlyLeuLysIleValLys 5
Oy	1365	TCCCTGCCGACAGCTCCCCGATATATTCAAGAATGTAATC
qq	512	spSerTyrGluValPheTrpGlnLysIleSe
Qγ	1419	AAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTC
qq	528	
Qγ	1479	CATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAÄGG
qq	546	
QY	1539	SAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTC
qq	547	 ValLeuLeuAsp
Qy	1599	CCGATGCGATGCCCAATGCCTATGCCATTGAGAAGGGCAAGCGT
qq	567	
Qy	1650	CCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG
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Search completed: May 16, 2003, 12:39:14 Job time : 73.5 secs

Title: Perfect score:

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Scoring table:

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Sequence 1068, Ap
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Sequence 10, Appl
Sequence 11918, A
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Sequence 958, 1
Sequence 57, At
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTOR: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT FALLING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR PILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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US-10-034-623-62

US-10-13-990-45

US-10-196-935A-2

US-10-196-935A-2

US-09-945-917-57

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US-09-945-917-918

US-09-945-917-918

US-09-909-567B-44

US-09-909-567B-426

US-09-815-242-11918

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US-10-100-049-23

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US-09-933-263-1068
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US-09-815-242-13382
US-09-815-242-13684
US-10-008-355-18
US-10-192-584-6
US-09-920-552-103
US-09-920-552-103
US-09-920-538-106
US-09-920-538-106
US-09-920-538-106
US-10-101-464A-979
US-10-171-311-83
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US-09-920-552-13
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ORGANISM: Porphyromonas
   Percent Similarity:
Best Local Similarity:
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LENGTH: 712
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-MODEL-frame+.n2p.model.-DEV=xlp
-Q-Acgn2_1/USPTO_spool/US10008355/runat_16052003_110341_9460/app_query.fasta_1.2311
-Q-Acgn2_1/USPTO_spool/US10008355/runat_16052003_110341_9460/app_query.fasta_1.2311
-Q-Acgn2_1/USPTO_spool/US10008355/runat_160Fix=n2p.rapb -WINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -SGRAT=1 -END--1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MATCH=0.0
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT—pto -NORM=ext -HRAPSIZE=500 -NINLEN-0
-MAXLEN=2000000000 -USER=CS10008355 (eCGN_1 1.25 (erunat_16052003_110341_9460
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                       APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Benbula, Agnieszka
TITLE OF INVENTION: Dipeptidyleptidases And
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
GlnCysProArgLeuIleGlnGluLeuLysLeuIle
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US-10-008-355-8
; Sequence 8, Application US/10008355
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10008355;
Patent No. US2002016475911
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Botempa, Jan S
TILE OF INVENTION: Dipeptidylpeptidases And Met;
FILE OF INVENTION: Dipeptidylpeptidases And Met;
FILE OF INVENTION: Dipeptidylpeptidases And Met;
FILE OF INVENTION: Dipeptidylpeptidases
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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US-10-008-355-9
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
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Best Local Similarity:
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
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Mismatches:
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Matches:
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                  60/246,827
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/2
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEO ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                          8.02e-69
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49.218
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US-10-008-355-7
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Query Match:
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LENGTH: 716
TYPE: PRT
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772 TCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACG 831 [11] [11] [11] [11] [11] [11] [11] [11	309 SerLysGlnAsnProAspileGlnValLysTyrAlaSerThrLeuAlaGlyLeuAsnAsn 328 994 TATTGGAAGAATTCGATGGGTATGACCGCGCTCTCGTCTTGACGTGATAGGTCGT 1053 329 ThrSerLysAsnPheAspGlyGlnLeuAspGlyPheArgArgIleAsnAlaIleGlyGln 348 1054 AAGCGTGCCGAGGAAAGACTTCGCAGATCCGTAACAACGGC	GlualaLeualaalaHisGlnThrLeuValaspLeuThrGluGlnTyr	1270	ValTrpLeuGlyAspGlyIleProAlaThrCaAGAATGTAATCGACAAGAATTCAAA ValTrpLeuGlyAspGlyIleProAlaThrLeuLysArgLeuGlyAspThrLysLeuSer GGCGACACGAAGAAGTATGCAGACTTCGATTCGACAAGAGTGTGGTTCTTATAGCGAC SerSerGluGluArg	GGATGCGCATTCCAAGAGCGTAATAGCTGCTGCTATTCAGGCGTT 160
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TATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAAC-----GGT
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F: Banbula, Agnieszka
INVENTION: Dipeptidylpeptidases And Methods Of Use
REBUCE: 235.00440101
PPPLICATION NUMBER: US/10/008,355
FILING DATE: 2001-11-08
FILICATION NUMBER: US 60/246,827
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q	71	tAsnAlaVallleSerLeuGlyGlyCysThrAlaSerPheValSerProLysGl 89	
λχ	246	CCTGATCTTTACCAACCACCACTGCGGTACGGTGCTATCCAGAGCCAAAGCACGGTGGA 305	
ą	83	yLeuValValThrAsnHisHisCysAlaTyrGlySerIleGlnTyrAsnSerThrProGl 109	
λ	306	36	
g	109	uLysAsnLeuLeuGlnAspGlyPheLeuAlaLysThrPheAlaAspGluLeuProAlaAl 129	
2y Op	363	TCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGAAGGTAGAAGG 422 	
· λ	423	ACAGCTCAAGGGTATCACTGACGAGGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCA 482	
q	149	aGlyLeuGluAsnLysThrGlyArgGluPheTyrGl 161	
λλ	483		
ą	161	nGlyValGluAsnGlnGluLysAlaLeuValAlaGluCysGluLysAspGluGlyTyrAr 181	
74	522	CTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATT	
Q C	181	20	
λ Sp	582	.CAAGGANGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATAC 641 ::: ::	
à	642	GGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGG 70	
q	221		. ,
λ	702		
q	241	::: :::	
λλ	762	CGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCC 821	
q	261	eLeuLysValSerAlaLysGlyValSerGluGlyAspPheValMetValAlaGlyTyrPr 281	
λλ	822	GGGCAGTACGGATCGCTACCTCTTGGGGTGGGAAGATCGTATCGAAAA 875	
අ	281	oGlyArgThrAsnArgTyrArgThrAlaThrCluValGlnAsnGluPheGluTrpAlaTy 301	
λλ	876	CGAGAACAATCCTCGTATCGAAGTTCCCGGTATCAAGCAAG	
දු	301	rProGluGlyLysMetLeuArgGluArgPheIleGluIleIleLysAlaThrAl 319	
λζ	936	GAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTA 995	10 (7
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qo	359	gLysAlaLeuGluAlaLysLeuAlaGluTrplleAlaLysAspSerSerArgGluAlaLy 379	
λά d	1113	CTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGCCAAGGCCAACGG 1	2
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Sy Ob	1173 398	TGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGT 122::	. 0
Σy	1221	TCGTTTTGCACAGTT	30
qq	416		

Qy		CAAAGAC
Op	426	InLeuProAspMetGlnArgGluProGlyPheGlnAspAr
δy	Ō	
g	445	eAspArgArgTyrAlaAlaSerValAspLysAlaValL
Qy	1338	GCCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGACAAGCTCCCGGATATT 1397
δλ	6	ATTCAAAGGCGACACGAAG14
QQ	483	alAsnGluAlaLysLeuAl 50
λ _o	π (AAGTATGCAGACTTCGTATTCGACAGAGTGTGGTTCCTTATAGGCGACAAGTTCCA 14
QQ Q	50	spLysMetTyrAlaLysThrGluLeuGlyAsnLysAspValArgLeuAl 520
0y	1494	AAGG
λŏ	J C	ACAGCTTCCAAGAGCCTA15
QQ	536	<pre>:::::: elleGlnPheAlaValAlaMetTyrAspThrAsnMetSerGluGluLysLysGluLysGl 556</pre>
Qy	1576	ATAGCTGCTGCTCGCGCTATTCAGGCCGATGGGATGG
Db	556	uLeuAspGlyGluLeuMetLysValArgProGlnTyrMetAspAlaIleIleAlaTy 575
δλ	(1)	9
q D	575	rAsnLeuGluGlnGlyLysProValTyr584
QY	1683	TGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGATA 1742
i i		9
Qy Db	1743	TGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCCAAGGGCGTATTGGAGAA 1802
οy	1803	CAGGATCCTAAGAGCGATGAGT
qq	621	s::
yo g	1863	CAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATC 19
a a	40	niystiniyitiyaprneiyimetiysserileAspservalriovalAsnrneLeuse bo
Qy Db	1917	
Qy	1977	GATCGGTCTTGCTTTCGATGCCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACC 2036
QQ	680	
Οy	3	0
qq	700	nGlulleAsnArgSerIleHisValAspSerArgTyrMetLeuTrpValMetLysTyrLe 720
Οy	2097	GGGTCAGTGCCCCCGTCTCAAGAGCTGAAGTTGATC 2136
qq	720	uAspHisAlaA
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TyrTyrLeuIleLysGlnLeuMetIleArgAspValArgLeuValTyrAlaProProGlu
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APPLICAMT: Travis, James
APPLICAMT: Travis, James
APPLICAMT: Barbula, Agnieszka
TITLE CANT: Barbula, Agnieszka
TITLE CO INVENTION: Dipeptidylpeptidases And Methods Of
FILE REFERENCE: 235.00440101
CURRENT PPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
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                               1642 CGTCTTTCTTTGCGGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG--
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APPLICANT: Banblia, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Met
FILE REFERENCE: 235.0044010119, CURRENT APPLICATION NUMBER: US.0110.008, 355
CURRENT APPLICATION NUMBER: US.0246, 827
PRIOR APPLICATION NUMBER: US.00/246, 827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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US-10-008-355-3
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LENGTH: 52
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APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATCHIN VOF: 2.1
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61 LysArgLeuAlaLysIleThrSerAsnLeuAspGly---LeuGluThrCysLeuAspTyr 79
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                    1990 TTCGATGGCAACTGGGAAGCTATGAGTGGTGAGTTCGAACTCGAACCCGATCTGCAGCGC
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Matches:
Conservative:
Mismatches:
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Publication No. US20030042381A1
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APPLICANT: Vandekerckhove
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DB:
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Sun May 25 15:40:17 2003

ò	628	TTCGGAGGCGATACGGACAACTGGATGTGGCGGCGTCACACGGGGGGGACTTCAGCGTATTC 687	_	
· 8	136	oProAlaValSerLys		
λ S	688	CGCGTGTATGCCGGCGACAACCGGCCGGCGGAATACAGGACAAGAACAATAAACCCTAT 747 :::		
žą ą	748	AAGC Ser		
Oy Dp	808	ACCATCGGTTTCCCGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGGAAGATCGT 867		
Qy Dp	868			
Oy Db	904			
y a	926	SRATIONG INSAFERS CAPACTAR SET 1 (1) SRATIONG INSAFERS SET 21 (1) STATE OF SET 21 (1) STATE OF SET OF SET 21 (2) STATE OF SET OF		
ر 20 م	943	GATCAGGCTACCGGTATCAAATATGCCAGCAAGTATGGTCAGGTGCTAACTATTGGAAG -:::::		
oy Dp	1003	AATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTCATAGGT		
Oy Dp	1051			
Oy Dp	1111			
O.y Db	330	CGTGAGATGACTTATTTGAGCGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTGCA 1230		
Oy Db	1231	CAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTT 1290 :::		
oy Oy	1291			
oy Og	1351	GATATTGTACGCCGGCGTATCCCTGCCGACAGCTCCCCGGATATATTCAAGAATGT :::		
Qy Db	1411			
Oy Db	1464	GAGTGGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGA 1520		
Oy Dp	1521	AAAGTTTGCCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAG 1571 ::	<u> </u>	
ογ	1572	CGTAATAGCTGCTCGC 1590		

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APPLICANT: BOGGETC, Thierry
APPLICANT: BOGGETC, Thierry
APPLICANT: Wandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: USE IN THE COMPOSITIONS CONTIANING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEO ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ATCACAGTGTCCGATCAGGGCCTGATC---------TTTACCAACCACCACTGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 TTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 CGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 GACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 GTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 TTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTC 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 LeuLysAsnLeuGlyLeuAsp------CysSerLysLeuThrLysThrAspIleAsp 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 GGATACGGTGCTATC---CAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGGT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              ; Sequence 4, Application US/09945917; Publication No. US20030042381A1; GENERAL INFORMATION:
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446 rIleValThrAlaIleArg 452
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148.50
37.48%
20.91%
3.89%
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Best Local Similarity:
Query Match:
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                                                         RESULT 9
US-09-945-917-4
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ACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGT 867	
3TATCAAGGAAGGCATCTGGA925 ::::: proSerSerArgSerSerGlyAsnAsnAsnValGlySerThrIleSerThrSerAlaLy 231	
SerLeuGluSerSerThrTyrSerSerIleSerAsnLeuAsnArgProThrSerG1 251	
ATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAG 1002 ::::::	
ATTCGATCG-:GTATGAACCGCGTCTCGCTCGTCTTGACGTGATAGGT 1050	
GTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT 1110 	
TCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	
GTGAGATGACTTATTTGAGGGAGGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCA 1230 :::::::: ::: ::: -	
AGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTT 1290 ::: LysIleAlaAla	
ACGACAAGTACCACCCCCCCGCCGCCGAAGGTGCTGCCGCCATGCTC 1350	
ATATTGTACGCCGCCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATC 1410 :::	
ACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAA 1463 	
AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGA 1520 	
AAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAG 1571 :::	
GTAATAGCIGCTGCTCGC 1590:	
68-108 108, Application US/09801368 . US20020128250A1 NFORMATION: T: Busby, Robert	 .
808 AC 868 AC 173 - 173	***Proclinierrangements*** ****Proclinierrangements*** ********************************

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APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT APPLICATION NUMBER: US 09/487,558
PRIOR PAPLICATION NUMBER: US 09/487,558
PRIOR PLING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PLING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 CGATTCCGGGTC---TTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 TAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 TATGCCAAGAACTGGCCAAAAAAAAAAATGCAGAGAGAACCAACTCTGCATCGTAGAGC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 ProserSerSerThrThrGluSerSerSerAlaProValThrSerSerThrThrGluSer 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| |||||| ::: :::::: :::||| ::: :::||| 355 ProValProThrProSerSerSerSerThrThrGluSerSerSerAlaProValThrSerSer 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 ThrThrGluSerSerAlaProValThrSerSerThrThrGluSerSerAlaPro 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TTGCCAATGCCGTGGTTATCTTCGGTG-----GCGGATGTACCCGGTATCACAGTGTCCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 ATCAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 TGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                Milne, Todd
No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
09-801-368-108
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145.00
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3.80%
Holtzman, Doug
                   Madden, Kevin
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ry Match:
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δο i	TGGTATTTGCTCCT	::: Db 835 SerSerValProValPro
3 8	occommentation and the contraction of the contracti	Qy 1664 GTGAGATGTACCCGGAC
<u> </u>	030 GUCLGCGICACACGGGCCAACTICAGCGIGITATICCGCGIGCCGGGCGGGCGGGCCGACGGGC /IS 441 DrovalThreadeacarmhrantcicorcarcaria	Db 855 SerSerSerThrThrGlu
3 8	CGGCCGAATACAGCAAAAAACCCTATAAAGCCCGTTTACT	Oy 1715 GTATGAGCTACGGCTCC
g.	 ThrGluSerSerSer	Db 875 IleThrSerSerAlaPro
. 0	764 CTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACGTTG	Qy 1763
7 a		Db 889 ThrGluSerPheSerTh
ογ	815 GTTTCCCGGGCAGTACGGATCGCTACCTCCTTGGGGTGTGGAAGATCGTATCGAAA 874	Qy 1805 AGGATCCTAAGAGCGATC
qq	::: ::	
٥٧	875 ACGAGAACATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG	Qy 1844 TCCTCGACCTCTTCCGCF
q	::: ThrGluSerSerSerAlaProValThrSerSerThrThrGluSerSer 635	Db 929 ThrSerValThrThrPro
οy	935 TGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACT 994	Qy 1877
Dp	:::	949
٥y	995 ATTGGAAGAATTCGATCGGTATGAACCGCGTCTCGCTCGTCTTGACGTGATAGGTCGTA 1054	1910
QQ		
Qy	1055 AGGGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCA 1102	1970
QQ		
δ	1103 AGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	2030
qq	687 ThrThrGluSerSerAlaProValThrSerSerThrThrGluSerSerAlaPro 706	7007
ò	1163 AGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTC 1222	
qq	707 ValProThrProSerSerSerThrThrGluSerSerAlaProvalPro 723	DD 1019 GIUINFALASEFGIUSEI
٥y	GTA	US-00-815-242-13382
qq	724 ThrProSerSerThrThrGluSerSerSerAlaProValProThrProSerSer 743	; Sequence 13302, Application; Patent No. US20020061569A1
δλ	1283 AATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCGCTCG	; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Rot
QQ	744 ThrThrGluSerSerSarAlaProValThrSerSerThrThrGluSerSerSerAlaPro 763	y APPLICANT: OHISSEN, MAIL y APPLICANT: Cyskind, Judi
oy	1343CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATA 1393	, APPLICANI: Wall, Daniel , APPLICANI: Trawick, John
QΩ	764 ValproThrProSerSerThrThrGluSerSerSerAlaproValProThrProSer 783	
ò		TITLE OF INVENTION: Identify TITLE OF INVENTION: Prob
g	784 SerSerThrThrGluSerSerSerAlaProValProThrProSerSerSerThrThrGlu 803	; FILE REFERENCE: ELITRA.01
ó d	AGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCG	CURRENT FILING DATE: 200 ; PRIOR APPLICATION NUMBER:
a .	Serservatatrovatrornrrroserserserserasniie	; PRIOR FILING DATE: 2000-0; PRIOR APPLICATION NUMBER:
oy B	1484 ACAAGTTCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543 	; PRIOR FILING DATE: 2000-0; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-0
δ	1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-1
QQ	833GluSer 834	
Oy	1604 ATGCGATGGCCAATGCCTATGCGATTGAGAAGGGCAAGCGTCTTTTTTTT	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-1

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CATCAAGGGATATGAACCGCAGGACGGTGCCT----- 1762
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alSerSerThrThrGluThrThrIleValProThrLysThrThr 928
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                                                                                                                                            ACGTGCTCTGCCGAGCGATGCCAACT-----TCACCATGC 17.14
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roSer-----SerIleProPheSerSerThr 888
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| roSerThrThrThrThrThrValCysSerThrGlyThr 948
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hrThrThrSerValThrThrSerSerThrThrThrIleThrThr 985
hrGlyThrThrValThrProSerSerSerLysTyrProGlySer 908
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PRIC PRIC NUMB SOFT SEQ I FEN TYP CRG	PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FeatSEQ for Windows Version 4.0 SEQ ID NO 13382 LENGTH: 883 TYPE: PRI ORGANISM: Streptococcus pneumoniae	Db Db	
Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB:	Alignment Scores: Pred. No.: 133.00 Matches: Score: 133.07 Percent Similarity: 3.03 Matches: Conservative: Mismatches: 166 Query Match: 10 Gaps: 24	ga ka a	
US-10-(US-10-008-355-1 (1-2139) x US-09-815-242-13382 (1-883)	gg ,	
Qy 5 Db	574 GATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT 609 11111111	ko qa	
Qy 6 Db	610 CCCAGCTCTGTAGGTAGGTCGGAGGCGATACGGACTGGATGTGGCCGCGTCACACG 669	oy D	1549 CCGGC 332 AlaLe
Oy 6 Db	670 GGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACCGGCCGG	do dy	
Oy 7 Db	730 AAGGACAATAAACCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAG 789	Qy Db	
Oy 7 Db	790 GCTGACGACTATGCCATGACCATGGTTTCCCGGCAGTACGGATCGCTACCTCACT 846	Oy Db	
Oy g	847 TCTTGGGGTGTGGAAGATCGTATCGAAACGAGAACATCCTCGTATCGAAGTTCGCGGT 906 ::: :::	Qy Dp	
Oy od	907ATCAAGCAAGGCATCTGGAAGGAAGCCATGAGGCGCAGATCAGGCTACC 954	Qy Dp	
Qy g	955 CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATC 1011	Qy Dp	1819 GATGA 435 AspGl
Oy 10	1012 GGTAFGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGA 1071 :::::: ::: ::1 147 ThrLeuaspGluGlyLeuSer	RESUUS-CUS-C	RESULT 12 US-09-815-242-1 ; Sequence 1368 ; Patent No. US
Oy 10 Db 1	1072 GCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGC 1119		GENERAL INFOR APPLICANT: H APPLICANT: APPLICANT:
Qy 11 Db	1120 GATGTATTGTCTTCTCGAAAGGCTTATAAG 1152 		APPLICANT: APPLICANT: APPLICANT: APPLICANT:
Oy 13	1153		APPLICANT: TITLE OF INV TITLE OF INV FILE REFEREN
0y 1.	1183 TATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC 1242 219 ThrargProGluthrMetPheGlyAspVal228		CURRENT APPL CURRENT FILI PRIOR APPLIC PRIOR FILING
0y 1:	1243 GCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTAC 1302		

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SGTACAACTATCATACGACAGGCAAGGCCGTATTGGAGAAGCAGGATCCTAAGAGC 1818
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                                                                ACTACCTCCCCTCG--------CTCGACCGTAAGGTGCTGCCGCCATG 1347
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-----AspProArgTyr 239
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TET Oblsen, Kari L.
TET Zyskind, Judith W.
TET Wall, Daniel
TET Wall, Daniel
TET Trawick, John D.
TET Yamancto, Robert T.
TET Yamancton Genes in
TERRACE: ELITRA, 011A
APPLICATION NUMBER: 05/191,078
TELING DATE: 2000-03-21
TELING DATE: 2000-03-21
TELING DATE: 2000-05-23
TELING DATE: 2000-05-23
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Matches:
Conservative:
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Indels:
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2010-12-16
PRIOR FILING DATE: 2010-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARRE: FASCERQ FOR WINGOWS VERSION 4.(5)
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REPERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR PPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TOKIYOSHI, Sachio
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                            Version #1.30
                                                                                                                26
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                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/192,584
FILING DATE: 11-Jul-2002
PRIOR APPLICATION NUMBER: US/09/077,098
FILING DATE: 19-May-1998
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1997
                                                                                                                                                                                                    US-10-008-355-1 (1-2139) x US-10-008-355-18 (1-26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,618
REFERNCE/DOCKET WUMBER: TOKUNAGA=1
TELECOMMUNICATION :
TELEPHONE: 202-628-5197
                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W.,
CITY: Washington
                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10192584
Publication No. US20030027987A1
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masashi
                                                                                                                                                                                                                                                                                                                                                                                                                        MATSUO, Kazuo
HAMADA, Fukusaburo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCE CHARACTERISTICS:
LENGTH: 2042 amino acids
                                                            ORGANISM: Porphyromonas gingivalis
US-10-008-355-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KORNBAU, Anne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
         SOFTWARE: Patentin version 3.0 SEQ ID NO 18 LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                CGTGAGCTCGGCTTTACG 144
                                                                                                                                                                                                                                                                                            21 ArgGluLeuGlyPheThr 26
                                                                                                             0.0237
122.50
96.15%
96.15%
3.21%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: USA
NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001
                                                                                                                                      Percent Similarity:
Best Local Similarity:
NUMBER OF SEQ ID
                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-10-192-584-6
                                     LENGTH: 20
TYPE: PRT
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DB:
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9
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GTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATC 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAAC 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTGGGTGGTACCGAGGTG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AlaLysSerAla-----GlyAsn-----GlnSerValSerLeuGlyGlnAsnSerTrp 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyTyrGlyAlaThrAsnAspArgSerAlaThrGlyAlaIleAlaLeuGlyVal---- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TATGCCATGACCATG 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AsnLeuAsnProSerGlyAlaGluSerValGlyThrAsnSerProGlnGlyValAlaile 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      925 AAGGAAGCCATGAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAG 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------Gln 163
                                                                                                                                                                                                                                                                                                                                                                           550 AACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTGCTCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GTGTATGCCGGTGCCGACAACCGGCCGGAATACAGCAAGGACAATAAAACCCTAT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        814 GGTTTCCCGGGCAGTACGGATCGCTACCTCACT------TCTTGGGGTGTGGAAGAT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||| ::::::|||| :::
73 LeuGluValTyrSerSerSerValLysLeuSerThrValSerAlaGlnSerAsnSerVal 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...---ValSerGluLeuAlaAsnAsnLysAspLysThrAlaSerGlnLysAsnThr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 HisAsnThrAlaPhePheGlnProLeuPheThrLysCysThrTyrLeuAlaLeuLeuIle 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- GlnLeuAlaAsnAlaLysTrp 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AsnLysValPheLysIleLysTyrSerValValLysGlnGluMetIleVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGAÏGTGGCCGCGCGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 AAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGAC----
                                                                                                                                                  2042
140
87
223
180
35
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| AsnGluSerThrAlaProSerSerValThrIleGlyLys-----
                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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9
                       MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                670 GGCGACTTCAGCGTATTCCGC-----
                                                                                                                                               0.636
118.50
36.038
22.228
3.108
TOPOLOGY: linear
                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Patent No. US20020094576A1

1319 CCCCCCATGCTCGATATTGTACCCCCCCTATATCCCCCCATACCTACC	1339 CCCCCCOMPGETCGATATTCTACCCCCCCCTCATACCCCCCCATACCCCCCCC	QQ	247ThrLysTyrAsnAspLysLeuProAlaThrAlaTrpAsnGlyThr 261	
22 Glythr	22 Glyth: ————————————————————————————————————	οy	339 CCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTC 139	
1399 AnGANGTORN	1999 AnGANGTORN	Dp	GlyThr	
214 SerGluteuTyrHatGlyLysGlnThrAsnGlyArgAspTyrAspThrThrArgAsp 293 1438	274 SerGluiceuTyrMetGlytyScluthrAsnGlytrgAspTyrAspTh;ThrThrAtgAsp 293 1488	٥y		
1438	1438	QQ	SerGluLeuTyrMetGlyLysGlnThrAsnGlyArgAspTyrAspThrThrThrArgAsp	
24 ProAssitysProclutalEpherytitysPheSerAspPheitysGilytysTalsaritr 113 1462 AAGAGTGTGTTCCT - TATACCCACACTTCCATGCTCACTCCACACACACACACAC	249 ProbantystroCiullaPheryriusPheSerbapPheSerba	٥y		
1462 AAAAGTGTGCTTCCT - TATABCCACAAGTTCCATGCACAAGTCCCATGGCACAAG 1518 314 PrOThtAlaSerPrOThtTytAlaGlyLysleuGlyAlalle 315 PROTHALASERPOTHTTYTALAGGLYLysleuGlyAlalle 317 FINE	1462 AAAAGTTGGTCTCTTATAGGGACAAGTTCCATGGACATGGATGTGATGGATGAGGACAGGGACAGGGACAGGGAGGAGGAGGAGGGAG	qq	ProAsnLysProGluAlaPheTyrLysPheSerAspPheLysGlyLysTyrValAsnThr	
314 Profitalsserbröthrfyjalasijvjaleudijajie; 1519 GAAAGTTGCCAAGGCAACAACATCGCAGATACAGCCTTCCAAGCCTA	314 Prothralaserbröthrüjkladlyüjsleudlyälie	οy	AAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG	
1519 GARANGTITGCCAAGGCTATCGAGAAGATCCGGAGTAGACCTTTCCAAGAGCGTA	1519 GAAAAGTTTCCAAGGCTATCCAGGATCAAGGATCAAGGCTATTCCAAGGCTATT-	qq	ProThralaSerProThrTyrAlaGlyLysLeuGlyAlalle	
328	328	٥y	519 GAAAAGTTTGCCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTA 157	
1576	1576ATAGCTGCTGCTGGCGATGCGCATGCGATGCCATGCC	QQ	AlaLeuGlySerArgThrIleAlaAlaGlyGluMetSerThrAlaValGly	
345 SerieukiaPhekiaLeukiaAspirgSerThrälake	345 SerieukiaPheklaieukiakspirgserthrälaket	٥٧	576ATAGCTGCTGCGCTATTCAGGCCGATGCGATGCCAATGCCTATGCCATTGAG 163	
1633 AAGGGCAAGCGCTCTTTCTTGCCGGTTTGCGGGAGATGTACCCGGACGTGCTCTGCCG 1692 1693 AGCGAAGCGTCTTTCTTTGCCGGTTTGCTGAGATGTACCCGGACGTGCTTGCT	1633 AAGGGCAAGCGTCTTTCTTGCCGGTTTGCGTGACATCTACCCGGACGTCTCGCG 1692 358GlyLeudgerhealthalling	Dp	SerLeuAlaPheAlaLeuAlaAspArgSerThrAlaMet	
1693 AGCGATGCC	358GiyLeuArgSerPheValilaLysaspialavalGlyGlTyhrAlaliteGly 374 1693 AGCGATGCC	οy	AAGGGCAAGCGTCTTTTGCCGGTTTGCGTGAGATGTÀCCCCGGACGTGCTCTGCCG 1692	
1693 AGCGATGCC	1693 AGCGATGCC	qq	GlyLeuArgSerPheValAlaLysAspAlaValGlyGlyThrAlaIleGly 374	
375 GludiuSerArgThrPheAlaLysAspSerValAlaIleGlyAshLyThrGluAlaSer 1720 AGCTACGGCTCCATCAAG	375 GludiuSerargThrPhealaLysAspSerValAlaIaleGlyAsnLyThrCluAlaSer 1720 AGCTACGGCTCCATCAGG	ογ	AGCGATGCCAGCTTCACCATGCGTATG 171	
1720 AGCTACGGCTCCATCAAG	1720 AGCTACGGCTCCATCAAG	QQ	GluGluSerArgThrPheAlaLysAspSerValAlaIleGlyAsnLysThrGluAlaSer	
395 ASIANAGUYSERMETALATYCLYTYLLYSALALYSALAVALGLYALAGUALAGUALAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUA	395 ASINALGIPSERMETALGLYTYLLYSALGLYSALGVARIGLYALGILEALG 1738GGATATGAACCGAGGACGGTGCCTGGTACAACTATCAACGACGCAAGGGGTA 1738GGATATGAACCGAGGACGGTGCCTGGTACAACTATCAACGACAGGCAAGGGGTA 119 11	οy	AGCTACGGCTCCATCAAG	
1738GGATATGAACCGCAGACGTCCTGGTACAACTATCATACCACGCAACGCGTA 115	1738GGATATGAACCGCAGGACGTCCTGGTACAACTATCATACGACGCAACGCGTA 115	QO	AsnaladlySerWetAlaTyrGlyTyrLysAlaLysAlaValGlyAlaGlyAlaIleAla	
115 IledlyThrGluValAlaAlaClySPhenSnScrHisGlnThrGlyAsnLeuLeu 1795 TTGGAGAAGCAGGATCCTAAGAGCGATGATTGCCGTA 135 GlnAspAsnAsnAlaTyrAlaThrLeuLySAsnAlaAspLySSerAspAspThrLys 1834 CAGGAGAATATCCTGCACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAACGGT 111	415 IledlyThrGluValAlaAlaClySPheAsnScrHisGlnThrGlyAsnLeuLeu 1795 TTGGAG	Οy	GGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTA	
1795 TTGGAGAGCAGGATCCTAAGAGCGATCAGAG 13 GlaspasnasnalaTyralaThrLeuLysasnalaAspLysSerAspAspThrLys 1834 CAGGAGAATATCCTCGACCTCTCCGCACAAAACTATGCCGATGCCGAACGGT 1845 ThrGlyAsnalaIleThrValPheThrGlnSerPheAspAsnMetLeuThrAsnGly 1894 CAGCTCCATATCGCTTTCCATACGACAACACGACATC	1795 TTGGAGAGCAGGATCCTAAGAGCGATCAGAGCGATCAGAGAGCGATCAGAGAGCGATCAGAAGAGCGATCAGAAGAGCGATCAGAAGAGCGATCAGAAGAGCGATCAGAAGAGCGATCAGAGAGAG	qq	lleGlyThrGluValAlaAlaGlyAlaLysPheAsnSerHisGlnThrGlyAsnLeuLeu	
435 GlnAspAsnAsnAlaTyrAlaThrLeuLysAsnAlaAspLysSerAspAspThrLys 1834 CAGGAGAATATCCTCGACCTCTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGT	435 GlnAspAsnAsnAsnAlaTyrAlaThrLeuLysAsnAlaAspLysSerAspAspThrLys 1834 CAGGAGAATATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGT	. λο	TTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTA	
1834 CAGGAGAATATCCTCGACCACAAAACTATGGTCGCTATGCCGAGAACGGT 454 ThrGlyAsnAlalleThrValPheThrGlnSerPheAspAsnMetLeuThrAsnGly 1894 CAGCTCCATATCGATCGAACAACGACTC	1834 CAGGAGAATATCCTCGACCACAAAACTATGGTCGCTATGCCGACAACGGT [1] :: ::	οp	GlnAspAsnAsnAlaTyrAlaThrLeuLysAsnAlaAspLysSerAspAspThrLys 4	
454 ThrGlyAsnalaileThrVailHeThrGlnSerPheAspAsnMetLeuThrAsnGly 1894 CAGCTCCATATGCCTTTCGAACAACGACATC	454 ThrGlyAsnalaileThrVallHI	٥y	CAGGAGAATATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGT 1899	
1894 CAGCTCCATATCGCTTTCTATCGAACAACGACATC	1894 CAGCTCCATATCGCTTTCTATCGAACAACGACATC	QQ		
473	473	0y	894 CAGCTCCATATCGCTTTCCTATCGAACAACGACATC	
1930ACGGGCGGTAACTCCGGTAGCCCGTATTCGATAAGAACGGCCGTCTGATC	1930ACGGGGGGTAACTCCGGTAGCCCGTATTCGATAAGAACGGCGGTTGATC	QQ	LeuProLeuValSerGluAsnGluThrTyrLeuThrThrSerAlaGlyAla	
490 IleLysLysThrAlaThrThrAspSerSerIalaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	490 IleLysLysThrAlaThrThrAspSerSerIaGlyGlyGlyLysAshalatlealaile 509 1981 GGTCTTGCTTCGATGGGAAGCTATGAGTGGTGACATCGACATCAGATCAGATCAGATCGACTACTCTCTTCATGATTAAC 209 2041 CTGCAGCGCACAATCAGCATCGACATCGATACTCTCTTCATGATTAAC 209 111	٥y	930ACGGCCGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATC	
1981 GGTCTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGACTCGACCCGAT 204	1981 GGTCTTGCTTTCGAACTGGGAAGCTATGAGTGGTGACATCGAGTTCCAACCCGAT 204	QQ		
510 GlySerLys-ThrPheAlaSerLysAlaAsnSerValAlaLeuGlySerTyrAlaie. 2041 CTGCAGCGCACAATCAGCGTGACGTTCTCTTCATGATTGAC :::::::	510 dlyserLys-ThrPhediaserLysalaAsnSerValalaLeuGlySerTyrAlaie 2041 CTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGAC	οy	981 GGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGACATGGACATCGAACCCGAT 204	
2041 CTGCACCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGAC :	2041 CTGCACCGCACAATCAGCGTGGACATCCGCTACGTTCTTCATGATTGAC :::::: ::: ::: 528 uAlaAspAlaGlnAsnAlaPheAlaLeuGlySerTyrSerPheValGluSerSerAlaTh 2092 AAATGGGGTCAGTGCCCGTCTCATCC 2119 548 rAsnThrIleThrIleGlyValGlySer 557 SULT 15 -09-920-552-103	qq	GlySerLys-ThrPheAlaSerLysAlaAsnSerValAlaLeuGlySerTyrAlaLe	
528 uAlaAspAlaGlnAsnAlaPheAlaLeuGlySerTyrSerPheValGluSerSerAlaTh 54 2092 AAATGGGGTCAGTGCCCGTGTTCATC 2119 1	528 ualaAspAlaGlnAsnalaPheAlaLeuGlySerTyrSerPheValGluSerSerAlaTh 54 2092 AAATGGGGTGGTGCCCCGTCTCATCC 2119 211 ::::: 548 rAsnThrIleThrIleGlyValGlySer 557 SULT 15 SOUTH 1	ōy.	CTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGAC	
2092 AAATGGGGTCAGTGCCCCGTCTCATCC	2092 AAATGGGGTCAGTGCCCCGTCTCATCC	qq	: : :::::!!!	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SULT 15 -09-920-552-103 Seminance 103. Application HS/M920652	oy Op	AAATGGGTCAGTGCCCCGTCTCATCC ::::::	
	SULT 15 -09-920-552-103 Sequence 103, Application US/099205			

```
SEQUENCE INFORMATION

APPLICANT: Griffiths, David J.

APPLICANT: Weiss, Robin A.

APPLICANT: Weiss, Patrich

TILE CANT: Weables, Patrich

TILE REFERENCE: Abbott Labs

CURRENT APPLICATION NUMBER: US/09/920,552

CURRENT APPLICATION NUMBER: US/09/920,552

CURRENT APPLICATION NUMBER: 09/280,329

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: GB 806649.1

PRIOR APPLICATION NUMBER: GB 8006649.1

PRIOR APPLICATION NUMBER: GB 8006649.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 TACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 TCTGCG-----CGTTTCTCGCAC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 GATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 GGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAG------ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 ----CGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 CGAGAACCAACTTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 CTACGATGTATTC-----AAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621 AGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tpro------177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 HisAlaPheValArgAlaValValGluMetSerProTrpPheLeuGlnGlnTrp-ArgGl 86
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162
89
252
251
251
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Matches:
Conservative:
Mismatches:
Indels:
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118.00
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521	1.743	534	1785	547	1818	567	1845	587	1857	607	1863	627	1914	647	1968	667	2028	687
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OM nucleic - protein search, using frame_plus_n2p model	126.5 3.3 666 1 D69103 DNA helicase
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Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 0.5 Fgapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0	Ladiselli Lactobacillia Penicillin bi DNA helicase valyl tran sy mucin - rat
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Database : PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Note: for a complete list of authors see reference number A59328 below A; Accession: G82627 A; Status: preliminary A; Molecule type: DNA
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	A;Residues: 1-716 <sina A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSP A;Experimental source: strain 95c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvareng</sina
\$ Query	Briones, M. K.S.; Bueno, M.K.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Casarbto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.
Score Match Length DB ID	J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E. chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Ma
1 907.5 23.8 716 2 GB2627 hypothetical prote 156 4.1 1791 2 T02345 hypothetical prote 3 154.5 4.0 1609 2 S25345 probable membrane 4 149 3.9 528 2 147141 gastric mucin (clo gastric mucin (clo f 143.5 3.8 136 1 S48478 C30C11.4 protein - 7 141 3.7 948 2 T116784 C30C11.4 protein - 7 141 3.7 948 2 T116784 hypothetical protein gastric mucin second f 139.5 3.7 1802 2 S69703 HKR1 protein precu gastric mucin f 547 (close J 139 3.6 477 2 S53362 mucin f 547 (close J 139 138 3.6 477 2 S53362	A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Oliveira, R.C.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A; Reference number: A59328 A; Contents: annotation C; Genetics: A; Genetics:
137 3.6 3570 2 T45025 133.5 3.5 1104 2 A60999 133 3.5 883 2 D97933 132. 3.3 571 2 C71528	Alignment Scores: 7.33e-54 Length: 716 Pred. No.: 907.50 Matches: 239 Percent Similarity: 49.21% Conservative: 135

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Best Local S Query Match: DB:	.1 Similarity: 31.45% Mismatches: 291 .ch: 23.76% Indels: 95 .ch: 2 Gaps: 21	
10-008	-355-1 (1-2139) x G82627 (1-716)	
п п	ATGCAAATGAAATTAAAAAGTATTCTTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG	60
61	GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT	120
121	CGAATGCGTGAGCTCGCTTACGCTCCCGTTGGATTCGCTCTACA	180
38	ProLeuLysGlnAlaGlyLeuGlnLeuSerProGluGlnLeuSerAsnLeuThrGlyA	_
181 58	. TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT :::	240 75
241	CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG::: ::	300
301	GTGGATCACGACTATCTGCGCGATGGTTTCTGCACGATGGGTGAGGAGCTTCCG :::::::::::: ::: ProLysLysAsnLeulleLysGluGlyPheAsnAlaLeuThrGlnAlaAspGluAlSer	360
361		417
	GAAGGACAGCTCAAGGGTATCACTGACAGAGTGGAGCGTCTGCGCAAAGCTCAGGAGTTTATTTA	477
1	TGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGA	n m
156	Phes	174
532	GAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTT	591 194
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652	ATGTGGCCGCGTCACACGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACACCITIIIIIIIIII	711
712	CGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTA	771
772		831.
m		891
275	AsnArgTyrAlaLeuVal	288
892	ATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGACC	933
m	ATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAA	6
309	::: SerLysGlnAsnProAspIleGlnValLysTyrAlaSerThrLeuAlaGlyLeuAsnAsn	328

-----GCCGGTATCCTCAAATCGCTTGAC 1293 ------GACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAA 1425 1426 GGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC 1485 1486 AAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAA 1545 1546 GATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTĠCTGCTCGCGCTATTCAGGCCGAT 1605 1840 AATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAAC----GGT 1893 ------CTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCC----- 1377 1606 GCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGT 1665 1666 GAGATGTACCCC-----GGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATG 1719 1720 AGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACG 1779 1780 ACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAG 1839 AAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTT 1221 424 GlualaGlyTyrGlnGluArgAspLeuProThrIleGluGlyAsnLeuLysGlnMetGlu 443 461 GluTyrAsnLysLeuPro------ValLysGlnArgValAlaalalleAsp 475 ||| :::||| ||| 476 ValTrpLeuGlyAspThrLysLeuSer 495 404 GlyvalAlaValAsnLeuTyrArgLeuAlaIleGluArgThrLysSerAspAlaGlnArg 423 501 -------LeuLysTrpPheAsnAlaAspArgAlaAlaPheGluSerSerGln 515 536 AsnLys1leArgThrGlyGluLeuLeuLysAlaArgProIleTyrLeuGlnAlaLeuAla 555 ||| :::|||||||::: ||| ::: 596 ThrLeuGlnGlyValMetAlaLys---AsnThrGlyValGluProPheAspSerProLys 614 369 GluAlaLeuAlaAlaHisGlnThrLeuValAspLeuThrGluGlnTyr-------1222 CGTTTTGCACACTTTGCCAACGCATTGGCT-----ACAAATCCTGATGCTCAT---1294 GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTG---------1054 AAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGC-349 1162 385 1336 1378 q οy qq δλ q δy qq Óγ qq δy qq δ Ωp Q QQ οy QQ οy g δ QQ QQ δý Qλ QQ οy QQ δ g Óγ d δ g ογ Q

Db 702ArgGlySerArgSerSerProGluProLysThrLysSerArgThrProProArgArg 720 Oy 498 AGAAAATGCAGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAA 551		Oy 552CGAATACTTCCTCATCGTCTACGATGT 578	Qy 579 ATTCAAGGACGTTCGTATGGTACTTTGCTCCTCCCAGCTCTGTAGGTAAGTT 629 Db 758ArgSerProSerValSerSerProGluProAlaGluLvsSerArgSerSer 774	630 CGGAGGCGATACGGACAACTGGATGTGGCCGCTCACACGGGCCACTTCAGCGTATTCCG 11111111	D.; Qy 690 CGTGTATGCCGGTGCCGACCGGCCGGCCGATACAGCAAGGACAATAAACCCTATAA 749 11	QY 750 GCCGGTTTACTTCGCTGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGAC 809 11 11 11 11 11 11 11	QY 810 CATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT 869	CGAAAACGAGAACAATCTCGTATCGAAGTTCGCGGTATCAAGCAAG	930 AGCCATGAGCGATCAGGCTACCCGTACAATATGCAGCAA 11 1 1 1 1 1 1 1 1	Qy 975 GTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	Qy 1035 TCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCG 1091	Oy 1092 TAAGAACGCAAGAGTG	QY 1134 TCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTCAGATGACTTATTTGAGCGA 1193 ::	Qy 1194 GA	QY 1224 TTTTGCACAGTTTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAA 1283	Qy 1284 ATGGCTTGACGACAAGTACAAAGACTACCTCGCTCGACCGTAAGGTGCTGCCGC 1343	YOY 1344 CATGCTCGATATTGTACGCCGGCGTATCCCTGCCG	OY 1379ACAAGGTCCCCGATATATTCAAGAATGTAATGGACAAAAAATTCAAAGGCGACACGAA 1436
Qy 1954 GTATTCGATAAGAACGCCCTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATG 2013	AGTGGTGACATCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTAC	675 SerSerasnTrpValPheaspProValMetThrArgThrIlealaValaspSerargTyr 694 2074 GTTCTCTTCATGATGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGCTGAAGTTG 2133	::::::	T02345 hypochtetical protein KIAA0324 - human (fragment) C.Species: Homo saptens (man) C.Spate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999	C; Accession: T02345 R; Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, re; J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998	Description: Sequencing or numan chromosome lbpl3.3. Reference number: Z14664 Accession: T02345 Status: preliminary; translated from GB/EMBL/DDBJ	MOLECULE type: DNA Residues: 1-1791 (RIC> Cross-references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650 Genetics:	Map position: 16 Introns: 1610/2; 1706/2 Note: KIAA0324	0.0236 156.00 34.42%	23.90% Mismatches: 2 Indels: 2 Gaps:	TCTCGGAGCAGCCTGCTGTTGGGTGCTTCAGGGTAGCCAAAGCCGACAAAGGCATGTG	011 SEKCIYSEKSERPKOGIUVAIASPSEKLYSSEKAKGT 87 GCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTT ::: ::: ::::	147 CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT	207 CGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTTACCAACCA	267 CIGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGG	327	381 GTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAAGGGTATCAC 1	441 TGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAA

Page 4

1437 GAAGTATGCACACTTCGTATTCGACAACAGTGTGGTTCCTTATACCGACAAGTT	A) RG C) CO C) CO C) CO C C C) CO C C C C	A;Residues: 1-1609 <fro> A;Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227; MIPS:YCR089 C;Genetics: A;Gene: SGD:FIG2 A;Cross-references: SGD:S0000685; MIPS:YCR089w A;Map position: 3R C;Keywords: transmembrane protein</fro>
Db 1038 erArgSerArgThrSerProValThrArgArgArgSerArgSerArgThrProProAlaI 1058 Qy 1536 TATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589 :: ::	F;4+ F;15 Alig Pred	s predicted <tml> status predicted <t length:<="" td=""></t></tml>
OY 1590 CGCTATTCAGGCCGATGCCAATGCCTATGCCATTGAGAGGGCAAGGTCTTTT 1649 11	Scor Pero Best Quer	154.50 ilarity: 35.18% Similarity: 21.19% ::
Qy 1650 CTTTGCCGGTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACCTCAC 1709	US-1	daps: 45 (1-1609)
1710 CATGCGTATGGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGTGCCTGGTACAA	Qy	74 ACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGGGTGAGC 133 :::
CTATCATACGACAGGCAAGGCGTATTGCAGAAGCAGGATCCTAAGAGCGATGAGTTTGC ::	QY	134 TCGCTTTACGCTCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATG 193 :::
1830 CGTACAGGAGAATATCCTCGACCTCTTCCGCACAAAAACTATGGTCGCTATGCCGAGAAA	Qy	194 CCGTGGTTATCTTCGGTGCCGGATGTACCGGTATCACAGTGCCGATCAGGGCCTGATCT 253 :: 812 ProLeuLeuSerThrSer 817
1890	Qy	254 TTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC 307
1950 CCCCGTATTCGATAGAACGGCCGTCTGATCGGTCTTGGTGTTCGATGGCAACCGGAAGC 1160 qp	Qy	308 ACGACTATCTGCGCGATGGTTTCTCGCACGATGGGTGGGGGGGCTTCCGATTCCGG 367
2010 TATGAGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGA	Qy	368 GTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGC 427 1
2064CATCCGCTACGTTCTCTTCATGATTGACAATGGGGTCAGTGCCCCGGTCT	. Qy	428 TCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC 487 :::::: 855 ThrGlnValSerAlaThr
	QV	488 IGGCCAAAAAAGAAAATGCAGAAAGCAATCTGCATCGTAGAGCCTTTCTATTCCA 547
SULT 3 SULT 3 SULT 3 SALA CONTRACTOR CONTRAC	QQ Dp	548 ACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTAT 601 ::: ::: :: :::
program members in youtherical protein (Saccharomyces Cerevisiae) N;Alternate names: hypothetical protein YCR1102 C;Species: Saccharomyces cerevisiae C;Date; 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000	oy Db	602 TTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAGCTGGATGTGGCCGC 661
R.Wilson, C.; Grisanti, P.; Frontali, L. Yeast 8, 569-575, 1992 **Affille: The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromos	Oy ob	662 GTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACA 709
FMID:1323009	Oy .	710 ACCGGCCGGATACAGCAAGACATAAACCCTATAAGCCCGTTTACTTCGCTGCCG 769 11
Frontall, L.; Grisanti, P. Endical, L.; Grisanti, P. Ibmitted to the Protein Sequence Database, March 1992 Acression S19504 Acression S19504	Oy Dp	770 TATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATGGGTTTCCCGGGCAGTA 829 ::: ::: ::: 952 LeuGlnThrGluAlaValGluValThrLeuSerSerHisGlnThrValThrMetSerThr 971
A;Molecule type: DNA		830 CGGATCGCTACCTCCTTGGGGTGTGGAAGATCGTATCGAAAACGAGA 880

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QQ	::: ::::::: :::: :::: ::::::::::::::::	991
Oy Dp	881ACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAA	931
δy	932 CCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTAG	
QQ	1012	1017
οy	992 ACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	1051
qq	1017	1017
٥y	1052 GTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTG	1111
QG	1018GerGluMetSerThrPheSerValSerThrGInSerLeu	1030
Οy	1112 TCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGCCAAGGCCAACC	1171
QQ	1031 ProLeuAlaPheThrCysSerGluLysArgSerThr	1042
٥y	1172 GIGAGAIGACTIAITIGAGCGAGACGCICTICGGIGGIACCGAGGIGGITCGTITIGCAC	1231
QQ	1043ThrservalserGlnTrp	1048
οy	1232 AGTITGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTG	1291
Ор	1049SerAsnThrValLeuThrAsnThrIleMetSerSerSerSerAsnValIle	1065
οy	1292 ACGACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCG	1342
QQ	1066 SerThrAsnGluLysProSerSerThrThrSerProTyrAsn	1079
٥y	1343 CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATTCAAGA	1402
qq	1080PheSerSerGlyTyrSerLeuProSerSerThrProSerGlnTyr	1095
οy	1403 ATGTAATCGACAAAAATTCAAAGGCGACACGAAGAAGTATGGAGACTTCGTATTCGACA	. 1462
Op	1096 SerLeuSerThrAlaThrThrThrIleAsnGly1leLysThrValTyrThrThr	1113
٥y	1463 AGAGTGGGTTCCTTATAGCGACAAGTTCCATGCCCATGGTCCATGGACAAGGAAA	1522
qq	1114TrpCysProLeuAlaGluLysSerThrValAlaAlaSerSerGlnSerSerArg	1131
oy G	1523 AGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGGGTAA	1576
20	277 TA 477 THE KONDURK TO TO THE KONDURK TO THE THE THE TO T	
g G	1151 le	
οy	1637 GCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCC	
QQ	::: ::: ::: 1158 laThrThrIleSerGlyLeuLysThrValTyrThrThrTrpCysProLeuThrS	1177
οy	1678GGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCT	1723
qq	::: ::: ::::::::::::::::::::::::::::::	1196
٥y	1724 ACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAG	1783
Dp	1197 SerAlaSerSerAlaThrSerThrSerIleSerThrSerThrGluSerThrGluSerThrGluSer	1216
Qy	1784 GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA	1843
С	1217 SerSerGlyTyrLeuSerLysGlyValCysSerGlyThrGluCysThrGlnAspValPro	1236
οy	1844 TCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCATA ::: :::	1903

Riturner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T. Gastroenterology 106, 200, 1994 A;Title: Pig gastric mucin: isolation and characterization of a cDNA clone with a nov A;Reference number: 147141; MUID:94102478; PMID:7506218 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rosidues: 1-528 <TUR>
A;Rossreferences: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
B;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T.
Biochem. J. 308, 89-96, 1995
A;Title: Isolation and characterization of CDNA clones encoding pig gastric mucin. A; TILLE: Isolation and characterization of CDNA clones encoding pig gastric mucin. A; Reference number: S55315; MUID:95275264; PMID:7755593 2065 2125 gastric mucin (clone PGM-2A) - pig (fragment) .
C:Species: Sus scrofd domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Nov-2000
C;Accession: I47141; S5315 ::: ||||||||| 1292 ThrSerLeuLeuSerThrSerLeuProSerProAlaPheThrSerSerThrLeuProThr 1311 ::: 1312 AlaThrAlaValSerSerSerThrPheIleAlaSerSerLeuProLeuSerSerLysSer 1331 1237 ThrGlnSerSerSerProAlaSerThrLeuAlaTyrSerProSerValSerThrSerSer 1256 1946 GTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGG 2005 1277 LeuLeuProSerSerSerser 1291 . 128 GTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTG 187 68 AAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAAGGAGAATCTGGATCGAATGC 127 248 TGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC 307 308 ACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGG 367 -----ProSerSer 41 A;Molecule type: mRNĀ A;Residues: 1-528 <TU2> A;Cross-references: GB:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208 C;Superfamily: pig submaxillary mucin 2006 AAGCTATGAGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACA 2066 TCCGCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 17 ---ThrThrSerValGInSer------SerSerSerVal 188 CCAATGCCGTGGTTATCTTCGGTGCCGGATGTACCGGTATCACAGTGTCCGATCAGGGCC 1904 TCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACT----Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 29 ProlleProSerThrThrSerValGln-----US-10-008-355-1 (1-2139) x 147141 (1-528) 0.0419 149.00 34.228 21.518 3.908 Percent Similarity: Best Local Similarity: A; Status: preliminary A; Accession: I47141 Alignment Scores: Pred. No.: Query Match: 1257 52 Score: ò q δ q Op qq QQ g QQ δ ò δy ò δ

Sun May 25 15:40:18 2003

1226 TIGCACAGTITGCCAAATGCTAAATCCTGAIGCTCATGCCGTATCCTCAAAT 128 267 SETThPPOILEPROSETThIThESETVALGINFROSETSETSET 282 1286 CGCTTGACGACAAGAACATCACCCCCTCGCTCGCTCGAAGGTGCTGCCCGCA 134 111	,	3 2 4 4 7 3 3 6 8 8 8 8 9 9 8 8 8 9 9 8 9 9 8 9 9 9 8 9	7
1286 CGCTTGACGACAAGTACAACTACCTCCCTCGACCGTAAGGTGCTGCCCGCCA 134 183 SerAlaProThrThrSerAlaThrSerValGlnProSerSerSerSerSerProPro 301 1346 TGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATG 140 302 11eSerSerThrIleSerValGlnProSerSer	% q		TTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAAT 1285 ::: :::
	25 25 25	286 283 346 302	134 301 140 312

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Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N.Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR01
C.Specias: Saccharomyces cerevisiae
C.Date: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 12.Nov-1999
C.Accession: S48478; A26877; B26877; S27281: JC6123
submitted to the EMBL Data Library, October 1994
A.Reference number: S48478
A.Accession: S48478
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A; Residues: 1-1367 < ROW>
A; Residues: 1-1367 < ROW>
A; Residues: 1-1367 < ROW>
B; Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A; Title: Gene fusion is a possible mechanism underlying the evolution of STAI.
A; Reference number: A91831; MUID:87194600; PMID:3106330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1871 ATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACGATCA 1930
1406 TAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGA 1465
                                                                                                                                                                                                              1526 TTGCCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTG 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1706 TCACCATGCGTATGAGCTACGGCT-----CCATCAAGGGATATGAACCGCAGGACGGTG 1759
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                                 313 ---SerSerSerProThrThrSerThrThrSerValGlnProSerSerGlySer 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 AlaProThrThrSerAlaThrSerValGlnProSerSerSerSerSerValProThrThr 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 ---SerSerSerSerProThrThrSerThrThrSerValGlnProSerSerGly 506
                                                                                                                                   32 AlaProThrThrSerAlaThrSerValGlnProSerSer------Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1466 GIGIGGITCCTIAIAGCGACAAGITCCAIGCCAIGCICCAIGGACAAGGAAAAGI
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A; Molecule type: DNA A; Residues: 1-242 <YAM>

A; Accession: B26877 A; Accession: B26877 A; Molecule type: DNA A; Accession: S72131 < YA2> A; Cross-references: EMBL:M16165; NID:9172523; PIDN:AAA35015.1; PID:9172526 A; Cross-references: EMBL:M16165; NID:9172523; PIDN:AAA35015.1; PID:9172526 FEBS Lett. 239, 179-184, 1988 A; Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A. FEBS Lett. 239, 179-184, 1988 A; Hitle: Similar short elements in the 5' regions of the STA2 and SGA genes from Sacchar A; Reference number: S27281; WUID:89031230; PMID:3141213	. oy 0y 0y	536 CITTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTA 595
9.1; PID:94552 1.S.	Db Oy Db	541 ProvalThrSerSerThrThrGluSerSerSerAlaProvalProThrProser 558 716 CGGCCGAATACAGCAATAAACCCTATAAGCCCGTTTAGTTCG 763 719 111 111 111 111 111 111 111 111 111
Mucl, a mucin-like protein that is regulated by Mssl0, is critical for pseudohy conumber: JC6123; MuID:96323237; PMID:8710886 ion: JC6123 ion: JC6123 ion: JC6123 ion: JC6123 ion: JC6123 ion: JC6124 ion: JC6125	oy od	764 CTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCG 814
Objecture type: Unambers 1-1367 clamb Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387 Gross-references: CB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387 Gross-references: CB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387 Gross-references: CB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387	Qy	815 GTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAA 874 1
Suctionaries MIPS:YIR019c: SGD:S0001458 osition: 9R family: yeast glucan 1,4-alpha-glucosidase homolog: glucan 1,4-alpha-glucosidase	Qy	875 ACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG
5-21/Domain: transmembrane #status predicted <tml> 1350-1366/Domain: transmembrane #status predicted <tml></tml></tml>	Qy	935 TGAGGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACT 994
0.118 Length: 1367 145.00 Matches: 160 33.69% Conservative: 95	QQ Dp	995 ATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG
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	QV Dp	1163 AGGCCAACGGTGAGATGACTTATTGAGCGAGAGCGCTCTTCGGTGGTACCGAGGTGGTTC 1222
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	Qy Db	1484 ACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543
IFINIGLUSEFSEFSEFALAPFOVALTNISEFSEFTNITNIGLUSEF 507	Qy	1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603

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C;Species: S4784
R;Favello, A.D.
Sequence of the C: elegans cosmid C30C11.
A;Description: Sequence of the C: elegans cosmid C30C11.
A;Reference number: S44782
A;Accession: S44784
A;Accession: S47784
A;Accession: S47784
A;Accession: S47784
A;Accession: S47784
A;Accession: S47784
A;Accession: S47784
A;Accession: S4778
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A;Accession: C;Genetics: C;Accession: C;Accession: C;Genetics: C;Accession: C;
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                                                                                                                                                                                                                                                  1715 GTATGAGCTACGCCTCCATCAAGGGATATGAACCGCAGGACGGTGCCT------ 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1805 AGGATCCTAAGAGCGATGAGT------1805 AGGATCCGTACAGGAGAATA 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GCTATGCCGAGAACGGTCAGCTCCATATCGCTT 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1970 GCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGT 2029
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                                        909 GlnThrGluThrSerValSerSerThrThrGluThrThrIleValProThrLySThrThr 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 IleThrSerSerAlaProSer------SerIleProPheSerSerThr 888
                                                                                                                                                                               2030 TCGAACCCG----------ATCTGCAGCGCACAATCAGCGTGGACATCC
                                                                                                                                                                                                                                                                                                                                                                                      889 ThrGluSerPheSerThrGlyThrThrValThrProSerSerSerLysTyrProGlySer
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949 AsnSerAlaGlyGluThrThrSerGlyCysSerProLysThrValThrThr-----
                                                                                      835 SerSerValProvalProThrProSerSerSerThrThrGluSerSerAlaProVal
                                                                                                                                                                                                                                                                                                                                                              ...--GGTACAACTATCATACGACAGGCCAAGGGCGTATTGGAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1019 GluThrAlaSerGluSerThrThrSerProThrThrProValThrThr 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2069 GCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCC 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1002 CysSerProLysThrIleThrThrValProCysSerThrSer----
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1118
87
189
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Matches:
Conservative:
Mismatches:
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C; Superfamily: heat shock protein 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.117
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Best Local Similarity:
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DB:
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1013 GTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAG 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SerAlaThrMetTyrGluProArgIleV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   893 TCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lualaHisTyralaGlnProAsnValValProHisAsnGlnValHisIleGlySerTrpL 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 CCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                833 ATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 lulleGlu------IleValGlyGlySerSerArglleProMetIleArgG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTATGCCAAGAACTGGCCAAAAAAGAA-------AATGCAGACGAG---- 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....----AlaIleLysAspThrGlnProTyrArgIleArgLeuSerT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCACACGGGGGGACTTCAGC-----GTATTCCGCGTGTATGCCGGTGCCGACAACCGGC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgAspGluValProPheSerLysLeuValSerLeuLeuArgSerGlyProPheAsnValG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 CGGCCGAATACAGCAAGGACAAT---AAACCCTATAAGCCCGTTTACTTCGCTGCCGTAT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ProGluGluIleAspG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGG 472
                                                                                                                                                                                                                                                                                                                                                                                                        291 uCysPheMetGluAspLysAspValThrGlyLysMetGln-ArgGlnGluPhe----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GluAspLeuAlaAlaProIlePheAsnArgIleLysGlnValLeuIleA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GTTCGTATGGTAT 601
                                             ATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCG 172
                                                                                                                                                                                GIGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGGATGGTTTCGTTTCTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 ITGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC
                                                                                                                                                                                                                                                                                     -----AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleTrpPheAsp------AlaLeuIleArgGluHisPheArgLysGluPheLys
                                                                                                                                                     ----GlyGlyAsnGlnLysVal---
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US-10-008-355-1 (1-2139) x S44784 (1-776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 GCACGATGGGTGAGGAGCTTCCGATTCCG-
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alGluGluValProAlaGluAlaMetGluValAspGlyAspAlaLysThrGluAlaProA 525 Db 54 LeuAspSerAsnThrThrSerAlaSerValGlnThrIleAlaIleSerGlnThrAspAsn	20 20 20 20 20 20 20 20	1149 Qy 608	565 Db 94 1198 Qy 662 584 Db 114	1252 QY 722 604 Db 134	1312 Qy 767 622 Db 150	CTCGATATTGTACGCGGCGTATCC 1372 QY 827 GTACGGATCGCTACCTCACTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAAACC	AAGAAATTCAAAGGCGACA 1432 QY 887 CTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAA	OY 947 AGGTACCGGTATCAAATATGCCAGGAGTAGTCAGAGTGCTCAGAGTGCTAATTGGAAGAATTTGGAAGAATTTTGAAGAATTTTGAAGAA	ICCATGGACAAGGAAAAGT 1525	QY 1067 AAAGAGCATTCGCAGACTGGATCCGTAAGAAGAGTGCTGTTTTGCGATGTATT 	qy 1127 TGTCTTCTCGAAAAGGATGAGGAGGCGAAGGCCAAGGCCAAGGCCAAGGCCAAGGCGAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGATGACTTATT	#text_change 16-Jul-1999	QY 1247 TGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACA :::	Qy 1298 AGTACAAAGACTACCTCCCTCGACGTAAGGTGCTGCCGCCATGCTGCTGGATGTTTTTTTT	Qy 1358	Db 307	Db 307 Qy 1394 Db 327	Db 307 ThrserThrLeuGlnP QY 1394 Db 327 SeralaLeuProThrT QY 1418 AATTCAAAGGCGACAC Db 347 ThrLysThrlleThrA
CATTCGCAGACTGGATCCGTAAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGT	CTTCTCTGAAAAGCTTAT		luSerIleProValSerTyrAspValGlnLysPheHisAsnLeuGluLeuGlnMetGlnGAAGGAAGGCAACCCAACCGTGAGATGACTTATTTGACCGAGACGC ::: ::	TCTTCGGTGGTACCGAGGTGGTTCGTTTTGCCACAGTTGCCTACGCTTGCTT ::::: :::::	CAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACC	TCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGT 	CTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGC ::: ::: :::	CGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT	GCGACAAGTTCCATGCCATGTCAAGTCCATGGACAAGGAAAAGT	TTGCCAAGGCTATCGAG 1542 alileAsnAlaileGlu 698	D10.06c - fission yeast (Sch	ce_revision 16-Jul-1999 #te> lood, V.; Rajandream, M.A.; Fileriam, Fileriam, M.A.; Fileriam, Fil	Submitted to the Embi Data Library, September 1998 A;Reference number: 217313 A;Accession: T11678 A;Status: preliminary; translated from GB/EMBL/DDBJ	.031536; NID:e1319499; PID:e			Length: Matches: Conservative:	Length: Matches: Matches: Conservative: Mismatches: Indels: Gaps:

us-10-008-355-1.n2p.rpr

à	1538	A; Not	e: sėguence extracted from NCBI backbone (NCBIN:144410, NCBIP:144411)
5 A	SerThrProIleSerGlySerPheProAspGly	A; Gen A; Cro	e: SGD:HKR1 ss-references: SGD:S0002828; MIPS:YDR420w
Qy Db	1598 AGGCCGATGCGAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTCTT	A; Map C; Key F; 1-2 F; 22-	A;Map position: 4R C;Keywords: calcium binding; glycoprotein; transmembrane protein E;1-21/Domain: signal sequence #status predicted <sig> F;22-1802/Product: HKRl protein #status predicted <mat></mat></sig>
٥y	1658 GTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGC 1714	F;148 F;164	3-1508/Domain: transmembrane #status predicted <tmm> 5-1656/Domain: calcium binding #status predicted <cal></cal></tmm>
Db Oy	417	Alignm Pred. Score:	0.317 Length: 139.50 Matches:
qq A	427 IleThrThrThrThrThrThrThrThrSerValSerAsnAsnThrGlnSerSerPheLeulle 444 1775 ataccacacacccacaaggggggggaaggaaggaaggaa	Best L Query	Acal Similarity: 21.798 Match: 2
		US-10	03 (1-1802)
Qy Db	1832TACAGGAGAATATCCTCGACCTCTTCCGCACCAAAACT 1870 :::	Qy Db	1 ATGCAAATGAAATTAAAAAGTATTCTTCTCGGAGCAGCCTGCTGTTGGGTGCTTCAGGG 60 ::: :::
Š Š	1870 1870 485 ProgergerflyttenGerashfrftenHisSerGerValClnSerSerClnSerSer 504	Qy	61 GTAGCCAAAAGCCAAAAGCATGTGGCTCCTCAACGAACTCAATCAGAAATCTGGAT 120 15
	ATGGTCGCTATGCCGAGAACGGTCACATATCGCTTTCCTATCGAACAACG	δλ	CGAATGCGTGAGCTCGGCTTTACGCTCCGGTTGGATTCGCTCTACAGTTTCGACAAGCCG
a v	1925 ACATCACGGCGGTAACTCCGGTAGCCCGGTATTCGATAAGAACGCCGTCTGATCGGTC 1984	g & t	
	TTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATC :::	Š Š	CAGGGCCTGATCTTTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGC
<u>a</u> 8	537 ProfirThrIleValSerSerSerPheGlnTyrSerSerLeuSerSerAsnValThrThr 556 2042 mgCagggaraamganggagaanamggaanggagaanggagaanggagaaaagagagag	Q ò	57APIGGRGGARCATCACGACTARCGGGARGTTTCTTTCTTTTCT
op Op	Tocascocachartascocachartacocachartascocacha	g g	ThribrithmetalaglyGluSerGlySerThrithEMetAsp
Oy Db	2102 AGTGCCCCGTCTCATCCAAGAGC 2125 111:::	Qy Db	352 GAGCTTCCGATTCCGGGCTTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGAC 411
RESULT	8 E	Οy	412 AAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGTGGAGCGTCTGCGCAAAGCTCAG 471
HKR1	1857/05 HKRI protein precursor - yeast (Saccharomyces cerevisiae) N.Alfarnate.names: protein VDR4200	qa	98 ThrThrGlnThrSerAspThrMetSerSerValLysLysSerThr 112
C; Spe C; Dat C; Acc	C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001 C;Accession: S69703; A53382	Oy Db	472 GAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAG 513 :::
Submi Submi A; Des	Riblerich F.S. Submitted to the EMBL Data Library, August 1995 A:Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 941 A:Reference number: S69555	Qy	514 AACCAACTCTGCATCGTAGAGACTTTCTATTCCAACAAGAATACTTCCTCATCGTCTAC 573 :::
A; Mol A: Res	A;Accession: Sos.Oo. A;Molecule type: DNA A;Residues: 1.1802 <die></die>	Qy	
A; Crc R; Kas	A)Cross-references: EMBL:U33007; NID:9927685; PIDN:AAB64857.1; PID:9927691; MIPS:YDR420w. R;Kasahara, S.; Yamada, H.; Mio, T.; Shiratori, Y.; Miyamoto, C.; Yabe, T.; Nakajima, T.	qq	
J. Ba A;Tit A;Ref	verexpression overcomes t	Οy Dp	634 GGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTG 693
A; Acc A; Mol A; Res A; Cro A; Exp	A;Accession: A3382 A;Molecule type: DNA A;Residues: 1-581,'A',583-593,'A',595-1802 <kas> A;Cross-treferences: BML:S69101; NID:9545659; PIDN:AAB30051.1; PID:9545660 A;Experimental source: YNN295</kas>	Qy Db	694 TATGCCGGGCGACAACCGGCCGGCCGAATACAGCAACAATAAACCCTATAAGCCC 753

NATIGETRATE names: CD91; LDL receptor related protein 1; low density lipoprotein rece C; Species: Gallus gallus (chicken)
C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 22-Jun-1999
C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 22-Jun-1999
C; Accession: A53102
R; Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.
J; Biol. Chen. 269, 212-219, 1994
A; Title: The somatic cell-specific low density lipoprotein receptor-related protein o A; Reference number: A53102; MUID: 94103212; PMID: 7506255 d protein.
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-bind C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-bind C; Keywords: beta-hydroxyaspartic acid; calcium binding; glyco C; Keywords: beta-hydroxyaspartic acid; calcium binding; glyco C; 1-17/Domain: signal sequence #status predicted <515x F; 18-3942/Domain: alpha-2-macroglobulin receptor #status predicted <515x F; 18-3942, 3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT> F; 29-66/Domain: LDL receptor ligand-binding repeat homology <LDLL> F; 74-110/Domain: LDL receptor ligand-binding repeat homology <LDLL> A; Modecule type: mRNA A; Residues: 1-4543 <NIM> A; Cross-references: GB:X74904; NID:g438006; PIDN:CAA52870.1; PID:g438007 C; Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-assoc 2052 AATCAGCGTGGACATCC------GCTACGTTCTCTTCATGATTGACAAATG 2096 1806 GGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAA 1865 ----- 1904 1992 CGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAACTCGAACCCGATCTGCAGCGCAC 2051 1932 GGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTT 1991 523 eralaProAlaAlaIleSerSerThrTyrThrSerSerProSerAlaProValAlaValS 563 erProSerAlaProValAlaValSerSerThrTyrThrSerSerProSerAlaProValA <YW05> <YW06> <YW08> < XW03> < X W 0 4 > <YW07> homology <EG4> receptor ligand-binding repeat homology <LDL3> receptor ligand-binding repeat homology <LDL4> homology homology YWTD-containing repeat homology homology homology homology 1866 AAACTATGGTCGCTATGCCGAGAACGGTCAGCTCC------repeat repeat repeat repeat repeat alpha-2-macroglobulin receptor precursor - chicken YWTD-containing YWTD-containing YWTD-containing YWTD-containing YWTD-containing 2097 GGGTCAGTGCCCCGTCTCATCCAAGAGC 2125 619 erProSerAlaProValAlaValSerSer 628 EGF homology <EGS2>
LDL receptor YWTD-co
LDL receptor YWTD-co A;Status: preliminary A;Accession: A53102 F;117-150/Domain: F;156-190/Domain: F;893-929/Domain: F;242-283/Domain: F;337-380/Domain: ;480-521/Domain: F;573-615/Domain: F;616-661/Domain: F;713-754/Domain: F;852-888/Domain: F;200-241/Domain: F;294-336/Domain: F;381-422/Domain: F;805-840/Domain: F; 423-470/Domain: F;662-712/Domain: F;755-797/Domain: RESULT 9 ò òy Db QΥ Db δ qq ōλ g δ δ

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F;4421-4443/Domain: transmembrane #status predicted <TMM>
F;444-4543/Domain: intracellular #status predicted <INT>
F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1
3488,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covale F;868,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
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                                                          F;4199-4230/Domain:
                                 F;4150-4181/Domain:
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LDL receptor YWTD-containing repeat homology <WW41>
alpha-2-macroglobulin receptor 85k chain *status predicted <85k>
85k chain extracellular *status predicted <8TY>
LDL receptor YWTD-containing repeat homology <YW42>
LDL receptor YWTD-containing repeat homology <YW43>
Thl. receptor YWTD-containing repeat homology <YW44>
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YWTD-containing
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homology <EG6>
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F) 934-969/Domain: LDE
F) 974-1009/Domain: LDE
F) 1013-1049/Domain: LDE
F) 1102-1138/Domain: LDE
F) 1102-1138/Domain: LDE
F) 1102-1138/Domain: LDE
F) 113-1139/Domain: LDE
F) 
                                 974-1009/Domain: L
1013-1049/Domain:
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λο	CCGGCCGAATACAGCAAGACAATAAACCCTATAAG	Db 4275 ysHisAsnAsnClySerCysThr
å ò	39/5 AspSerGlyArgAspVallleGluValAlaGlnMetLySGlyGluAsnArg 3991 751 CCCGTTTACTTCGCTGCCGTATCCAAGGCTACAAGGCTGACGACGACTATGACC 810	Qy 1666 GAGATGTACCCCGGACGTGCTCT
7 A		4293
Oy 1	GGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATC	Qy 1726 GGCTCCATCAAGGGATATGAACCC ::: ::: Db 4311 ysGluAsnAsnGlyVal
o ò	400/ VAIASPFIOLEUARGGIYINIMETIYITIPSERASPIIPDGLY	RESULT 10
2 g		mucin 5AC (clone JER47) - human (; C;Species: Homo sapiens (man)
Qγ	931 GCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAGGTAT 978	C, Date: 28-Oct-1996 #sequence_rev.
đ	4037 ThrLeuvalGlnAspAsnIleGlnTrpProThrGlyLeuAlaValAspTyr 4053	A; or you would be a second of the A; or you will be a second of the A; or you will be a second or the second of the second or t
0y	979 GCTCAGAGTGCTAACTATTGGAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	A. Reference number: S53361; MUID: A. Accession: S53362
g G	4054 HisAsnGluArgLeuTyrTrpAlaAspAlaLysLeu 4065	A; Status: nucleic acid sequence no A; Molecule type: mRNA
δò	1039 GACGTGATAGGTGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAAC 1098	A; Residues: 1-477 <guy> A; Cross-references: EMBL: Z34277</guy>
gg ,	IeargLeuAsn	A; Experimental source: clone JER4 R; Porchet, N.
ò á	1099 GGC	Submitted to the EMBL Data Librar. A. Reference number: S71065
3 (ory in aspriovatvaratiens pasiily stysciy beuser fiskrorneser ile	A; Accession: S/1055 A; Molecule type: mRNA
γο d	1102AAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAGGCT 1146 1::: -	A; Residues: 1-211, 'S', 213-224, 'AR A; Cross-references: EMBL: 234277; A; Exposimental Course, 1900
3 8	SOFITE INCOLUDIORITY FILE OF TAKE THE TYLLEGOSHOSHOLGENGE GENERAL GENE	A) axper interior source: croile JEK4
6 6	HisLysPhedlyHisLySerValThrAsnLeuThrSerClyLeuAsnHis	A; vene: GDB:m0C3AC A; Cross-references: GDB:454136; OI A; Map position: 11p15.5-11p15.5
Oy	1207 GGTACCGAGGTGGTTTGTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCT 1266	C; Keywords: glycoprotein; tandem
ф		
δλ	1267 CATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTC 1314	SCORE: 138.00 Percent Similarity: 41.188. Rect Incel Similarity: 29.038.
qa	4150	-
QY	1315 CCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC 1366	-10-008-355-1 (1-2139
0		Qy 1413 CAAGAAATTCAAAGGCGACACGA
7 점	4182 ILeuIleProSerProThrAlaSerAlaval-ValProThrThrAspThrCysAspLeuV 4202	ysį
ΟŸ		Qy 1473 TCCTTATAGCGACAAGTTCCATG
qq		75
δ	1483 GACAAGTICCAIGCCAIGCICAAGICCAIGGACAAGGAAAAGIIIGCCAA 1532	1527
qq	::	00 t
Οy	1533GGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTA 1575	OY 158/ TCGCGCTATTCAGGCCGATGCGA
අ ପ	4235 ysSerAspTyrCysGlnAsnGlyGlyLeuCysThrAlaSerProSerGlyMetProThrC 4255	1647
y g	1576 ATAGCTGCTGCTGCTATTCAGGCCGATGCGATGGCCAATGCCTAT 1623 1576 ATAGCTGCTGCTGCTATTCAGGCCGATGCGAATGGCCAATGCCTAT 1623 4255 vsAtaGvsProThtGlvPheThtGlvPheThtGvsAshGlnGlnVallvsThtAshTvrr 4275	106
QY		Oy 1703ACTTCACCATGC

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: human mucin gene MUC5AC: a consensus cysteine-rich d
                                                                                                                                                                                                                                                .P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galieg
   :
rValAsnGlnGlyAsnGlnProAsnCysArg----- 4292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTACCCCGGACGTGCTCTGCCGAGCGATGCCA---- 1702
                                         TGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTAC 1725
                                                         :vision 07-Feb-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCT 1646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR',227-259,'S',261-477 <POR>
. NID:9563374; PIDN:CAA84031.1; PID:9563375
347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LeuValCysArgAsnGlnAspGlnGlnGly 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----Cys 90
                                                                                                                   CGCAGGACGGTGCCTGGTACAACTATCATACGAC 1781
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                         (fragment)
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Page 14

Db 2963 AlaThrMetSerThrIleHisProSerSerThrProGluThrThrHisThrSerThrVal Qy 281 CTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGGGGATGGTTTCGTTTCTC Dh 2983 LeuThrThrLysalaThrThrArgalaThrSerThrSerThrPro	338	Qy 395 TCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCTCAAGGGTATCACTGACGAGATGGAGCTGAAGGACAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGGAGATGAAGGAGAAGGAGAAGGAGAAGGAGAAGGAAGGAGAAGGAGA	OY 455 GTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAAA	Qy 515 ACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACG ::	Qy 575 ATGTATTCAAGGACGTTC	Qy 617 CTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC	Oy 662 GTCACACGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACACCGGCCGG	alternat Qy 782 GCTACAAGGCTGACGACTATGCCATGACCATGGGTTTCCCGGGCAGTACGGATCGCTACC ::	TGGAA rpTh	3164	Qy 959 TCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCG ::: ::::::::::::::::::::::::::::::::	OY 1013 GTATGAACCGCGGTCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCG	Oy 1064	QY 1169 ACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTG
125 lyCysProValThrSerThrProValThrAlaProSerThrProSerGlyArgA 143 1752 GGACGGTGCTGGTACAACATCATACGACAGGCGTATTGGAGAA 1802 1753 GAACGGTGCTGGTACAACATCATACACAGCAGGCGTATTGGAGAA 1802 173 laThrSerPro	GCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTCCGCAC ::	1863 CAAAAACTATGGTCGCTATGCCGAGAACGGTCAGATCGCTTTCCTATCGAACAA 1922 	1923 CGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCG 1973 	1974 TCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACAT 2024 11	2025 CGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTTCAT 2084 ::::	2085 GATTGACAAATGGGGTCAGTGCCCCGTCTCATCCAAGAGC 2125 	RESULT 11 T45025 mucin MUC5B, tracheobronchial [imported] - human (fragment) C:Species: Homo sapiens (man) C:Species: Homo wapiens (man) C:Accession: T45025 R:Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.	odes various	tus: preliminary: translated from GB/EMBL/DDBJ ecule type: DNA 1ducs: 1-3570 <des> iss-references: EMBL:272496; NID:91834502; PIDN:CAA96577.1; PID:91834503 erimental source: placenta</des>	A;Gene: MUC5B	Artylmment Scottes: 0.631 Length: 3570 Score: 137.00 Matches: 154 Percent Similarity: 33.29% Conservative: 94 Boart Local Similarity: 30.57% Minmatches: 94	3.59% Intellections 2 Gaps: Gaps:	65 CCAAAGCCAAAGGCATGCGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAA 124 65 CCAAAGCCGAAAAGCCAAAGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAA 124 65 CCAAAGCCGAAAAGGCATGGCTCCTTCAACGAACTCAATCTGGAATCTGGATCAAGCTCTCAAGATTTCGACAAGCCGTCA 184 65 TGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGACAAGCCGTCCA 184 66 TATATATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TTGCCAATGCCGTGGTTATCTTCGGTGGCGGAGCTC

Sun May 25 15:40:18 2003

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A;Title: The nucleotide sequence of an alpha-amylase gene from an alkalopsychrotrophin, A;Reference number: A60999
A;Accession: A60999
A;Molecule type: DNA
A;Residues: 1-1104 <KIM>A;Residues: 1-1104 <KIM>A;Residues: 1-1104 <KIM>A;Residues: 1-104 <KIM>A;Periorical (B:X55799; NID:g296762; PIDN:CAA39321.1; PID:g296763
C;Function: A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
A;Pathway: glycosidase; hydrolase; polysaccharide degradation
F;1-32/Pomain: signal sequence #status predicted <SIG>F;33-1104/Product: alpha-amylase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1051 CGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 AsnValArgLysGlnIleIleAsp---TrpGlnThrAspTrpIleGluLysAlaThrThr 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 ThrTrpMetGlnPheLysAsnAlaLeuThrGluLysMetProGluPheLysMetIleGly 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluThrSerGluProTyrTyrGlyTyrHisGlyTyrTrpAlaAsnAsnPheGlyGluLeu 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 ArgAsnMetLysIleMetValAsp-----ValValVal 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                772 TCCATGCAAGGCTAC----AAGGCTGACGACTATGCCATGACC-----ATCGGT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 AsnHisThrGlyTyrGlyLeuLysGluIleAspGlySerValThrAsnProProAlaGly 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 TyrProSerAspAlaAspArgAlaArgPheSerAspLeuLeuArgGlnGlyAlaAspVal 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TGGGGTGTGGAAGATCGTATCGAAAACGAGAAC 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         943 GATCAGGCTACCCGTATCAAATAT------GCCAGCAAGTATGCTCAGAGTGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 ValGluAsnIleLysTyr---------AspValArgTyrTyr 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGG-----ATG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 TGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGC---GTGTATGCCGGTGCCGACAAC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 CGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 CAAGAACTGGCCAAAAAAAAAATGCAGAGAGAACCAACTCTGCATCGTAGAGCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 TATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: ::: |||
550 GluAsnGlyAsnThrIleAspTyrPheArgValAspThrValLysHisValGluAspAla
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1138
138
94
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173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-008-355-1 (1-2139) x A60999 (1-1104)
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133.50
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Best Local Similarity:
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ΩΩ	590 G	GluAlaraspAsnThrLeu	009
ð í		GTCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGGA	1161
QQ	601 G	GlyTyrLeuGluThrGlyThrMetAspSerLeuLeuAspPheGlyPheLysGluThrAla	620
οy	1162 A		1194
QQ	621 A	ArgSerPheValAsnGlySerLeuGluAlaAlaAsnAlaSerLeuThrAlaArgAsnAla	640
οy		ACGCTCTTCGGTGGTACCGAGGTGGTTGTT	1236
q	641 L	LysLeuAspAsnThrAlaThrLeuGlyGlnPheLeuGlySerHisAspGluGluGlyPhe	099
ογ	1237 G	GCCAACGCATTGCTACAAAT	1257
QQ	661 г	GlyA	680
Οy	1258 -	CCTCAAATCG	1305
QQ	681 A	AlaLysGlyGlnProValIleTyrTyrGlyGluGluLeuGlyGlnThrGlyAla	869
٥y	1306 G	SGTA	1365
Q	699 A	ASINASOTYTPTOGINTYTASPASNATGTYTASPPHEALGTTPASP	713
ογ		CGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAA	1425
g	714 G	GlnValGluGlyAsnGluIleLeuAlaHisTyrThrLysIleLeuAsnPheArgGlu	732
ò á		GGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC	1485
2		sıyıyrserLysvalPneAlaLysGlyGluArgThfLeuValGlyGlySerAsp	
δ			1545
qq	751 L	LysAspGlnPheLeuLeuPheSerArgAspTyrGlnAspGlnLysValTyrValGlyLeu	770
oy D	1546 G	GATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATT :::	1596
à		######################################	1652
2 6	790	ValThrAspAlaTyrSerGlyThrGluTyrThrAlaThrAlaGlyLys	805
è			1713
S 8		second in ejentrantic reconstruction of the control	1/13 822
ò	1714 C	CGTATGAGCTACGGCTCCATCAAGGGA	1740
Dp		::: ::: ValGluGlyGlyAsnIleThrGlyValAlaLysAspAsnGlyGluValValValGlu	841
οy	1741 -	TATGAACGCAGGACGGTGCTGGTACAAC	1770
Dp	842 L	.:: LeuValProGluAsnAsnIleArgIleHisTyrLysArgGluAspAsnValTyrLysAsn	861
οy	1771 T	TATCATACGACAGGCCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCC	1830
qq	862 T	GlyAlaTrpLeuTrpAsnAspValAlaSerPro	878
ογ	1831 G	GTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAG	1887
Dp	879 V	ValGlyAlaThrMetPheGluLysThrAspSerTyrGlyAlaTyrIleAspVal	968
οy		AACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTT111	1938
Q O	897 P	ProLeuAlaAspGlyAlaLysAsnIleGlyPheLeuValMetAspIleThrAlaGly	915
λοί		AACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGC	1998
g	916 A	AspAlaGlyLysAspGlyGlyAspLysGlyPheThrIleSerSerProGlnAlaAsnGlu	935

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Cispecies: Streptococcus pneumoniae
Cispecies: Oct-2001 #sequence_revision 22-oct-2001 #text_change 03-Jun-2002
Cispecies: D3-oct-2001 #sequence_revision 22-oct-2001 #text_change 03-Jun-2002
Cispecies: D3-oct-2001 #sequence_revision 22-oct-2001 #text_change 03-Jun-2002
R;Hoskins: J3-Alborn Jr. W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
Cispecies: D3-oct-2001 W; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, J.; P.; Sun, P.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, T.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-883 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99296.1; PiD:g15458063; GSPDB:GN00174
C;Genetics:
1999 AACTGGGAAGCTATGAGTGGTGAC-----ATCGAGTTCGAACCC---GATCTGCAGCGC 2049
                                                                                      111 GluserPhereuThriysValTrpGluTrpLysAsp------GluTyrAlaThr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    846
                                                                                                                            956 Asn---ThrValArgIleHisTyrThrArgGluAlaValAspTyrAspAspPheGlyIle 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AAGGACGTTCGTATGGTATTGCTCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGCGTCACACG 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730 AAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           847 TCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGT 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 Gly------HisAla 57
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104
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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| FroAsnValThrGlyLysLeu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: valine-tRNA ligase C; Keywords: ligase
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133.00
33.078
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3.488
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: D97933
A; Status: preliminary
A; Molecule type: DNA
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Sun May 25 15:40:18 2003

<u>ک</u> و	955 CGTATC 127 Thrile	CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATC	1011	
7.4 Op	1012 GGTATG ::: 147 ThrLeu	GGTATGAACCGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGA :::: :::	1071	
λά 90	1072 GCATTC 159 ValPhe	GCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGC	1119	
ZY QC	1120 GAT 179 ASPPIC	GATGTATTGTCTTCTCTGAAAGGCTTATAAG	1152	
7.		GAAGGAGCCAAGGCGAGCGTGAGATGACT	1182	
g 75	an m	AlaphetyrhisMetAsnTyrMetLeuGluAspGiySerArgAlaLeuGluValAlaThr TATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC :::	218 1242	
ල . අ	219	ProGluThrMetPheGlyAspVal	228	
ž 2	1243 GCATTE 	ocartoscracarariccisatocicarocceratocicaaaricerracacadaaci :: ::: AlailealavalasnProGluAspFroArgTyr	1302	
<u>ک</u> ۾	1303 AAAGAC 240 LysAsp	AAAGACTACCTCCCCTCG	1347 259	
λ 4	1348 CTCGAT	Clubicalasenbroothubboothubboothubatustreatustreatustreatus	1368	
		OCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGC		
ą	114 280 AspPro		299	
λ 2	1429 GACACC 300 Aspasi	GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGGGTTCCTTATAGCGACAAG	1488	
ž q	1489 TTCCAT 317 PheGlu	TTCCATGCCATGCTCAAGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGAT	1548	
ž a	1549 CCGGCR 332 AlaLeu	CCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCT	1593 351	
γ̈́α	1594	ATTCAGGCCGAT	1605	
QQ	352 ValVal	::: ValValGluProArgLeuSerThrGlnTrpPheValLysMetAspGlnLeuAlaLysAsn	371	
Sy Op	1606 GCGATC : : 372 Alalle	GCGATGGCCAATGCCATTGAGAAGGCCAAGCGTCTTTCTT	1665	
λά Gb	1666 GAGATC 383 GluPhe	GAGATGTACCCCGGACGTGCTCTGCCGAGC	1698	
ς G	1699 GCCAAC 403 TrpVa	GCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGT :::::::::::::::::::::::::::::::::::	1758	
ζζ	1759 GCCTGC 417 AlaTr	GCCTGGTACAACTATCATACGACAGGCGTATTGGAGAAGCAGGATCCTAAGAGC		

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probable pts pep phosphotransferase - Chlamydia trachomatis (serotype D, strain UW3/C C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13.5ep-1998 #sequence_revision 13.5ep-1998 #text_change 21-Jan-2000
C; Accession: C71528
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia the A; Reference number: A1570; MUID: 99000809; PMID: 9784136
                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <ARN>
A;Coss_references: GB:AE001306; GB:AE001273; NID:g3328748; PIDN:AAC67931.1; PID:g332
A;Cross_references: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: pts1
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I F;17-565/Domain: phosphotransferase system enzyme I homology <PTl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1575 TACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGGCAAACTTTTCCTT 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1479 ATAAGGAACCACACTCTTGTCGAA-----TACGAAGTCTGCATACTTCTTCGTGT 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ATTTGTAGCCAATGCGTTGGC 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LysAsnAlaGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 ThrAlaThrArgValAspArgValGlnAspIleHisAspIleSerAsnArgValIleGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 LeuGluLysGluAlaLysGlyLysGlnGlyTyrGlnGluIleAlaSerIleLeuGlnAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 IleValProGlyIleGlyLeuGlyLysAlaLeu-------
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115
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186
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
1819 GATGAGTTTGCCGTACAGGAGAATATCCTCGAC 1851
                    US-10-008-355-1 (1-2139) x C71528 (1-571)
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25 15:40:18 2003

Sun May

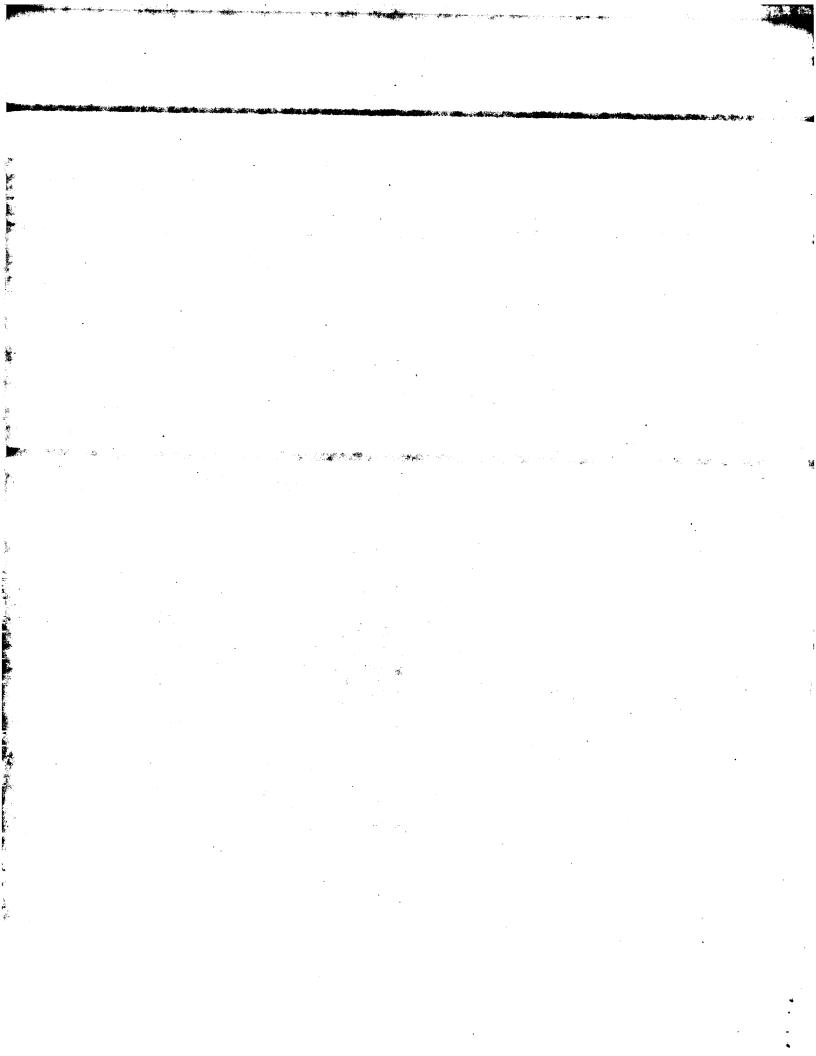
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λa a	1191G 198 ValSerLeuGluGlyA		1147
λά	-		1117
QQ	::: 212 SerLeuAlaLysAsnI	::: SerLeuAlaLysAsnIleProTyrValAlaAsnPheThrThrGluLeuTrpAspThrIle	231
ά		ATAGACAGCACTCTTGCCGTTCTTACGGATCCAGTCTGCGATGCTCTTTC	1066
g g		ThrLeuValLeuIleAsnGlyAspLysGlyGluIleThrPheAsn	251
2 G	252 ProGlnLeuSerThri		1030 271
γά	1029 GAGACCGCGGTTCATA	GAGACCGCGGTTCATACCGAATGTTCCAATAGTTAGCACTCTGAGCATACTTGCT	970
Q.	272 ProvalGlnvalGlnT	ThrGlyLysAsnLeuProLeuIleSer-LeuSerAla	288
yo da	969 GGCATATTTGATACGG 289	GGCATATTTGATACGGGTAGCCTGATCGCCTCATGCTTCCATGCCTTGCTT :::::::::::::::: ::GlnIleValSerThrGluGluLeuProMetIl	910 299
λά	909 GATACCG	GATACCGCGAACTTCGATACGAGGATTGTTCTCGTTTCGATACGATCTTC	859
e e	299 eGluArgGluSerPro	oglyThrSerValGlyLeuPhe	311
οy	858 CACACCCCAAGAAGTG	CACACCCCAAGAAGTGAGGGATCCGTACTGCCCGGGAAACCGATGGTCATGGCATA :::	. 664
8	312	ArgSerGluPheMetAlaPh	318
λo 4	798	GTOGTCAGCCTTGCATGCATACGCAGCGAAGTAAACGGGCTTATAGGGTTT	739
ò	738	G	336 736
qq	338	InPheGInCysSerAspIleHisValLeuArgLeuPheAspPheGlyGluAspLysGluC	358
à	735	GTCCTTGCTGTATTCGGCCGGCCGGTTGTCGGCACCGGCATACACGCGGAATACGCTGAA	676
2	675		01.0
S 6	. 4	GINGLULYSVALLeuLysGluGluLeuGlnAlaIleAlaIleValSer	389
ž g	618 AGAGCTGGGAGGAGCA 1 390 ArglleGlyArgLeuL	AGAGCTGGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAA	559 406
λά	558 GTATTCGTTGTTGGAA		499
q	::: ::!!! 407 IleAlaLeuVal	::: ::: ::: ::: ::: IlealaLeuValLysArgLeuPheGlnGluGluIleArgLeuLysGlyIle	424
λĊ	498 TTTTTGGCCAGTTCT		439
q	425 SerGluAsnIleLeuT	SerGluAsnIleLeuTrpGlySerMetIleGluIleProSerAlaValTrpMetIleGlu	444
તે તે	38	GATACCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGGCAGATACTT	379
3		serser ruevalaleuciyinrasnaspleualacınıyrinr	404
දු ද	378 CACGGAAAGACCCGGA ::: 465 LeuGlyThrSerArgG	CACGGAAAGACCCGGAAACCTCCTCACCATCGTGCGAGAAACGAAACCATCGCG	319
λ t	18	CAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGTATCCGCAGTG	265
2	485 VallleArgMetileH		504

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date 10 Nov-1997 #sequence_revision 10 Nov-1997 #text_change 08-Oct-1999
C; Accession: PC4395 #sequence_revision 10. Nov-1997 #text_change 08-Oct-1999
C; Accession: PC4395 #sequence_revision 10. Nov-1997 #text_change 08-Oct-1999
B; Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Ein Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A; Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem re A; Reference number: PC4395; MUID:97445141; PMID:9299468
                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-648 <VAN>
A;Cross-references: DDBJ:AF016692; NID:g2454614; PIDN:AAB71685.1; PID:g2454615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GlySerThrLeuSerThrProSerValValThrSerThrProValThrThrSerThrGlu 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 Val-------------ThrSerSerGluAlaSerThrProSerThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 GCG--------TGTATGCCGGTGCCGACAACCGGCCGGCCGAATACA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ThrProThrProProGluValIleThrLeuProMetSerThrProSerGluValSerThr 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 GCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACA 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LeuAspSerThr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 CTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATG---TATTCAAGGACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------CGGACAACTGGATGTGGCCGCGTCACGGGGCGACTTCAGCGTATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788 AGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 GlnValSerSerProValThrProGluGlyThrThrMetProIleTrpThrLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GTATCGAAAACGAGAACA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATA--
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173
234
34
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F;1-59,60-118,119-177,178-236,237-295/Region: repeat
F;296-565/Region: semi-unique #steutus predicted
F;566-582,583-599,600-616,617-633,634-647/Region: repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
264 GTGGTTGGTAAA-----GATCAGGCCCTGATC 238
                     US-10-008-355-1 (1-2139) x PC4395 (1-648)
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Pred. No.:
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ò	962	AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGA 1018	
qq	00	Pr	
ΟŊ	1019	TTGACGTGATAGGTCGTAAGCGTG	
qq	292	ThrPro	
οy	1079	CAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCG 1138	
qq	311	SerlleProSerValTyrThrSerMetSerMetThrThr 323	
Qy	1139	AAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGC 1198	
Op	324		
δy	1199	TCTTCGGTGGTACCCAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATC 1258	
QQ	327	GlySerSerSerProThrThrLeuGluGly 336	
Οy	1259	TCAAATCGCTTGACGACAAGTACAAAG	
QQ	337	ThrThrThrThrMetProMetSerThrThrSerGlu 347	
δý	1319	CGCTCGACCGTAAGG1GCTGCCCGCCATGCTCGATATTG 1357	
Dp	348	:: ArgSerThrLeuLeuThrThrValLeuIleSerProIleSerValMetSerProSerGlu 367	
ΟŊ	1358	TACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAA 1408	
qq	368	::: :: AlaSerThrLeuSerThrProProGlyAspThrSerThrProLeuLeuThr 384	
οy	0	TCGACAAGAAATTCAAAG	
QQ	385	ysAlaGlySerPheSerIleProAlaGluValThrThrIleArgIleSerIl	
δy	1445	CAGACTICGIAITGGACAAGAGIGIGGITCCITAIAGCGACAAGIICCAIGCCAIG	
οp	405	ThrSerGluArgSerThrProLeuThrThrLeuLeuValSerThrThrLeuProThrSer 424	
Οy	1505	AGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGC 1561	
q O	425	PheProGlyAlaSerIleAlaSerThrPro	
δλ	1562	TTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCT 1621	
qq	434	434	
οy	1622	TCTTTGCCGGTTTGCGTGAGATGT	
QQ	435	 ProLeuAspThrSerThrThrPheThrProSer 445	
Οÿ	1682	GTGCTCTGCCGAGCGATGCCAACCTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGAT 1741	
qq	446	ThraspThralaSerThrProThrIleProValalaThrThrIleSerValSerVal 464	
δy	1742	ATGAACCGCAGGACGGTGCCTGGTACACTATCATACGACAG 1783	
qq	465	III IIII IIII IIIIIIIIIIIIIIIIIIIIIIII	
δy	1784	GCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA 1843	
qq	485	SerThrAlaAspValPheProAlaThrThrGlyAlaValSerThrProVal1le 502	
ΟY	1844	TCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCC 1900	
QQ	503	GluLeuAsnThrProSerThrSerSer	
οy	1901	ATAICGCITICCIAICGAACAACGACAICACGGGCGGTAACICCGGTAGCC 1951	
οp	517	ThrThrThrSerPheSerThrThrLysGluPheThrThrProAlaMetThrThrAlaAla 536	

2011	542	2071	561		
1952 CCGTATTCGATAAGAACGCCCGTCTGATCGGTCTTGCTTTCGAGGCAACTGGGAAGCTA 2011		2012 TGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCT 2071	6	2072 ACGITCITCATGATGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125	562 SerThrLeuSerAlaThrSerThrProHisThrSerThrSer 575
1952	537	2012	543	2072	562
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Search completed: May 16, 2003, 12:38:15 Job time : 131.5 secs



Sun May 25 15:40:19 2003

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1 DNAK_PORPU 1 GLGB_AGRTU 1 VIVC_BPT7 1 VG46_YEAST 1 RTR1_CHLMU 1 DAN4_YEAST 1 WEB1_YEAST 1 PLE1_RAT 1 CN16_HAEIN 1 EST2_CABEL 1 PPOL_HUMAN 1 DPOZ_YEAST 1 VKL6_CABEL 1 HY1_ECOLI	11.5 2.9 2410 MOKI_SCHPO Q9usk8 110.5 2.9 498 FLID_BACSU P39738 110.5 2.9 498 FLID_BACSU P39738 110.5 2.9 1039 SYI_METJA Q58357 109.5 2.9 681 MP10_HUMAN Q58357 109 2.9 3672 LML2_CAREL Q0566 Q0566 Q1855 Q5855 Q5	RESULT 1 FIG2_YEAST ID FIG3_LEAST TO P25633. AC 01-MAY-1992 (Rel. 22, Last sequence update) DT 01-MAY-1992 (Rel. 37, Last sequence update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DE Factor induced gene 2. GN FIG2 OR YCR089W OR YCR102. OS Saccharomyces cerevisiae (Baker's yeast). OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes; ON NCBI_TAXID=4932; RN [1] RP SEQUENCE FROM N. A. RX MEDLINE=9239754; PubMed=1523889; RA Wilson C., Grisnati P., Frontall L.; RA Wilson C., Grisnati P., Frontall L.; The complete sequence of a 6146 bp fragment of Saccharomyces	cerevisiae chromosome III contains two new open 'Yeast 8:569-575(1992). -! FUNCTION: REQUIRED FOR EFFICIENT MATING!- INDUCTION: BY MATING PHEROMONES. This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the Buropean Bioinformatics Institute. There are use by non-profit institutions as long as it modified and this statement is not removed. Usa entities requires a license agreement (See http: or send an email to license agreement (See http: or send an email to license agreement (See http: PIR; S19504; S19504. PIR; S25345; S25345. SGD; S0000685; FIG2. SEQUENCE 1609 AA: 166049 MW; 7D66AD7F85A7B85 Ignment Scores: 0.0162
	Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 0.5 Ygapop 10.0, Ygapext 0.5 Ygapop 10.0, Ygapext 7.0 Delop 6.0, Polext 7.0 Searched: 112892 seqs, 41476328 residues Total number of hits satisfying chosen parameters: 225784 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Maximum DB seq length: 2000000000	Maximum Match Listing first Insting first D. Maximum Match S. Model -DEV-x1 S. D. Model -DEV-x1 S. D. THR. SC MT- FOO -THR. SC MT- FOO -THR. SC MT- Pto -NORM-C GCGN_1_1_47_C MP -LARGEQUERY THREADS=1 -XC THREADS=1 -XC EXT-0.5 -DELOP- SWISSPICT_40:† SWISSPICT_40:	Result Query Query Duery Description No. Score Match Length DB ID Description 1 154.5 4.0 1609 1 FIG2 YEAST POE553 saccharomyc POE640 2 accharomyc POE640 3 accharomyc POE640 3 accharomyc POE640 3 accharomyc POE640 3 accharomyc POE650 3 and AMM-YEAST POE640 accharomyc POE650 3 and AMM-YEAST POE640 accharomyc POE650 3 and AMM-YEAST POE670 2 and AMM-YEAST POE770 2 and AMM-YEAST POE7772 YIB AMM-YEAST POE75772 YIB AMM-YEAST POE757772 YIB AMM-YEAST POE75772 YIB AMM-YEAST POE757772 YIB AMM-YEAST POE757772 YIB AMM-YEAST POE757772

Query	Match: 4.04% Indels: 214	Qy .	10
DB:	I caps:	qq	101
US-10-008		Qy	111
y S	74 ACAAAGGCATGTGGTCCTCAACGAACTCAATCAGGAAATCTGGATCAATGCGATGCGTGAGC 155 T :::	QO	103
οy	TTCGCTCTACAGTTTCGACAAGC	Q G	11.
qq	799 ThrvallleThrServalThrAlaThrSerSerThr	a è	, ,
ογ	194 CCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCT 253	g qa	107
QQ	812 ProLeuLeuSerThrser 817	ò	129
ογ	TTACCAACCACCACTGCGGATACGGTGTATCCAGAGCCAAAGCACGGTGGATC	op Op	10(
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οy	GTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACA 70	Dp	11
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ογ		qq	11
QQ	ThrGluValValThrSerLysGlyThrProSerAsnGlyHisSerSerGlnThr	Qy	17
δ i	TATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTA	qa	12
Op	LeuGinThrGluAlavalGluValThrLeuSerSerHisGinThrValThrMeLSerLin	QY	18
οy	CGGATCGCTACCTCCTCTTGGGGTGTGGAAGATCGTATCGAAACGAGA	Db	12
QQ	972 GluvalCysSerAsnSerIleCysThrProThrValIleThrServalGlnMetArgSer 991	δŏ	19
Ολ		QO	12
qa	992 ThrProPheProTyrLeuThrSerSerThrSerSerSerLeuAlaSerThrLysLys 1011	Oy	19
٥y	ATGCTCAGAGTGCTA	ΩD	12
qq		Qy	20
δλ	ACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	qa	12
qa	1017 1017	Qy	20

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ά	5 N	AAGCGTGCCGAGGAAAAGAGCATTCGCAGAACGGTGCGTAAGAAAGA	
qq	1018		_
Qy	1112 TC	TCTTCTCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACC 117	_
QQ	1031 Pr	0	~
Qy	1172 GT	SAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCAC 123	_
qq	1043	ThrSerValSerGinTrp1	m
δy	1232 AG	GCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTG 129	_
qq	1049	SerAsnThrValLeuThrAsnThrIleMetSerSerSerSerAsnValIle 106	ю
οy	1292 AC	ACGACAAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTGCCG 1342	0
QQ	1066 Se		0
Qy	1343 CC	CCATGCTCGATATTGTACGCCGGCGTATCCTGCCGACAAGCTCCCCGATATATTCAAGA 1402	7
QΩ	1080		2
Qy	1403 AT	TGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACA 1462	7
qa	1096 Se	SerLeuSerThrAlaThrThrThrIleAsnGly11eLysThrValTyrThrThr 1113	ω.
QY	1463 AG	152	7
Ωp	1114	113	П
δy	1523 AC	TTGCCAAGGCTATCGAGAAGGTTCCGGCAGTAGAGCTTTCCAAGAGCGTAA 157	9
Op	1132 Se	115	Т
Qy	1577 TA	3CTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGG 163	9
qq	1151 16	uSerThrA 115	8
Qy	1637 GC	167	7
qq	1158 18	::: :: aThrThrIleSerGlyLeuLysThrValTyrThrTrpCysProLeuThrS 117	7
Οy	1678		e
Dp	1177 eı	rLysSerThrLeuGlyAlaThrThrGlnThrSerSerThrAlaLysvalArgIleThr- 119	9
δy	1724 AC	CGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAG 178	m
QQ	: 1197 Se	 SerSerAlaThrSerThrSerIleSerLeuSerThrSerThrGluSerGluSer 121	9
Qy	1784 G	CAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGATA 184	en
Dp	: 1217 Se	0 123	9
Οy	1844 T	TCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATA 1903	ē
Db	1237 T	r 125	19
Qy	1904 T	CGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCG 194	S
Db	1257 S		. 9
Qy	1946 G	GTAGCCCCGTATTCGATAAGAACGCCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGG 2005	ζ.
qq	1277 i	SerileSerAlaSerSerProSerSer 129	
Qy	2006 A	AAGCTATGAGTGACATGGAGTTCGAACCCGATCTGCAGCGCACAATCAGGGTGGACA 2069	52
qq	1292 T	hrSerLeuLeuSerThrSerLeuProSerProAlaPheThrSerSerThrLeuProThr 131	۲.
Qγ	2066 T	TCCGCTACGTTCTTCTTCATGATTGACAAATGGGGTCAGTGCCCCÇGTCTCATCCAAGAGC 212	22

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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
"Similar short elements in the 5' regions of the STA2 and SGA genes
from Saccharomyces cerevisiae.";
FEBS Lett. 239:179-184(1981)
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.
-!- SIMILARITY: TO S.POMBE SPRC215.13.
-!- SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
Glycoprotein;
                                                                                                                ANYH_YEAST STANDARD; PRT; 1367 AA.

D08640; P08068:

D1-40G-1988 (Rel. 08, Created)

O1-FEB-1995 (Rel. 31, Last sequence update)

G1ucoanylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-9lucosidase) (1,4-alpha-D-9lucan glucohydrolase).

STAI OR STA2 OR MALS OR YIRO19C.

Saccharomyces (Baker's yeast).

Eukaryota; Pungi; Ascomycota; Saccharomycetina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Barkin=S288C / AB972;
Barcola B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Deviin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamashita I., Nakamura M., Fukui S.; "Gene fusion is a possible mechanism underlying the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLOCOAMILASE S1/S2.
SER/THR-RICH.
N-LINED (GLCNAC. . ) (POTENTIAL).
MW: 91C00E2DBD61AA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Polysaccharide degradation;
Signal; Multigene family.
SIGNAL 1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-242 AND 762-1331 FROM N.A. MEDLINE=87194600; Pubmed=3106330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-31 FROM N.A.
STRAIN-SPX101-1C;
MEDLINE-89031230; PubMed-3141213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 169:2142-2149(1987)
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EMBL; M16164; AAA35014.1; --
EMBL; M16165; AAA35015.1; --
EMBL; X1387; CAA32069.1; --
PIR; B26877; B26877.
PIR; A26877; A26877.
PIR; S48478; S48478.
SGD; S0001458; MUCI.
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AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

BD 10-1000

BD 610coar

BD 7 10-1000

BD 82chary

BD 82chary

BD 82chen

BB 82c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 ThrGluSerSerSerAlaProValThrSerSerThrThrGluSerSerAlaProVal
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                                                  Conservative:
Mismatches:
  Length:
Matches:
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                                                                                                                                                                        US-10-008-355-1 (1-2139) x AMYH_YEAST
0.0657
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21.148
                                                  Percent Similarity:
Best Local Similarity:
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1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603
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                                                                                                                        687 ThrThrGluSerSerSerAlaProValThrSerSerThrThrGluSerSerAlaPro
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| AsnSerAlaGlyGluThrThrSerGlyCysSerProLysThrValThrThr----
                             GluSerSerSerAlaProValProThrProSerSerSerThrThrGluSerSerAla
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                                                                              1970 GCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGT 2029
                                                                                                                  986 Thrval-------CysSerThrGlyThrAsnSerAlaGlyGluThrThrSerGly 1001
                                                                                                                                                            ---ATCTGCAGCGCACATCAGCGTGGACATCC 2068
                                                                                                                                                                                                     1002 CysSerProLysThrIleThrThrThrValProCysSerThrSer-----ProSer 1018
1910 TCCTATCGAACAACGACATCACGGCGGTAACTCCGGTAGCCCCGGTATTCGATAAGAACG 1.969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coulson A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Lalsster N.,
Latrellle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonhhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                         2069 GCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCC 2119
                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 86.9 kDa protein C30C11.4 in chromosome III.
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PROSITE; PS01036; HSP70_3; 1.
HYPOTHELICAL protein; ATP-binding; Multigene family.
SEQUENCE 776 AA: 86896 MW; 20FA975FB649FA9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                   776 AA
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Matches:
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MEDLINE=94150718; PubMed=7906398;
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InterPro; IPR001023; Hsp70.
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143.50
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SEQUENCE FROM N.A.
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AATCGCTTGACGACAAGTACAAAGACTACC 1312
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                                  CGATAGGTCGTAACCGTGCCGAGGAAAGAG 1072
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|nTyralaGluPheIleThrProAlaAlaA 604
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|hrSerThrGluAspTrpLeuTyrAspGluG 622
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-----AspVal<sup>†</sup>fyrGluLysArgLeu- 634
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covalvalGluArgTyrArgGluSerGluT 653
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|InSerIleMetArgValArgLysAlaTyrG 673
                                                         || ||| ||| ::: |||| alaspGlyAspAlaLysThrGluAlaProA 525
                                                                                                                                       ysLeuValProValAspLeuGluValileG 545
                                                                                                                                                                                                                                 /sPheHisAsnLeuGluLeuGlnMetGlnG 565
                                                                                                                                                                                                                                                                                                 spalaLysAsnSer---LeuGluGluTyrV 584
-SerAlaThrMetTyrGluProArgileV 505
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Furuichi Y.;
risiae gene whose overexpression
sr toxin, which inhibits
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LLER TOXIN.
embrane protein (Probable).
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aromycotina; Saccharomycetes;
ae; Saccharomyces.
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SER/THR-RICH.

12 X 28 AA TANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-A-P-A-A-I-S-S-T-
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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252 N-LINKED (GLCN...
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Indels:
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                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                               PROTEIN 1
SIMILARITY: SOME, TO YEAST MSB2
                                                                                                                  SGD; S0002828; HKR1.
Glycoprotein; Transmembrane;
SIGNAL 1 21
                                                                                                        EMBL; S69101; AAB30051.1; -.
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SEQUENCE
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TCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGGC 1109
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--ThrSerAspThrMetSerSerValLysLysSerThr 112
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                                                                                                   AAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAG 471
                                                                                                                                                                                                                                                             GlulleAlaThrProSerSerSerIleValProThrProLeuGlnSerTyrSerAspGlu 132
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DOMAIN
  TGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAA 1640
                                                                                                                                                                                                                                                                                    1701 CAACTICACCATGCGTAIGAGCIACGGCTCCATCAAGGGATAIGAACCGCAGGACGGIGC 1760
                                                                                                                                                                                                                                                                                                                                                                                 1821 TGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTA 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                --- ATATCGCTTTCCTATCGAA 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1920 CAACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGAT 1979
1380 CAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAAT-----TCAAAGGCGA 1430
                                                                                                                                          ------CCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGC 1580
                                                                                                                                                                                                                                      1641 GCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGC 1700
                                                                                                                                                                                                                                                                                                                                   1761 CTGGTACAACTATCATACGACAGGCAAGGGGGGTATTGGAGAAGCAGGATCCTAAGAGGGA 1820
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                                                                                                                                                                                                               463
                                                                                                                                                                                                                                                                                                                                                                                                463 hrSerSerProSerAlaSerValValValProSerAlaTyrAlaSerSerProSerValP 483
                      371 erAsnThrPheAlaValSerSerIle---SerThrThrAsnPheIleValSerSerAlaS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roValAlaValSerSerThrTyrThrSerSerProSerAlaProAlaAlaIleSerSerT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2001 (Rel. 40, Last annotation update)
Low-density lipoprotein receptor-related protein 1 precursor (LRP)
(Alpha-2-macroglobulin receptor) (A2MR).
                                                                                                                                                                                                                                                                                                                                                 1980 CGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 eralaProAlaAlaIleSerSer-----ThrTyrThrSerSerProSerAlaP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 ----ThrSerSerProSerAlaProValAlaValSerSerThrTyrThrSerSerProS
                                                            :: :: ||||||| ::: |||| erAspThrValValValSerThisSerT
                                                                                                                                                                                                                                                               TALT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 alSerSerThrTyrThrSerSerProSerAlaProAlaAlaIleSerSerThrTyr----
                                                                                           1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTG-
                                                                                                                   410 hrPheValHisAlaThrSer-----SerSerThrTyrlleSerSerSerLeuT
                                                                                                                                                                426 yrSerSerProSerLeuSerAlaSerValSerSer---HisPheGlyValAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2085 GATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 hrTyrThrSerSerProSerAlaProvalAlaValSerSer 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUE=Liver, and Ovary;
                                                                                                                                                                                                                                                             450 erPheSerSerValProValAlaValSerSerThr----
                                             1431 CACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCGAGAACGGTCAGCTCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRP1_CHICK
ID LRP1_CHICK
AC P98157;
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MEDLINE-94103212; PubMed=7506255; Nimpf J., Stifani S., Bilous P.T., Schneider W.J.; Mingt J., Stifani S., Bilous P.T., Schneider W.J.; The somatic cell-specific low density lipoprotein receptor-related protein of the chicken. Close kinship to mammalian low density lipoprotein receptor gene family members."; J. Biol. Chem. 269:212-21911994).
-i- FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
                                                                                                                                                                                AND ACTIVATED ALPHA 2 "MACROGLOBULIN, AS WELL AS THE LOCAL METABOLISM OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR ENDOGENOUS INHIBITORS, BINDS VITELLOGENIN, CALCIUM AND ALPHA 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- ALTERNAHIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-:- TISSUE SPECIFICITY: SOMATIC.
-:- PIM: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LRP-85) AN A 515 KDA LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-COVALENTLY ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
EGF-LIKE 2,
EGF-LIKE 3,
EGF-LIKE 3.
EGF-LIKE 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Endocytosis; Glycoprotein;
EGF-like domain; Coated pits;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: CONTAINS 22 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR00172; LDL_recept_A.
InterPro; IPR00003; Ldl_recept_A.
Pfam; PF00008; EGF; 14.
Pfam; PF00057; Idl_recept_a; 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00010; ASX_HYDROXYL; 3. PROSITE; PS00022; EGF_1; 5. PROSITE; PS01186; EGF_2; 7. PROSITE; PS01107; EGF_CA; 2. PROSITE; PS01209; LDLRA_1; 27. PROSITE; PS50068; LDLRA_2; 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00057; ldl_recept_a; 31. pfam; PF00058; ldl_recept_b; 33. PRINTS; PR00010; EGTBLOOD. PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00179; EGF_CA; 3.
SMART; SM0010; EGF_like; 18.
SMART; SM00192; LDLa; 31.
SMART; SM00135; LY; 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X74904; CAA52870.1; -. HSSP; Q07954; 1CR8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4543
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                                                                                                                                                                                                                                                                   MACROGLOBULIN.
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1100 1140 LDL-RECEPTOR CLASS A 9. 1141 1180 LDL-RECEPTOR CLASS A 10. 1121 1220 EGF-LIKE 6. 11534 1577 EGF-LIKE 6. 12512 2191 EGF-LIKE 7. 12512 2191 EGF-LIKE 9. 12513 2191 EGF-LIKE 9. 12514 2512 EGF-LIKE 9. 12515 2512 LDL-RECEPTOR CLASS A 11. 12516 2556 LDL-RECEPTOR CLASS A 13. 12517 LDL-RECEPTOR CLASS A 13. 12518 2514 LDL-RECEPTOR CLASS A 14. 12519 LDL-RECEPTOR CLASS A 15. 12519 100-RECEPTOR CLASS A 16. 12519 2510 LDL-RECEPTOR CLASS A 16. 12510 2510 LDL-RECEPTOR CLASS A 16. 12510 2510 LDL-RECEPTOR CLASS A 19. 12511 2511 LDL-RECEPTOR CLASS A 21. 12511 2511 LDL-RECEPTOR CLASS A 22. 12511 2511 LDL-RECEPTOR CLASS A 22. 12511 2511 LDL-RECEPTOR CLASS A 23. 12511 2511 LDL-RECE	4374 EGF-LIKE 21. 4409 EGF-LIKE 22. 3942 RECOGNITION PROCESSING (4506 ENDOCYTOSIS 42 BY SIMILARIT 66 BY SIMILARIT 87 BY SIMILARIT 87 BY SIMILARIT 87 BY SIMILARIT	100 BY SIMILARITY 110 BY SIMILARITY 110 BY SIMILARITY 111 126 BY SIMILARITY 112 113 110 BY SIMILARITY 113 110 BY SIMILARITY 110 110 BY SIMILARITY 110 BY SIM
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	qq	4163	ProSer-GlyPro	/alCysThrCysPro/	AsnGlyLysArgLeuAs	pAsnGlyThrCysVa 4182	
	δy	1367	GTATCCCTG	CCGACAGCTCCCCG	CTATCCCTGCCGACAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAATTC	ATCGACAAGAAATTC 1422	
	qq	4182		ProThrAlaSerAlaV	/al-ValProThrThr	spThrCysAspLeuV 4202	
	QY	1423	AAAGGCGACACGA	AGAAGTATGCAGACTT	AAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGC	GIGGIICCITAIAGC 1482	
	qq	4202	-	Phe	AsnAlaArg	4215	
	QY	1483		CCATGCTCAAGTCCAT	GACAAGTICCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAA	GCCAA 1532	
	QQ	4215		sArgCysGlnProArg	gTyrAsnGlyGluArgC	ysglnIleAsnGlnC 4235	
	οy	1533	GGCTATCG	GGCTATCGAGAAAGATCCGGC	AGTAGAG	-AGTAGAGCTTTCCAAGAGCGTA 1575	
	Db	4235		sGlnAsnGlyGlyLeu	ysSerAspTyrCysGlnAsnGlyGlyLeuCysThrAlaSerProSerGlyMetProThrC	erGlyMetProThrC 4255	
	QY	1576		ATAGCTGCTCGCGCTATTCAGGC	-CGATGCGATGGCCAA	TGCCTAT 1623	
	Db	4255		: rGlyPheThrGlySeı	ysArgCysProThrGlyPheThrGlySerArgCysAspGlnGlnValCysThrAsnTyrC	alCysThrAsnTyrC 4275	
	δy	1624	-	GCCATTGAGAAGGCAAGCGTCTTTT)	CTTTGCCGGTTTGCGT 1665	
	qq	4275	ysHisAsnAsnGl	ySerCysThrValAsı	ysHisAsnAsnGlySerCysThrValAsnGlnGlyAsnGlnProAsnCysArg-	snCysArg 4292	
	Qγ	1666		SACGTGCTCTGCCGAC	SCGATGCCAACTTCACC	ATGCGTATGAGCTAC 1725	
	qq	4293	TIL	orhrPhelleGlyAsp	CysProProThrPheIleGlyAspArgCysGlnTyrGlnGlnCysPheAsnTyrC	::: :lnCysPheAsnTyrC 4311	
	Qy	1726		SATATGAACCGCAGG	ACGGTGCCTGGTACAAC	TATCATACGAC 1781	
	Dp	4311	ysGluAsnAsnGl	yval	ysGluAsnAsnGlyValCysGluMetSerArgAsp	etSerArgAsp 4322	
	RESULT 6	T 6 YEAS1	£			ESULT 6 M96 YEAST	
	! 11	96MY	YEAST STA	NDARD; PRT	; 1140 AA.		
	DI.	01-N	93; OV-1997 (Rel.	35, Created)			
	TO TO	01 - NC 01 - NC	OV-1997 (Rel.	35, Last sequend 35, Last apportat	ce update)		
	DE	Нуро	thetical 113.1	kDa protein in	PRE5-FET4 inter	renic region.	
	N S	YMR3.	17W OR YM9924. haromyces cere	09. visiae (Baker's	veast).		
	888	Euka	ryota; Fungi;	Ascomycota; Sace	charomycotina; Sa	ccharomycetes;	•
	3 x	Sacci NCBI	naromycetales; _TaxID=4932;	Saccharomyceta	ceae; Saccharomyo	es.	
	RN	[1]	ENCE FROM N A				
		STRA	IN-S288c / AB9	72;			
		Chur.	cher C.M., Lou itted (NOV-199	is E.J., Barrel. 5) to the EMBL/(Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., 1 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.	um M.A., Walsh S.V.; bases.	
		-1-	DOMAIN: CONTAI	NS MANY SER/THR	-RICH DOMAIN AND	REPEATS.	
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		or se	end an email t	o license@isb-s	ib.ch).		. !
		EMBL	; Z54141; CAA9	0835.1;			
	SOW	Hypor	Hypothetical protein; Repeat. SEQUENCE 1140 AA; 113070 M	Χ,	0153EBCA24FE5427	CRC64;	·
	110	nment	Scores:				
	Pred.	red. No.: Score:		0.195 137.50		1140 131	
_	Perce	int s	ercent Similarity:	36.73%		96	

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21.20% Mismatches:	Query Match: 3.60% Indels: 145 DB: 1 Gaps: 21	US-10-008-355-1 (1-2139) x YM96_YEAST (1-1140)	QY 533 AGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTC 592	Db 233 SerThrSerSerProAlaSerSerThrIleSerGluThrLeuProPheSerSerThrIle 252	Qy 593 GTATGCTACTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGA 652 1:	653 TGTGGCCGCGTCACACGGCGACTTCAGCGTATTCCGCGTGTATGCCG	::: ::: ::: ::: Db 270 SerSerValSerSerGluAlaSerSerThrSerSerSerValSerSerGluAlaPro 289	701 GTGCCGACACCGGCCGGCCGAATACAGCAAGG	AlaŤ	Oy 740AACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTG 793 Oh 310 corclustancescenth-carcarcarcarcarcarcarcarcarcarcarcarcarc	10	325 SerSerThrThrSerSerSerValSerSerGluAlaProLeuAlaThrSerSerValVal	Qy 851GGGGTGTGGAAGATCGTAAAACGAGA 880	Db 345 SerSerGluAlaProSerSerThrSerSerSerValSerSerGluIleSerSerThrThr 364	881		Oy 932 CCATGAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTAGAGTGCTA 991	992 ACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	::: ::::::::::::::::::::::::::::::::::	1052	.Db 425 SerSerValMetSerSerGluValSerSerAlaThrSerSerLeuValSerSerGluAla 444	OY 1112 TCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	1172 GTGAGATGACTTATTTGAGCGAGAGCTCTTCGGTGGTACCGAGGTGGTTTTGCAC		Qy 1232 AGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCC 1279	Db 479	Oy 1280 TCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTGGTCGTAAGGTGCTGC 1339	1340 CCCCBRCCRCBRRARGERACCSCCRARGERACCRCACACACACACACACACACACACACACACACACA	5340 CCGCCRICCTCORING TOTAL CCCCCCGCCACACCTCCCCTATTICA 1:: :::	Qy 1400 AGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCG 1453 	1
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                                                                                                                                                                                 AAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTG 1585
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---TATTCGACAAGAGTGTGGTTC 1474
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| IllePheGlyAsnSerSerThrValThrThrSerProSerAla 558
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aSerProLeuProSerValTrpSerAspIleThrSerSerGlu 578
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rSerGluThrThrAsnGluSerAsnLeuAlaThr---SerSer 636
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nLysAlaThrAlaArgSerLeuSerThrSerAsnAlaThrSer 656
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                                                                                                                                                                                                                                                                                                                  -----AsnAsnSerThrIle 599
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aSerGlyAspValThrSerSerLeuAlaAlaHisAsnLeuThr
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----GCTCAAATAAGTCATCTCACGGTTGGCCTTGGCTCCTTCTTATA 1147
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                                                                                                            138 ThralaThrargValaspargValGlnaspileHisAspileSerasnargValIleGly 157
                                                                                                                                                                                                               158 HisLeuCysCysGlnHisLysSerSerLeuGlyGluPheAspGlnAsnLeuIleValPhe 177
                                                                                                                                                                                                                                                                                                                        178 SerGluGluLeuThrProSerGluAlaAlaAsnAlaAsnProGluTyrIleArgGlyPhe 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuAlaLysAsnIleProTyrValAlaAsnPheThrThrGluLeuTrpAspThrIle 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      798 GTCGTCAGCCTTGTAGCCTTGCATGGATACGGCAGCGAAGTAAACGGGCCTTATAGGGTTT 739
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IleAlaLeuVal-----LysArgLeuPheGlnGluGluIleArgLeuLeuLysGlyIle 424
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     118 PheValPheSerSerValMetGlyGluIleGluLysSerLeuCysAlaValGlnLysThr 137
                                                                                                                                                                AAACTGTGC-----AAAACGAACCACCTCGGTACCACCGAAGAGCGTCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 LysGluPheSerGlyThrLeuValLeuIleAsnGlyAspLysGlyGluIleThrPheAsn
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(See http://www.isb.sib.ch/announce/
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                                                                        SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDBATE ACTIVE TRANSPORT SYSTEM. ENZYME I TRANSFERS THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE (PEP) TO THE PHOSPHORYL CARRIER PROTEIN (HPR).
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                      Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                    ENZYME I IS COMMON TO ALL PTS (BY SIMILARITY).

CATALYTIC ACTIVITY: Phosphoenolpyruvate + protein L-histidine pyruvate + protein N(pl)-phospho:L-histidine.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PEP-UTILIZING ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluHisGluIleSerArgTyrTyrLysAlaLeuLysArgSerArgSerAspLeuAlaAla
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InterPro; IPR000121; PEP_utilizers.
Pfam: PF00391; PEP-utilizers; 1
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  MEDLINE-99000809; PubMed-9784136;
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                                                                                                                                                                                                                                                                                                                                                                                                                            18 X APPROXIMATE TANDEM REPEATS, SER/THR-
                                                    319
                                                                         484
         GATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A CORE SUBUNIT.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
AND/OR BY CARBOHYDRATE-MEDIATED COVALENT CROSS-LINKS (POSSIBLE).
                                                                                                                                                                                                                                                                                                                                                            Roy A., Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.;
"The AGAL product is involved in cell surface attachment of the
Saccharomyces cerevisiae cell adhesion glycoprotein a-agglutinin.";
Mol. Cell. Biol. 11:4196-4206(1991).
                      485 ValileArgMetileHisHisValValGluGlnAlaLysGlnLysAsnValProValSer
                                                    CACGGAAAGACCCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACCATCGCG
                                                                       LeuGlyThrSerArgGluArgSerLeuLeuGlyGluArgSerArgValProHisProSer
                                                                                               CAGATAGTCGTGATCCACCGTGCTTTG-----GCTCTGGATAGCACCGTATCCGCAGTG
                                                                                                                                                                                                                                                                                              Saccharomycetes;
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2 X APPROXIMATE REPEATS.
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                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Agglutinin attachment subunit precursor.
AGAI OR YNRO44W OR N3431.
                                                                                                                                                    ||| ||||::: ||| ||||::: ValCysGlyGluMetAlaGlyAspProAlaLeuLeu 516
                                                                                                                                        GTGGTTGGTAAA-----GATCAGGCCCTGATC 238
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Glycoprotein; Cell adhesion;
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AC Q09624; Q			OX NCBI_TaxII RN [1] RP SEQUENCE RC STRAIN=Br		RA Durbin R. RL Submitted CC -!- SUBCE CC -: SIMIL	This betwe the E	mo en or	DR EMBL; Z48 DR EMBL; Z48 DR EMBL; Z48		Interl Interl Pfam; Pfam;		FT DOMAIN FT DOMAIN FT DOMAIN FT TRANSMEM		FT TRANSMEM FT TRANSMEM FT TRANSMEM FT TRANSMEM	FT TRANSMEM FT TRANSMEM FT TRANSMEM SQ SEQUENCE	Alignment Scor Pred. No.: Score:	Percent Simila Best Local Sim Query Match: DB:	US-10-008-355-
IleSerThrThrIleProSerPheSerMetSerThrTyrPheThrThrValSerGlyVal 405	GAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACT 1182 	TATTTGAGGGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC 1242 ::: ::: SerMetHisGluThrValThrThrAspAlaThrValCySThrHisGluSerCySMetPro 445	GCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGAC 1296 ::: ::: ::: ::: SerGlnThrThrSer-LeuIleThrSerSerIleLysMetSerThrLysAsnValAlaTh 465	AAGTACAAAGACTACCTCCCTCGACCGTAAGGTGCTGCCCGCCATGCTC 1350 	GATATTGTACGCGGGGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATC 1410	GACAAGAAGAGCGAC 1431 ::: rThrLysSerTrpValSerSerMetThrThrSerAspGluAspPheAsnLysHisAlaTh 525	ACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTC 1491	CATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCG 1551	GCAGTAGACTTTCCAAGAGCGTAATAGCTGCGCTGTGTATTCAGGCCGATGCGATG 1611 :::	GCCAATGCCTATGCCATGAGAGGGCAAGCGTCTTTTCTTTGCCGGTT 1660 :::::::: ::	TGCGTGAGATGTACCCCGGACGTGCTGCCGAGCGATGCCAACTTC 1707 ::: :::: ovalThrThrLeuGlnIleSerSerThrSerGluIleLeuGlnProThrSe 615	ACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTAC 1767	AACTATCATACGACAGGCCAATTGGAGAACAGGATCCTAAGAGCGATGAGTTT 1827 	GCCGTACAGGAGAATATCCTCGACCTTTCCGCACCAAAACTATGGTCGCTATGCCGAG 1887	AACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACGGGGGGGG	AGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCATGGCAACTGGGAA 2007	ACATCGAGT 2029 111 1 PhrSerSer 690	
IleSerThrThrIlePr	GAAAAGGCTTATAAGGA ThrThrMetTyrThrTh	TATTTGAGCGAGACGCT.:: :: SerMetHisGluThrVa	GCATTGGCTACAAATCCTGATGCTC ::: ::: ::: SerGlnThrThrSer-LeulleThrSer	AAGTACAAAGACTACCT rervalserThrserT	GATATTGTACGCCGGCG		ACGAAGAAGTATGCAGA 	CATGCCATGCTCAAGTC 	GCAGTAGAGCTTTCCAA ::: SerHisLeuLeuSerTh	GCCAATGCCTATGCCAT ::::::: SerAspSerThrIle-L	TGCG : oValThrThrLeuGlnI						GCTATGAGTGGTG7 ::: rIleGlnTyrGln7	L CARDANDADA
Db 386	Qy 1138 Db 406	Qy 1183 Db 426	Qy 1243 Db 446	Qy 1297 Db 465	Qy 1351 Db 485	Oy 1411 Db 505	Oy 1432 Db 525	Qy 1492 Db 545	Qy 1552 Db 560	Qy 1612 Db. 579	Qy 1661 Db 598	Qy 1708 Db 615	Oy 1768 Db 616	Oy 1828 Db 636	Oy 1888 Db 652	Oy 1948 Db 663	Qy 2008 Db 683	RESULT 9 YS89_CAEEL

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                                                                                                    bditis elegans.
a; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
dae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                              d (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EELUUAR LOCATION: Integral membrane protein (Potential).
LARITY: CONTAINS 1 GPS DOMAIN.
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Matches:
Conservative:
Mismatches:
Indels:
            995 (Rel. 32, Created)
002 (Rel. 41, Last sequence update)
002 (Rel. 41, Last annotation update)
ical protein ZK945.9 in chromosome II.
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GLY/SER-RICH.
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ro; IPR001024; Lipoxygenase_LH2.
ro; IPR001024; Lipoxygenase_LH2.
ro; IPR000203; PKD_cys_rich.
PF00520; ion_trans; 1.
PF01825; GPS: 1.
SM00303; GPS: 1.
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...-CTTTCCGTG 378

346 GGTGAGGAGCTTCCGATTCCGGGT-----

qq		qq
Oy Db	379 AAGTATCTGCGCAAGATCGTGAAG	op Op
Oy Dp	409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAG 453	Qy
Qy Dp	454 CGTCTGCGCAAAGCTCAGGAGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAG 513	Oy Dp
O Op	514 AACCAACTCTGCATCGTAGACCTTTCTATTCCAACAACGAATAC 558	Qy
Q Op	559 TTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCT 618 ::: ::: 285 rValThrSerThr289	Oy Dp
Oy Db	619 GTAGGTAAGTTCGGAGGCGATACGGACAGCTGGATGTGGCGGCGTCACACGGGCGACTTC 678 1 1 1 1 1 1 1 1 1 1	Qy Dp
Qy Dp	679 AGCGTATTCCGCGTGTGCCGGCGACAACCGGCCGAATACAGCAAGGACAAT 738 .	Qy Dp
Oy Db	739 AAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGAC 795 1	Oy Dp
Oy Db	796 GACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGT 855 ::: 330	Qy
Q Op	856 GTGGAAGATCGTATCGAAAACAACGAGAACCATCTCGAAGTTCGCGGTATCAAGCAA 915	oy Og
Oy Dp	916 GGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCGGTATCAAATATGCCA 970	Qy Dp
. yo	971 -GCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGC 1023	Qy
Oy Op	1024 GGTCTCGCTCGTCTTGACCTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGAC 1083	Qy Db
Oy Db	1084 TGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGAAAAG 1143 	Qy
Oy Db	1144 GCTTATAAGGAAGGACCAAGGCCAACCGTGAGATGACTTATTTGAGCGACACGCTCTTC 1203 1::	Qy Dp
λο ά	1204 GGTGGTACCGAGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGAT 1263	Oy Dp
3 6 8	GCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCG	Qy
λ̈́ο	CTCGACCGTAAGGTGCTGCCCGTCGATATTGTACGCCGGCGTATCCCTGCCGAC	RESULT COLA_(ID (

Op	446	SrSerThrValThrThrSerProSe	454
Qy	1381	AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGA	1440
QQ	454	rThrSerProvalThrSerThrValThrSerSerSerSerSe	471
Qy	1441	TATGCAGACTTCGTATTCGACAAGAGTGTGGGTTCCTTAT:	1500
qq	472	-ValThrThrProThrSerThrGluSerThrSerPhrSerP	486
οy	1501	CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAG	1542
qq	486	rSerThrValThrThrSerThrThrAlaProSerT	909
Qy	1543	AAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTC	1598
Op	206	rSerSerThrProSerSerThrAlaSerSerValSerSerThrAlaSerSerThrG	526
οy	1599)) -	1614
QQ	526	nSe	546
Qy	1615	:	1658
qq	546	rAspGlyThrAsnProAspPheTyrPhe	999
Qy	1659	TTTGCGTGAGATGTACCCCGGACGTGCTCTGC	1718
qq	266		575
Qγ	1719	GAGCTACGGCTCCATCAAGGGATATGAA	1746
QQ	575	rGlyLeuGlyIleIleGlyTyrGln	594.
Qy	1747	CCGCAGGACGGTGCCTGGTACAAC	1770
Db	594	. ::: rAsnTyrValSerThrThrLysAspGlyAlaCysPheThrLysSerValSe	614
QY	1770		1770
QQ	614	$\tt gLeuGlyGlyThrTyrProAlaSerThrPheValGlyProGlyAsnTyrThrPheArr$	634
QY	1771		1795
QQ	634	аТh	654
Qy	1796	Ĭ	1853
Db	654		674
Οy	1854	CTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACG	1898
QQ	674		694
Qy	1899	199 CCATATCGCTTTCCTATCGAACAACAACAACGGGGGGGGG	1958
qq	694	erThrArgSerSerAspSerThrThrThrSerAlaGlySerThrThrThrLeuGlnGluS	714
Qy	1959) CGATAAGAACGGCCGTCTGATCGGTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGG	2018
qq	714	erThrThrThrSerGluGluSerThrThrAspSerSerThrThrThrIleSerAspThrS	734
٥y	2019	TGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCT	2078
qa	734	erthrThrSerSerSerTroSerSerThrThrAlaAspSerThrSerThrLeuS	752
Qy	2079	CT 2080	
QQ	752		
RESI COL! ID	RESULT 10 COLA_CLOPE ID COLA_C) DE CLOPE STANDARD; PRT; 1104 AA.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50093; PKD; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Zymogen; Signal; Complete proteome.
SIGNAL 1 39 POTENIAL.
                                                                                                                                                                                                                                                                                                                                                                                        Matsushita 0.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Digestion of native collagen in the triple helical region at Xaa -! Gly bonds. With synthetic peptides, a preference is shown for Gly at P3 and P1'; Pro and Ala at P2 and P2'; and hydroxyproline, Ala or Arg at P3'.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M9.
         01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Microbial collagenase precursor (EC 3.4.24.3) (120 kDa collagenase).
                                                                                                                                   STRAIN=NCIB 10662;
MEDLINE=94110220; PubMed=8282691;
Matsushita 0., Yoshihara K., Katayama S.-I., Minami J., Okabe A.;
"Purification and characterization of Clostridium perfiingens 120-kilodalton collagenase and nucleotide sequence of the corresponding
                                                                                                                                                                                                                                                                                       Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                      Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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ZINC (CATALYTIC) (BY S
L -> F (IN REF. 1).
I -> M (IN REF. 1).
G -> E (IN REF. 1).
V -> E (IN REF. 1).
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Interpro; 1PR000601; PKD_domain.
Interpro; 1PR000130; Zn_MTpeptdse.
Pfam; PF00801; PKD; 1.
Pfam; PF01752; Peptidase_M9; 1.
PRINTS; PR00931; MICOLLPTASE.
                                                                                                                                                                                                                           Bacteriol. 176:149-156(1994).
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1073-1104 FROM N.A. STRAIN=NCIB 10662;
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PubMed=11792842;
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                                                                                                             NCBI_TaxID=1502;
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349 GAGGAGCTTCCGATTCCGGGTCTT-----TCCGTGAAGTATCTGCGCAAGATCGTG 399
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|LeuPheArgHisGluPheThrHisTyrLeuGlnGlyArgTyrVal
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                                                                          CRC64;
     T -> A (IN REF. 1).
A -> E (IN REF. 1).
I -> T (IN REF. 1 AND 3)
WW; F4B7377194ED021C CRC
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Matches:
Conservative:
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629	696	675	1026	695	1086	1 .	1143	1176	749	1236	763	1281	477	1341	785	1401	794	1443	814	1479	829	1518	849	1551	698	1593	688	1644	606	1659	929	1698	949	1758	696
AsnAsn1leAspAsnLeuAspValProLeuValSerAspGluTyrValAsnGly	CAAGGCATCTG			SerAsnIleLysAspLeuSerSerAsnValGluLysSerGlnPhePheThrThrTyrAsp	CTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGG :::		AICCGTAAGAACGCAAGAAGTGCTGTCTATGGCGAATGTTGTCTTTTCTCTCGAAAGG LysAspMetAsnSerLysLeuAsnAspTleLcaLysGluLeuSerLysEys		SerTrpAsnGlyTyrLysThrValTh			GCCAACGCATT	AspThrAsnThrA	AAATCGCTTGA		GCCATGCTC	IleValGluGluGluIleAsn		GlyThrGluSerLysAspGluAspGlyGluIleLysAlaTyrGluTrpAspPheGlyAsp				::: :::::: ThrGlyGluTyrGluValLysLeuThrValThrAspAsnAsnGlyGlyIleAsnThrGlu		SerLysLysLleLysValValGluAspLysProValGluValIleAsnGluSerGluPro	GCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCT			:::		LysIleThrLeuAsnAsnLeuAsnSerValGlyIleThrTrpThrLeuTyrLysGluGly				LysThrLeuGluProGlyArgTyrTyrLeuSerValTyrThrTyrAspAsnGlnSer
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hyaluronare.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: The partially purified protein from strain CPN50 is
-!- CAUTION: The partially purified protein from strain CPN50 is approximately 70 kba smaller than the sequence indicated here.
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                                                                                                                                                                                                                                             1759 GCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGC 1818
                                                                                                                                              1879 TATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGT 1938
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                    970 -----ThrTyrThrValAsnValLysGlyAsnLeuLysAsnGluValLysGluThr 986
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"Molecular genetic analysis of the nagH gene encoding a hyaluronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Putative virulence factor which is likely to act on connective tissue during gas gangrene.
-!- CATALYTIC ACTIVITY: Random Mydrolysis of 1.4-linkages between Naccetyl-beta-D-glucosamine and D-glucuronate residues in
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                                                                        1819 GATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGC
                                                                                                                                                                                  -----AsnAsnAsp-----
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15-JUN-2002 (Rel. 41, Last annotation update)
Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                          987 AlaLysAspAlaIleLysGlu------
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Mol. Gen. Genet. 243:215-224(1994)
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MEDLINE=94232189; PubMed=8177218;
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Db 225 AspProTyrHisAsnSerLysTrpArgAspLeuTyrProGlu 238 Qy 943 GATCAGGCTACCGGTATCAAATATGCCAGCAAGTATGGTCAGAGTGCTAAGAAGTGTAATGGAAG 1002	Db 239 GluLysLeuSerGluIleLysLysLeuAlaGlnValGlyAsnGluThrLys 255 Qy 1003 AATTCGATC	Qy 1033CGTCTTGACGTGATAGGTCGTAAG	Oy 1063 GAGGAAGAGCATTCGCA1080	Oy 1081	OY 1111 GTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAGGAAGGA 1158	Qy 1159 GCCAAGGCCAACCGTGAGATGACTTATTGAGCGAGACGCTTT 1203 ::: ::: ::: Db 354 SerSerAlaGInLeuLysGluLeuAsnLysAlaGluAspAsnValSerIleValMetThr 373	Qy 1204 GGTGGTACCGAGGTGGTTGGTTTGCACAGTTTGCCAACGCATTGGCTACA 1254	Qy 1255 AATCCTGATGCTCATGCGGT	Qy 1291 GACGACAAGTACAAAGACTACCTC	QY 1321 CTCGACCGTAAGGTGCTGCCCCCATGCTGATATTGTACGCCGGCGTATCCTGCCGAC 1380 :::	Oy 1381 AAG	Oy 1426 GGCGACACGAAGAGTATGCAGACTTCGTATTC 1458	Qy 1459 GACAAGAGTGTGCTTATAGCGACAAGTTCCATGCTCAAGTCCATGGAC 1515	QY 1516AAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGGTTTCCAAGAGC 1572	Oy 1573 GTAATAGCTGCTGCTGCTATTCAGGCCGATGCGATGGCCAATGCCTAT 1623 :::	Qy 1624 GCCATTGAAAGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGT 1683	Qy 1684 GCTCTGCCGAGCGATGCC
CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).	EMBL; M81878; AAAZ EMBL; AP003185; BA PIK; S27540; S2754 InterPro; IPR0021C InterPro; IPR00042	PF00404; Dockerin_1; 2. PF00754; F5_F8_type_C; 1 SM00231; FA58C; 1. ase; Glycosidase; Toxin;	SIGNAL 1 1528 CHAIN 31 1628 DOMAIN 703 1032 PEPEAT 703 748	REPEAT	VARIANT 520 520 V 7 M (IN STRAIN VARIANT 558 558 D -> E (IN STRAIN VARIANT 614 614 G -> E (IN STRAIN VARIANT 614 61 S -> E (IN	VARLANT 944 944 1 -> V (IN STRAIN VARLANT 979 979 T -> I (IN STRAIN VARLANT 979 979 T -> I (IN STRAIN VARLANT 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 I -> I (IN STRAIN T 982 982 982 982 I -> I (IN STRAIN T 982 982 982 982 982 982 982 982 982 982	1042 1042 I -> F 1043 1628 MISSING 1628 AA; 182474 MW; D42	.75 Length: 21.00 Matches: 2.24% Conservative:	St Local Similarity: 20.09% ery Match: 1 1 1	CTCATCGTCTAC	111 VAIVAIASPASHIYFPHEABHLYSASHIITEFIOHISASPOLUSEEFHEETTTTTT VAIVAIASPOLUSEEFHEETTTTTT VAIVAINTEEFT VAIVAINTE	634 GGCGATACGGACACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTG	694 TATGCCGGTGCCGACAGCCGAATACAGCAAGACAATAAACCCTATAAGCCC ::: ::	754 GITTACTICGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATC 111111111111111111111111111111111	814 GGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATC	DD 185 AlahisangGiryPhelieGiuGiyiyrTyrGiyashFroirpSerashGiuAspArgAla 204 Qy 871 GAAAAGGAGAAC 882 Ch 205 GirishMatrusDhadiuGiuGiuanamurringtanamurrin	200 GILLEUMELLYSFIEGGIYGIYASPIYLLYSLEUNSHGIHIYIYYYELEUNSHGIHIYYYYSSP 883 AATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGCCATGAGCGCA !::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=El Tor N16961 / Serotype 01;

STRAIN=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                        1875
                                                                                                                                                                                                                                                                                            GCTTTCCTATCGAAC---AACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGAT 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
           -TATGAACCGCAGGACGGTGCCTGG 1764
                                                                                                                                                                                                          646
                                                                                                                                                                                                                                                                                                            Chorans., Nature 406:477-483(2000).
-!- FUNCTION: This protein promotes the GTP-dependent translocation the nascent protein chain from the A-site to the P-site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-G/EF-2 SUBFAMILY.
                                587 AlaileGlyTyrLeuLysSerAlaIleAlaIleGluGlyAspAspGluAlaAlaTrp
                                                                TACAACTATCATACGACAGGCCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                      1825 TTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGT-----
                                                                                                                                                                                             -----SerLysThrTyrGlyPheHisTyr
                                                                                                                                                                                                                                                                647 MetGlyGlnAsnLeuSerValValIleGlySerIleValAspProAsnArgIleIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                   ||||||| :::
| 607 AlaAsnTyr---SerGluAlaGlnGlyAlaPheGluLys-------
                                                                                                                                                                              -----CGCTATGCCGAGAACGGTCAGCTCCATATC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
FUSA OR VC0361.
                                                                                                                                                                                                                                                                                                                                                                                                                                      698 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004124; AAF93534.1; -. HSSP; P13551; 1ELO.
TIGR; VC0361; -.
        1720 AGCTACGGCTCCATCAAGGGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                  1963 AAGAAC 1968
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                                                                                                                                                                                                                                                                                                                                                                            686 AsnAsn 687
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125 ThrValTrpArgGlnAlaAspLysTyrGlyValProArgMetValPheValAsnLysMet 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GAAGGACAGCTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GlnIleLysHisArgLeuGlyAlaAsnProValProIleGlnLeuAsnIleGlyAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 GluGluGluPheLysGlyValIleAspLeuIleLysMetLysAlaIleAsnTrpAsnGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 ACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ATTCTTCTCGGAGCAGCCCTGCTGTTG----GGTGCTTCAGGGGTAGCCAAAGCCGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 GlnAlaValLeuAspAlaValIleGluPheLeuProSerProThrAspValProAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 TACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATC------
                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
F44FDA4DB8FC4ECC CRC64;
                                                                      Pfam; PF00679; EFG_C; 1.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF00144; GTP_EFTU, 1.
TIGRPAMS; TIGR00484; EF-G; 1.
TIGRFAMS; TIGR00231; SEACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                               698
120
83
202
246
26
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 GACTATCTGCGCGATGGTTTCGTTTCT-------
                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-008-355-1 (1-2139) x EFG_VIBCH (1-698)
InterPro; IPR000640; EFG_C.
InterPro: IPR0004161; EFTU_DS.
InterPro; IPR000795; EF GTPbind.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 AAG---GTAACGGACAAGGTA----
                                                                                                                                                                                                                                                                                                       76927 MW;
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118.00
31.18%
18.43%
3.09%
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92
145
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Query Match:
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                                                                                                                                                                                                                                                                NP_BIND
NP_BIND
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οy	490	GCCAAAAAAAAAAATGCAGACGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAAC 549
Db	304	SerValGluArgHisAlaAspAspAsn
٥y	550	
op O	317	SerLeuAlaPheLys1leAlaThrAspProPhe
οy	610	CCCAGCTCTGTAGGTAA
QQ	328	328
Qγ	670	GGCGACITCAGCGIATICCGCGIGIATGCCGGIGCCGACAACCGGCCGGCCGAATACAGC 729
qq	329	
Qy	730	
qq	349	AsnSerValLysGlnLysLysGluArgPheGlyArgIleValGlnMetHisAlaAsnLys 368
οy	790	
qq	369	ArgAspGluIleLysGluIleArgAlaGlyAspIleAlaAlaAlaAlaAlaGlyLeuLysAsp 388
δy	816	816
QQ	389	
οy	817	TTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTG
QQ	409	
οy	877	GAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG
qq	417	
٥y	937	AGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGT 987
QQ	437	
Qy	988	
QQ	457	SerGlyMetGlyGluLeuHisLeuAspIleIleValAspArgMetLySArgGluPheGly 476
Qy dy	1015	ATGAACCGCGGTCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAA 1
gg	4//	
ΟŊ	1069	AGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGC 1119
Db	497	
οy	1119	1119
QQ	517	LeuLysIleGluProAlaGluProGlyGlnGlyPheValPheValAspAlaIleAlaGly 536
οy	1120	GATGTATTGTCTTCTCGAAAAGGCTTATAAG 1152
qq	537	
οy	1153	GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212
qq	557	
οy	1213	GAGGTICGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCAT 1269
qq	577	PheHisAspValAspSerSerGluMetAlaPheLysIleAlaGlySerMetAlaPheLys 596
ΟŊ	1270	GCCGGTATCCTCAAATCGCTT1290
QQ	597	LysGlyAla
οy	1291	GACGACAAGTACAAAGACTACCTCCCTCGACCGTAAGGTGCTG 1338

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                                                                                                1339 ------CCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Hess J., Wels W., Vogel M., Goebel W.;

"Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence.";
FEMS Whicrobiol. Lett. 34:1-11(1986).
:::||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || :: || ::: || ::: || :: || :: || :: || :: || :: || :: || :: || :: 
                                                                                                                                                                                                                                                                                    ||| ::::::|||
| 655 ---LeuSerGluMetPheGlyTyrAlaThrAspLeuArgSerAlaThrGlnGlyArgAla 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 178:5422-5430(1996).
FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
-!- PIM: PALMITOXLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                                                                                        Stanley P., Packman L.C., Koronakis V., Hughes C.,
Fatty adviation of two internal lysine residues required for the
toxic activity of Escherichia coli hemolysin.";
science 266:1992-1996(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid IncI2 pHLV152.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis, of the in vivo activation of hemolysin (HlyA) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                  1381 AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1024 AA.
                                                                                                                                                                                                                                                                                                                                                                          1420 ---TTCAAAGGCGACACGAAGAAGTATGCAGAC 1449
                                                                                                                                                                                                                                                                                                                                                                                                                  674 SerTyrSerMetGluPheAlaGluTyrAlaAsp 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE-96404790; Pubmed=8808931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE=95099325; PubMed-7801126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemolysin, plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
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397 GTGAAGGTAACGGACAAGGTAGAAGGACAGCTC---AAGGGTATCACTGACGAGATGGAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 GATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 GGCGATACGGACAACTGGATGTGGCCGCGTCACAGGGCGACTTCAGCGTATTCCGCGTG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 TATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAAACCCTATAAGCCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 AlaValThrLeuAlaIleSerProLeu-------SerPheLeuSerIleAla 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ThrThrSerLeuValGlyAlaProValSerAl 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 AspLysPheLysArgAlaAsnLysIleGluGluTyrSerGlnArgPheLysLysLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 GTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATC
                                                                        PRINTS; PRODOS; TANANORPT.
PRINTS; PRO1488; RYXTOXINA.
PROSITS: PSO0330, HEMOLYSIN_CALCIUM; 4.
Hemolysis; TOXIN; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                    PALMITATE.
W; 83944917F76C945B CRC64;
                                                                                                                                           POTENTIAL.
POTENTIAL.
16 X REPEATS, GLY-RICH.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                          PALMITATE.
                                                                                                                                   POTENTIAL
                 InterPro; IPR001343; Hemiysn_Ca_bind.
InterPro; IPR003355; RTXtoxin_N.
InterPro; IPR003995; RTXA.
Pfam; PF00353; hemolysinCabind; 6.
Pfam; PF02382; RTX; 1.
          EMBL; M14107; AAA98233.1; -.
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20.06%
3.08%
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Best Local Similarity:
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TRANSMEM
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δλ	-	GTTTCCCGGCAGTA
qq	397	uValGlyAlaValThrGlyIleI
QY	830	CGGATCCCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAAC 882
qq	417	 Valile-AlaGluTrpGluLysL
Οy	883	AATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCC 933
qa	437	aAlaPh
Qy	934	SCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCA
q	457	heLysIleLeuSerGlnTyrAsnLysGluTyrSerValGluArgSerValLeuIle-Thr 476
Qy	988	GCTAACTAGTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG
qq	477	GlnGlnHisTrpAspThrLeuIleGlyGluLeuAlaGlyValThrArgAsn 493
Qy	1048	AGCATTCGCAGACTGGATCCGT
QQ	494	AspLysThrLeuSerGlyLysSerT
Qy	1108	⋖
qq	507	Ar
Qy	1168	TGAGATGACTTATTTGAGCGAGAC
qq	514	GluLysLys***AspGluPheGlnLysGlnValPhe525
Qy	1228	STATCCT
qq	526	sGlyAsn
Qy	1288	ACAAGTACAAAGACTACCTCCCTC
qq	535	LysPh
Óγ	1348	CGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATG
qq	554	lleArgGluArgArgGlnSerGlyLysTyrGluTyrIl
Qy	1408	ATCGACAAGAAATTCAAAGGGGACACGGAGAGAAGTATGCAGACTTCGTATTCGACAAG 1464
qa	569	ThrGluLeuLeuValLysGlyValAspLysTrpThrValLysGlyValGlnAspLysGly 588
.0y	1465	ATGCCAT
qa	589	Glr
QY	1522	AAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTT 1563
qq	909	AspLysValPhe
Qy	1564	TCAGGCCGATGCGATGGCCAATGC
qq	626	SerAlaGlySerAlaAsnIleTyr 633
Qy	1624	GCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATG 1671
QΩ	634	AlaGlyLysGlyHisAspValValTyrTyrAspLysThrAspThrGlyTyrLeuThr 652
Οy	1672	TACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGC 1728
QQ	653	IleAspGlyThrLysAlaThrGluAlaGlyAsnTyrThrValThrArgValLeuGlyGly 672
δλ	1729	TCCATCAAGGATATGAACCG 1749
qq	673	AspValLysValLeuGlnGluValValLysGluGlnGluValSerValGlyLysArgThr 692

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US-10-008-355-1 (1-2139) x TEAL_SCHPO (1-1147)
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Best Local Similarity:
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NEDLINE=21844401; Pubbmed=11859360;

Neod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squoros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gonlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gonlins M., Connor R., Cronin A., Davis P., Hudell T., Fraser A.,

Gonlins M., Connor R., Challingworth T., Hurkhell T., Fraser A.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Nonory P., Woules S., Mungall K., Murphy L., Niblett D., Odell C.,

Rutherford K., Parson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Taylor R.S., Saunders D., Seeger K., Sharp S.,

Skelton J., Simmonds M., Squares S., Stevens K.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Nodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodel C., Frohs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Allbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
   ---CATACGACAGGCAAGGGCGTATTGGAG 1800
                                                                    ------CCTAAGAGCGATGAGTTTGCC 1830
                                                                                                                                                                                                                                                                              1918 AACAACGACATCACGGGGGGGTAACTCCGGTAGCCCCGTATTC-----GATAAGAACGGC 1971
                                                                                                                                                                                                        1858 CGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCG 1917
                                                                                                                                                                                                                                                                                                                                               1972 CGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTC 2031
                                                                                                     713 ThrAspAsnLeuTyrSerValGluGluLeuIleGlyThrThrArgAlaAspLysPhe--- 731
                                                                                                                                                                         751
                                                                                                                                                                                                                                                                                                             764 AsnAspThrLeuSerGlyGlyAsnGlyAspAspGlnLeuTyrGlyGlyAspGlyAsnAsp 783
                                                                                                                                                                                                                                                                                                                                                                     Mata J., Nurse P.;
"teal and the microtubular cytoskeleton are important for generating global spatial order within the fission yeast cell.";
[Cell 89:339-949(1997).
                                  693 GluLysThrGlnTyrArgSerTyrGluPheThrHisIleAsnGlyLysAsnLeuThrGlu
                                                                                                                                                                       732 PheGlySerLysPheThrAspIlePheHisGlyAlaAspGlyAspAspLeuIleGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41 Last annotation update)
Tip elongation aberrant protein 1 (Cell polarity protein teal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                          752 AsnAspGlyAsnAspArgLeuTyrGlyAspLysGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1147 AA.
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                                                                                                                                       1831 GTACAGGAGAATATCCTCGACCTCTTC
1750 CAGGACGGTGCCTGGTACAACTAT---
                                                                  1801 AAGCAGGAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEA1 OR SPCC1223.06.
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NCBI_TaxID=4896;
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TEA1_SCHPO
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602 TIGCTCCTCCCAGCICTG---TAGGIAAGTICGGAGGCGATACGGÁCAACTGGATGTGGC 658

518 GluValSerProThrLeuSerPheValProSerSerHisSerMetGluGlnGlyAsnGly

478 SerileLeuGinProSerTyrAsnLeuAsnSerHisSerSerAspArgArgAsnThrAsn 497

533 AGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACG---

-----ATGTATTCAAGGACGTTCGTATGTAT 198 AspAspAspGlnSerSerLeuAsnSerGlnGlnLeuSerAsnGlnAlaLysAlaGlnGly

575

473 AGGTATGCCAAGAACTGGCCAAAAAAAAAATGCAGAGGAGGAACCAACTCTGCATCGTAG 532

Length:
Matches:
Conservative:
Mismatches:

4.53 117.00 36.99% 21.00% 3.06%

Indels:

719 CCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGC 778

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         INFLUENCE MICROTUBULAR ORGANIZATION, AFFECTING THE MAINTENANCE OF AS INCLE CEMPRAL AXIS.
SUBCELLULAR LOCATION: PRESENT AT BOTH POLES OF THE CELL THOUGHOUT THE CELL CYCLE WHETHER THEY ARE GROWING OR NOT. LOCATED AT THE MICROTUBULES GROWING TOWARDS THE CELL POLES. AN INTACT MICROTUBULAR SKELETON IS REQUIRED TO MAINTAIN THE LOCATION AT THE CELL TIPS; ON THE OTHER HAND, A NORMALLY ORGANIZED ACTIN
  Sanchez M., del Rey F., Benito J.,
                           Forsburg S.L.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Ben Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                           ACT AS AN END MARKER
                                                                                                                                                                                      MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
W/ 7BE65F6C666EF4F8 CRC64;
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KELCH 1.

KELCH 2.

KELCH 3.

KELCH 4.

KELCH 4.

COILED COIL (POTENTIAL).
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92
70
168
109
                                                                                                                                                        -!- FUNCTION: CELL POLARITY PROTEIN. MAY ACT AS AN EN DIRECTING THE GROWTH MACHINERY TO THE CELL POLES.
                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON IS NOT REQUIRED. SIMILARITY: CONTAINS 5 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y12709; CAA73246.1; -. EMBL; AL031579; CAA20875.1; InterPro; IPR001798; Kelch. Pfam; PF01344; Kelch; 5.
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198
303
351
402
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DOMAIN
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Db 550

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||| :::||| :::||| SerSerSerSerSerGluValCysThrGluCysThrGluThr------- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCA-----TTGCCAATGCCGTGGTTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerSerGluVal------CysThrGluCys------Thr 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 ACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 GluThrGluSerThr-SerTyrValThrProTyrValSerSerSerThrAlaAlaAlaAS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 ATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 nTyr------------------------ThrSerSerPheSerSerSerGluva 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                 169 HYPOTHETICAL PROTEIN YRR102W
169 HYPOTHETICAL PROTEIN YRR102W
109 SER/THR-RICH.
1157 N-LINKED (GLCNAC. .) (POTENTIAL)
1157 N-LINKED (GLCNAC. .) (POTENTIAL)
1167 N-LINKED (GLCNAC. .) (POTENTIAL)
1168 N-LINKED (GLCNAC. .) (POTENTIAL)
1178 N-LINKED (GLCNAC. .) (POTENTIAL)
1189 N-LINKED (GLCNAC. .) (POTENTIAL)
1180 N-LINKED (GLCNAC. .) (POTENTIAL)
1181 N-LINKED (GLCNAC. .) (POTENTIAL)
                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 122.2 kDa protein in SIR1 3'region precursor.
                                                                                                                                            Gailion L., Dujon B.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: CELL WALL (BY SIMILARITY).
--- PTM: EXTENSIVELY O-GLYCOSYLATED (BY SIMILARITY).
--- SIMILARITY: STRONG, TO YEAST PROTEIN FLOI.
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161
87
287
204
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Matches:
Conservative:
Mismatches:
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SGD; S0001810; YKR102W.
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Qy Dp	383 463	ATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTG 44.	2 6
مي و	443	AGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAA 50 ::: ::: ::: :::	20
δ		52	
QQ	499	:: erThrSerTyrValThrProTyrValSerSerThrAlaAlaAlaAsn-TyrThrSer 518	æ
Οy	521	58	30
Dp	519	SerPheSerSerSerGluValCysThrGluCysThrGluThrGluSerThrSerThr 53	
Qy Dp	581	TCAAGGACGTTCGTATGGTATTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATA 64 :::	40
Qy	641	7	00
qq	559	 GluThrGluSerThrSerTyrValThrProTyrValSerSerSerThrAla 57	5.
٥y	701	GTGCCGACAACCGGCCGGATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACT 760	09
QQ	576	5	87
δλ	761	TCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCC 820	50
qq	588	GluvalCysThrGluCysThrGluThrGluSerThrSerThrSerThrProTyrAlaThr 607	70
δ	821	CGGGCAGTACGGATCGCTACCTCACTTCGGGGTGTGGGAAGATCGTATCGAAAACGAGA 880	30
QQ	608	SerSerThrGlyThrAlaThrSerPheThrAlaSerThrSerAsnThrMet 624	24
ΟŊ	881	ACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGA 92	55
QQ	625	THIS THIND THIND THE	13
δy	926	AGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGA 98	35
QQ	644	GluHisThrAsnAlaProThrSerSerValGluSerAsnAlaSerThr 65	69
QY	986	!	1027
qq	099	PhelleSerSerAsnLysGlySerValLysSerTyrValThrSerSerIleHisSerIle 67	67
δy	1028	TCGCTCTTGACGTGATAGGTCGTAGGCGTCCGAGG 106	990
qq	680	ThrProMetTyrProSerAsnGlnThrValThrSerSerSerValValSerThrProIle 69	66
Qγ	1067	AAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGACTGCTGTCTATGGCGATGTAT 112	126
qq	700	ThrSerGluSerSerGluSerSerAlaSerValThrIleLeuProSer71	15
οy	1127	TGTCTTCTCGAAAAGGCTTATAAGGAAGGACCAAGGCCAACCGTGAGATGACTTATT 118	186
QQ	716	ThrileThrSerGluPheLysProSer7hrIleThrSerGluPheLysProSer7	. 54
δλ	1187	AGGTGGTTCGTT	246
Q	725	ThrMetLysThrLysValValSerIleSerSerProThrAsn 73	39
ο _γ	1247	TGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATGCTTGACGACAAGTACAAG 13	1306
QQ	740		15
Qy	1307	ACTACCTCCCCTCGACGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC 136	366
qq	746	ThrThrSerLysAspSerThrValGlySerSerThrSerSerValSerLeuIleSerSer 76	55

Search completed: May 16, 2003, 12:29:53 Job time : 88.5 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

nucleic - protein search, using frame_plus_n2p model

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י מסדוות דדמוווב הדתפ הודלה וווסתפי	3, 12:21:16 ; Search time 164.5 Seconds (without alignments) 5358.478 Million cell updates/sec	55-1 saattaaaaagaagagctgaagttgatctaa 2139	Xgapext 0.5 Ygapext 0.5 Ygapext 7.0 Delext 7.0	, 206047115 residues	ying chosen parameters: 1343160		tch 0% tch 100% rst 45 summaries	Command line parameters: -MODEL-frame+_n2p.model -DEV=xlp -WODEL-frame+_n2p.model -DEV=xlp -WODEL-frame+_n2p.model -DEV=xlp -CopolLUSPTO_Expol_VOR10008355,runat_16052003_110338_9352/app_query.fasta_1.2311 -DB-SPTEMBL_21 -OFMT-fastan -SUFFIX-an2p.rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT-0 -UNITS-bits -START=1 -END1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCOREP=COT -THR_MXX=100 -THR_MIN-0 -ALIGN=15 -WODE-LCCAL -OUTFWT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000 -USER-USI0008355_ECGN_11_238_@runat_16052003_110338_9352 -NCPU-6 -ICPU-3 -WARN_TINEOUT-30 -THREADS-1 -REG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120 -WARN_TINEOUT-30 -THREADS-1 -SGAPOP-10 -XGAPEXT-0.5 -FCAPOPP-6 -FCAPEXT-7	:* ea:* n:* n:* n:* al:* al:* al:* al:* al:* al:* al:* al	er of results predicted by chance to have a equal to the score of the result being printed, lysis of the total score distribution.	SUMMARIES h DB ID Description
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ow merete proce	Run on: Ma	Title: US Perfect score: 38 Sequence: 1	Scoring table: BLXg	Searched: 67	Total number of hi	Minimum DB seq len Maximum DB seq len	Post-processing: M M	Command line parameters: -MODEL-frame+_n2p.modelA-Cap2_1/USPFO_SPOOL/U -DB-SPTERBL_21 -OFWT-Fa -LOOPEXT-0 -UNITS-bitsLIST-45 -DOCALIGN-200MODE-LCAL -OUTFMT-pto -USER-US10008355_@CGN_1 -NO_XLDAY -NO_MAAP -LARG -WANL_TIMEOUT-30 -THERBAL -VGAPOP-10 -VGAPEXT-0.5	Database : SP 1: 1: 1: 1: 1: 1: 1: 1	Pred. No. is score greate. and is deriv	

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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
R. Krieger J.E., Kuramee E.E., Laigret F., Lambais M.R., Lefte L.C.C.,
Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Ouggio R.B., Poberto P.G., Rodrigues V., de Rosa A.J.M.,
de Silva A.C.R., da Silva A.M., da Silva W.A. Jr.,
da Silva A.C.R., Jr., Silva W.A. Jr.,
Ad Silva A.C.R., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., Jr., Silva W.A. Jr.,
Ad Silva A.C.R., Santelli R.Y., Sawasaki H.E.,
Ad Silva A.C.R., Jr., Silva W.A. Jr.,
Ad Silva A.C.R., Santelli R.Y., Sawasaki H.E.,
Ad Silva M.A., Verjovski-Almeida S., Vettore A.L.,
Nalada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Anture 406:151:159(2001)
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|PheSerLysGlnGluIleAlaLysCysGluGlu---GluGlnGlyTyrArgCysGlnPhe
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---ThrHisAlaGlyGluGlyMetTrpValProGlnGlnLeu---ProGluIleAlaGly
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994 TATTGGAAGAATTCGATCGCTATGAACCGCGGTCTCGCTCTTGTGTGGTAGGTCGT 1053
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                                                                                                                                                                                                                                                                                                                                       891
175 PheSerPheAlaGlyGlyAsnThrTyrArgValPheLysAsnLeuGluIleLysAspVal 194
                                                      235 LysProAlaSerPheSerLysGluAsnIleProTyrArgProLysHisTrpLeuLysPhe
                                                                                                                                                                                                                                                                                                  SerAspGlnProLeuGlyAspGlyAspPheValMetValAlaGlyTyrProGlyArgThr
                                                                                                                                                                                                                                                                                                                                                          289 TrpThrTyrProValI1eGlyGlnHisPheLysAsnLeu11eAlaLeuI1eGluAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         934 ATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||::::::||||||| ||| ||| ||| ||| |||| |||| |||| LysGlnSerGluGluThrAlaValLeuAlaTrpLeuLysGlnGlnGluThrAlaValLeuAlaTrpLeuLysGlnGlnGlyIleArgGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GluAlaLeuAlaAlaHisGlnThrLeuValAspLeuThrGluGlnTyr------
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596 ThrLeuGlnGlyValMetAlaLys---AsnThrGlyValGluProPheAspSerProLys 614
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                                                                                                                                                                                                                                                                                                               556 AspTyrAsnLysSerHisGlyLysPheValTyrProAspAlaAsnSerSerLeuArgIle
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           ----TCCTCAACGAACTCAATCAGGAGAATCTGGATC 121
                                                                             593 CysCysGluThrProLysGlyCysProValThrSerThrSerValThrAlaProSerPro
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AGGCTGCTGTTATGCGGATGTATTGTCTTCTCCGAAAGGCTTATAAGGAAGG	GTCTATGGGGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG		
SerLysThiseTaladaThrSerSerThrThiseClySerGlyThrThrProSerPro AGGCCAACCGGAACTTGCTATTGCGAACACCTTTGGTTGCTTGC			_
AGGCCAACCGTGAGATGACTTATTGAGGGACGCTCTTCGTGGTACCGAGGTGGTTC VallIIII AATCGCTGACCGCATGGCATGGCTACAAATCCTGAGGTCCTGCGGGTATCCTCA CTTTGCACAGTTTGCCAACGCATGGGTACAAATCCTGACGTCGTGCCGG SEH18ValSerValSerIySThrThTH18SerGInProvalThrAcgAspCy8H18Pro CCATGGTCG AATCGCTGCACCAACGCCAAAGACTCCTCCCCCCCCCC	CGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGT ILThr		금 :
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SerHisvalSerVallerLysThrThrHisSerGlnProvalThrArgaspySHisPro CCARGCTCGATATTGTACCCGGGGTATCCCTGCGGAGGTCCCCGATATTGTACCGGGGGTATCCTGCGAGGTCCCCCGATATTTTATATCAGAATGTAATCGACAAGAATTTAAAGGCGACGGA AspLysGluThrTyfsanasnile-IlaArgSerGlyGluLysIleCysArgArgArgA AspLysGluThrTyfsanasnile-IlaArgSerGlyGluLysIleCysArgArgArgArgA AGAAGTATGCAAGTCCATGGACAAGGTGTGGTTCCTTATAGGGACAAGTTCCATG :: :: :: ::	GACGACAAGTACAAAGTACCTCCCTCGGTCGGTAAGGTGCTGCC	134	<u> </u>
CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCGG			
AspLysGluThrTyTcAaGAATGTAATCGACAAGAAATTCAAAGGCGACACGA AspLysGluThrTyTsanAsnIle-IleArgSerGlyGluLysIleCysArgArgProGl AGAAGTATGCAGACTTCGTATTCGACAAGAGTGGTTCCTTATAGCGACAAGTTCCATG [1] [::		388£
ASPLYSGIUTHTYTAGNASAILE-ILEATGSERGIYGIULYSIIECYSATGATGPOOL AGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATG ::: :::	ATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACAC	143	
AGAAGTATGCAACTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATG [uThrTyrAsnAsnIle-IleArgSerGlyGluLysIleCysArgArgPro		
CCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCCAAGGCTATCGAGAAAGATC	GTGGTTCCTTATAGCGACAAGTTCC	149	-
	SAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGA		- S
CGGCAGTAGAGCCTATCCAAGAGCGTAATAGCTGCGCGCTATTCAGGCCGATGCGA	::: 	966 -	
TGGCCAATGCCTATGAGAGGGCAAGCGTTTTCTTTGCGTGGTTTGGGTGAGA :::	GAGCTTTCCAAGAGCGTAATAGCTGCTGCGCTATTCAGGCCGATGC		
### ### ##############################	rgcctatgccattgagaagggcaagcgtcttttctttgccggttgcgtga		
TGTACCCCGGACGTGCTCTGCCGAGCGATGCCA	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: :		. a
TYGLUVALARGVALLeuCySCySGLUThrPPTOLySGLYCySPFOVALThrSerThrPPTO GTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATC [GGACGTGCTGCGAGGATGCCAACTTCACCAT		8
GIAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11ArgValLeuCysCysGluThrProLysGlyCysProValThrSerThrP	103	<u> </u>
ATACGACGAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCG	JACGGCTCCATCAAGGGATATGAACGCAGGGAGGGTGCCTGGTACAACTA 	177	6 B
	GGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGC		6
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	SAATATCCTCGACCTCTTCCGCACAAAACTATGGTCGCTATGCCGAGAA :::		8
	ThrSerThrThrSerThrProGlnThrSerThrThrSerAlaProT		ă
	CCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTA-::		δ
	nrIleProAlaSerThrProSerThrThrSerAlaProThrThrSerThrT		<u>-</u>
		197	δ
	OThrThrSerThrThrSerAlaProThrHisArgThrThrSerGlyProT		<u>~</u>
1976 TGATCGGTCTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAAC 2035	CTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGACTTCGA	203	<i>6</i>

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85 rProileileThrGluSerThrSerSerThrSerRerAlaSerThrThrGlySerSerSe 105
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
pombe SPBPJ4664.02
SPAPB189-04C.
SCHIZOSACCHAROMYCES pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Sch
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STRAIN=972H-;
O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell is Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AL691402; CAD27470.1; -. SEQUENCE 800 AA; 79351 MW; F65488E43FE7089A CRC64;
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GGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCGCGCTATTCAGGCCGATGCGAT :::::: hrSerSerAsnTyrThrIleSer
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CATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACCAACTATCATACGACGGGCAAGGG
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erPheAlaSerGluSerSerSerPheTyrSerAsnValThrThrSerSerThrValS
CCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATC
GAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGAÏAAGAACGGCCGTCT : : : : :
GATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACC
CGAFCTGCACCCCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATG ::: ::: erGlySerSerSerSerSerTyrThrProAlaSerSerThrThrThrThrSerS
GGGTCAGTGCCCCGTCTCATCCAAGAGC
PRELIMINARY; ; 014650; -1998 (TrEMBLrel. 0)

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SerPhe-----SerSerIleThrThrThrThrProLeuHisSerThrPro 284
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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mismatches:
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                                        Mucin (Intestinal mucin) (Fragment).
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01-NOV-1998 (TrEMBLrel. 08,
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                                                                  GlyLeuProSerTrpValThrThrThrLySThrThrSerHisIleThrProGlyLeuThr
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                                   CCGGTTTGCGTGAGATGTACCCCGGACGTG------CTCTGCCGAGCGATGCCAACT 1705
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| ProSerThrThrProCysProGlyThrIleThrIleThrIleThrIleValProAlaSerProThr
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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215 GATGTACCGGTATCACAGTGTCCGATCAGG-------GCCTGATCTTTACCAACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerIleThrThrSerGluThrProSerHisSerThrProSerSerThrSerLeuIleThr 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrihrLysThrThrSerHisSerThrProSer-----PheThrSerSerIleThr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ThrThrThrGluThrAsnSerHisSerThrThrSerPheThrSerSerIleThrThrThr 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 AATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::
SerPhe-----SerSerIleThrThrThrGluThrProLeuHisSerThrPro 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGTGGCCGCGTCACACACGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770 TATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SerIleThrThrThrGluThrThrSerGluSerThrProSerLeuSerSerSerThr 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 CGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ThrSerSerIleThrThr 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrGluThrThr-----SerHisAsnThrArgSerPheThrSerSerIle 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLeuThrSerTrpValThrThrThrLysThrThrSerHisIleThrProGlyLeuThr 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 ATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 ATGCAGACGAGAACCAACTCT----GCATCGTAGAGGCCTTTCTATTCCAACAACG
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SerSerIleThrThrThrGluThrThrSerHisSerThrProGlyPheThrSer-----
                                                                                                                                                                                                                                                                                                                                       0783A4003C969664 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 ThrThrGluThrThrSerHisSerAlaArgSerPhe------
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170
93
289
245
32
Biophys. Res. Commun. 263:728-736(1999),
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                         PROSITE; PS00022; EGF_1; UNKNOWN_2
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50024; SEA; 1.
EGF-like domain; Glycoprotein.
                 EMBL, AF113616; AAF13032.1;
InterPro; IPR000561; EGF-like.
InterPro; IPR000082; SEA_domain.
Fam; PF01390; SEA; 1.
SNART; SN00181: EGF; 2.
SNART; SN00200; SEA; 1.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1217 AA; 129171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         0.0302
157.00
33.00%
21.33%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                               NON_TER
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Sun May 25 15:40:19 2003

Db 678 AspProCysValGlu	Qy 1732	1732	1733		1844		1961 797	813		RESULT 6 Q8TDH7 ID Q8TDH7 AC Q8TDH7;				RA Gum J.R. Jr., Crawle RT "MUC17, a novel memb RL Blochem. Blophys. Re DR EMBL; AF430017, AAL8		larity: imilarity:	Ouery Match: 4 DB: 4 US-10-008-355-1 (1-2139)	Qy 536 CTTCTATTCCAACA.
342IleTyrSerThrValSerThrShrThrAlaile 353	890 GTATCGAAGTTCGCGGTATCAAGCAACGCATCTGGAAGGAA	950	1010 TCGTATGAACCGCGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTG 1060	1061	1103 AGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	1163 AGGCCAACCGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTC 1222	1223 GTTTGCACAGTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCA 1282 :: :: ::	1283 AATCGCTTGACGACAAGTACA	1313 TCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCC 1372	1373	1379	1418 AATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTC 1474 	1475CTTATAGGGACAAGTTCCATGCCTCAAGTCCATGGACAAGGAAAGTTTG 1528	1529 CCAAGGCTATCGAGAAGATCCGGCA	1555 618	1595 TTCAGGCCGATGCGATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTG 1654	1655 CCGGTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGGGATGCCAACT 1705	1706 TCACCATGCGTA 1732
q	QY Db	Qy .	Qy	Qy Db	Qy Db	Oy OD	Qy	Oy Op	Qy Db	Oy	Oy Dp	Oy Db	Qy Db	Qy	O _Y	. Qy	Qy Dp	ογ

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CGCACCAAAAACTATGGTCGCTATGCCGAGAACG---GTCAGCTCC 1900
                                                                                                            1732
                                                                                                                                                                                      GGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAG 1783
                                                                                                                                                                                                                                                              GAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA 1843
                                                                                                                                                                                                                                                                                                                                                                                                              TCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCG 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTG 2020
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                                                                                                                                                                                                                                                                                                                                                            ------Thr 762
                                                                                                                                                                                                                                                                                                                                                                                                                                   eThrThrGluMetValThrCysProThrSerIleSerIleGlnThr 717
                                                                                                                                               rmetAspThrSerSerMetMetProGluSerGluSerSerIleSer 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rLysSerThrHisProSerProProThrThrArg----- 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTA 595
uMetAspProSerThrGluAlaThrSerProProThrThrProLeu 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ubMed=11855812;
ey S.C., Hicks J.W., Szymkowski D.E., Kim Y.S.;
bbrane-tethered mucin.";
tes. Commun. 291:466-475(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ).
: Chordata; Craniata; Vertebrata; Euteleostomi;
; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108320 MW; 5E1AD19E4BE948E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGGTCAGTGCCCCGTCTCATCCAAGAGC 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rArgIleThrSerGlnMetThrThrGlnSer 843
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147
63
230
205
29
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Liel. 21, Last sequence update)
Liel. 21, Last annotation update)
e mucin MUC17 (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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156.50
32.56%
22.79%
4.10%
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Qy 1418 AATTCAAAGGCGACACGAAGAAGTATGCAGACTTC	Qy 1478 ATACCGACAAGTTCCATGCCATGCTCAAGTCCATG ::	Oy 1538 TCGAGAAAGATCCGGCAGTAGAG ::: Db 458 ThrThrIleSerValSerVallleThrGluGlySe	Oy 1586 CTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC :::1 1	Qy 1646 TTTTCTTGCCGGT	1676	Qy 1709 CCATGCGTATGAGCTACGGCTCCATCAAGGGATAT :: Db 530 ProAlaMetThrThrAlaAlaProLeuThrTyrVa	Qy 1769 ACTATCATACGACAGGCAAGGGCGTATTGGAGAAG :: Db 550 ProArgThrThrSerArgGlyCysThrThrSerAl	1829		<pre>Qy 1916 CGAACAACGACATCACGGGGGGGGTAACTCCGGTAGC </pre>	1976	Qy 2036 CCGATCTGCAGCGCACAATCAGCGTGGACATCGGC	Qy 2096 GGGGTCAGTGCCCCC 2110 Db 659 ProThrSerThrPro 663	SULT 7 JQ36 Q9UQ36 PRELIMINARY; Q9UQ36;			RN 11) RP SEQUENCE FROM N.A. RA Ohtaki S., Umeki K., Sawada Y.; RR 'Homo sapiens mRNA for RNA binding prote
104 MetSerThrProSerGluGlySerSerSerLeuThrThrMet	656 GGCCGCGTCACACGGGCGACT	557 FIGSELVATASPALGSSTINITIONALINIS IN SELTINIS INSTITUCULUM 677TCAGCGTATTCCGCG	692 TGTATGCCGGTGCCGACAACCGGCCGCCCGAATACACCAAGACAATA	740AACCCTATAAGC 195 ProValAsoThrProValTJ=ThrSeTThrProValTJ=ThrSeTThrProValTJ=ThrSeTProValThrP	752 CGGTTACTCGCTGCGTATCCATGCAGGGCTACAGGCTGACGAGT	800	860 AAGATCGTATCGAAAACGAGAA ::: ::: 254 SerValValThrSerThrP	920	980CTCAGAGTGCTAACTATTGGAAGATTCGATCGGTATGAACCGCGGTCTCGCTCG	1037 TTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGCGATCCGTAAGA 1096 111	1097 ACGGCAAGAGTGCTGTCTATGCCGATGTATTGTCTCTCTC	1157 GAGCCAA 335 GluGlyT	1217 TGGTTCGTTTTGCCAACGCATTGGCTACAAATCTGATGGTCATGCGGTA	/ 1277 TCCTCAAAT 1285. 	7 1286 CGCTTGACGACAAGACAAAGACT	/ 1310ACCTCCCTCGACCGTAAGGTGCTGCCGCCATGCTCGATATTG 1357 	/ 1358 TACGCCGCGTATCCCTGCCGACAAGCTCCCGATATATTCAAGAATGTAATCGACAAGA 1417. :::
90 20 20 20	Š d	e vy	Qy Db	Š d	oy og	Oy Db	Q P	Qy Db	QY Db	oy Op	Q D	Qy Db	Q D	Qy Db	O.Y DD	Qy Db	OY Db

ACCTTTCCAAGAGCGTAATAGCTGCTG 1585 CCTATGCCATTGAGAAGGGCAAGCGTC 1645 STITGCGTGAGATGT-----ACC 1675 AGCAGGATCCTAAGAGCGATGAGTTTG 1828 ACGGTCAGCTCCATATCGCTTTCCTAT 1915 CTATGAGTGGTGACATCGAGTTCGAAC 2035 SCTACGTTCTCTTCATGATTGACAAAT 2095 CGTATTCGACAAGAGTGTGGTTCCTT 1477 ATGAACCGCAGGACGGTGCCTGGTACA 1768 SCCCCGTATTCGATAAGAACGGCCGTC 1975 GGACAAGGAAAAGTTTGCCAAGGCTA 1537 |||| :::::: ||| |SnProGluAlaValThrThrMetThr 629 ||| ||| |SerThrProGlyThr------ 473 heSerThrThrLysGluPheThrThr 529 |||||||:::::::: ; Vertebrata; Euteleostomi; ni; Hominidae; Homo. tein, partial cds."; nce update) ation update) 75 AA.

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB016091; BAA83717.1; NON_TER 1 1 SEQUENCE 1275 AA; 136869 MW; 45C2B2F85E98A6F6 CRC64;		Db Oy Db
ment Scores: 0.0363 Length: 1275 No.: 156.00 Matches: 184 int Similarity: 34.42% Conservative: 81 Local Similarity: 23.90% Mismatches: 276 Match: 4.08% Indels: 229 4 Gaps: 35		. Oy
(1-2139) x Q9UQ36 (1-1275)		go (
TCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGGGTAGCCAAAAGCCGACAAAGGCATGTG 	scargrg 86 ::: Leu 114	å da
GCTCCTCAACGAACTCAAGAAAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT ::: ::: :::	TTACGCT 146 134	oy O
CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT Pro	TATCTT 206 135	Oy Dp
CGGTGGCGGATGTACCGGTATCACAGTGCCCGATCAGGGCCTGATCTTACCAACCA	ACCACCA 266	Qy Dp
CTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGG 	GCGATGG 326 Acgarg 158	Qy Dp
TTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAA 	CCTGAA 380 SerThr 178	oy Op
GTATCTGCGCAAGATCGTGAAGGTAACGGACAGGTAGAAGGACAGCTCAAGGTATCAC :::::::::::::::::::::::::::::::::	3TATCAC 440	Qy
GACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAA 	-GGCCAAAAA 497 :::::: OProargarg 211	Oy Dp
AGAAAATGCAGACGAACCTGCATCGTAGAGCCTTTCTATTCCAACAA 	N 551 SerArg 231	oy op
CATCGTCTACGATACTTCCTCATCGTCTACGATGT	ACGATGT 578	qa
ATTCAAGGACGTICGTATGGTATTIGCICCTCCCAGCTCTGTAGGTAAGTT	STAAGTT 629 SerSer 265	oy Op
CGGAGGCGATACGGACACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCG 	ATTCCG 689 Thrser 280	Oy Dp
CGTGTATGCCGGTGCCGACACCGGCCGGCCGATACAGCAAGGACATAAACCCTATAA 	CCTATAA 749	oy Db
GCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGAC	CCATGAC 809	Oy Dp
CATCGGITTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT	AGATCGTAT 869 :::	Oy Dp

qq	305ThrArgThrThr 308
0y	AACGAGAACAATCCTCGTATCGAAGTTCGCG
qa	llllli::: lySerSerGln
Qy	930 AGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAA 974
Q	rArgSerA
Oy	975 GTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG
qq	346 gSerProAlaArgGlnGluSerSerArgThrSerSerArgArgArgArgGlyArgSerAr 366
δλ	1035 TCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGACCATTCGCAGACTGGATCG 1091
QC	<u>~</u>
Qy	AAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTT
qa	386 gSerArg-SerArgAlaSerProAlaThrHisArgArgSerArgSerArgThrProLeuI 406
Qy	CTCGAAAAGGCTTATAAGGAAGGAGGCCAAGGCCAACCGTGAGATGACTTATTTGAG
QQ	406 leSerArgArgSerArgSerArgThrSerProValSerArgArgArgSerArgSerA 426
Qy	1194 GA
qq	426 rgThrSerValThrArgArgArgSerArgSerArgAlaSerProValSerArgArgArgS 446
δy	ACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATC
qq	446 erargSerargThrPro
Qy	1284 ATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCGCTCG
QQ	
Qy	₽
qo	475 rovalThrargargargargSerargSerargThrProProvalThrargargargSerargS 495
Qy	1379ACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
qq	495 erargThrSerProlleThrargArgArgSerArgSerArgThrSerProValThrArgA 515
Qy	1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTT 1490
qq	515 rgArgSerArgSerArgThrSerProValThrArgArgArgS 529
QY	1491 CCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGC 1535
QQ	529 erargSerargThrSerProValThrArgArgArgSerArgSerArgThrProProAlai 549
Qy	ATCGAGAAAGATC
qa	:: hrProLe
٥y	1590 CGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT 1649
qa	563LysargSerargSerargSerProLeualaIleargargSerargSera
0y	ATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACT
qa	580 rgThrProArgThrAlaArgGlyLysArgSerLeuThrArgSerP 595
Oy	1710 CATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAA 1769
qq	595 ro
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Oy 18	1830 CGTACAGGAGATATCCTCGACCTCTTCCGCACAAAACTATGGTCGCTATGCCGAGAA 1889	Qy	207 CGG
9 qa	617 roalaThrargasnHisSerGlySerArgThrPro	^q Ω .	644
Qy 18	1890 CGGTCAGCTCCATATCCTATCCTATCGAACACGACGGCGGGAAACTCCGGTAG 1949	Qy	267 CTG
9 qa	AsnSerSerArgMetSerCysPheSerArgProSerMetSerProT	qu	651
Qy 19	1950 CCCCGTATTCGATAAGAACGGCCGTCTGGTCTTGGTTTCGATGGCAACTGGGAAGC 2009	Qy	327 TTT
9 qa	651 sp	qa	667 Ser
Qy 20	2010 TATGAGTGGTGACATCGAATCTGCAGCGCGCACAATCAGCGTGGA 2063	δò	381 GTA
9 qa	659 euGluProLeuGlySerSerArgThrProMetSerValLeuGln-GlnAlaGlyGlySer 678	qa ,	687 Glu
Qy 20	2064CATCCGCTACGTTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCT 2114	. Qy	441 TGA
9 qa	679 MetMetaspGlyProArglleProAspHisGlnArgThrSerValProGluAsn 698	qq	701
Qy 21	2115 CATCCAAGAGCTGAAGTTGATCTA 2138	QY	498 AGA
9 qa	699 HisalaGinSerargilealaLeu 706	q _Q	720 Arg
RESULT 015038	ω	Qy	552
ID OI	.5038 PRELIMINARY; PRT; 1783 AA.	Dp	740 Ser
	reat	Qy	579 ATT
DT 01	01-DEC-2001 (TrEMBLIAL) 19, Last annotation update) KTAA0324 protein (Fragment)	qa .	757
	KITAN324. Homo sanions (Human)	Qý	990 069
	(I) ±	qa	774 Arg
		Qy	690 CGT
	11) THE STREET OF THE STREET O	. qa	 789 Arg
	984; PubMed=9205841; Chim Mobil Manager Manage	QY	750 GCC
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		Qy	810 CAT
	COGE 101 INTIGE PICCETUS IN VICTO. ; COGE 101 INTIGE PICCETUS IN VICTO. ; FWRIT. BAD00342 BAB20782 3	qa	813
	ENON_TER 1 1 1000.00 MM. 66030256enA176AB CECEA.	δŏ	870 CGA
Alianme	TOO MY, TOOME IM, COCOCEECEDATIONS	qα	817 Arg
Pred. N		Qy	930 AGC
Percent Best Lo	tive:	qa	835 Ser
Query Match: DB:	4.08% 4	οy	975 GTA
US-10-008	08-355-1 (1-2139) x 015038 (1-1783)	qa	
Qy	27 TCTCGGAGCAGCCCTGCTGGTGGTGCTTCAGGGGTAGCCCAAAGCCGACAAAGGCATGTG 86	δλ	1035 TCT
		qa	874 gTh
Οy	87 GCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT 146	δy	1092 TAA
9 qa	::: :::	qq ,	
0y 1	147 CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT 206	δο i	
9 qq	643 Pro 643	ga .	914 168

ΟŊ	207	GATCAGGGCCTGA
q Ω .	644	31.7
Qy	267	CTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGG 326
qq	651	ror
Qy	327	TGGGTGAGGAGCTTCCGA
QQ	667	gSerGly
δλ	381	CGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCT
qq	687	GluSerSerProGluHisProProLysSerArgThrAlaArg 700
QY	441	TGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAA 497
qq	701	ArgGlySerArgSerSerProGluProLysThrLysSerArgThrProProArgArg 719
δλ	498	AGAAAATGCAGAGAGCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAA 551
qq	720	ArgSerSerArgSerSerProGluLeuThrArgLysAlaArgLeuSerArgArgSerArg 739
Qy	552	CGAATACTTCCTCATCGTCTACGATGT 578
Op	740	SerAlaSerSerProGluThrArgSerArgThrProProArgHisArg 756
Qy	579	PATGGTATTTGCTCCTCCCAGCTCTGTAG
qa .	757	Serse
Qý	630	CGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCG 689
Dp	774	Argarg
Qy	069	CGTGTATGCCGGTGCCGACAACCGGCCGGATAACAGCAAGGACAATAAACCCTATAA 749
qq	789	ArgargGlyArgSerProSerProLysProArg799
δλ	750	CTGCCGTATCCATGCAAGGCTACA
qq	800	
Οy	810	CATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT 869
qq	813	ThrargThrThr 816
δy	870	CGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG
Dp	817	::: :::: ArgargargaspargserGlySerSerGlnSerThrserargargargang 834
Οy	930	
qq	835	SERARGSERARG-SERARGVAITHRARGARGARGARGGLYGLYSERGLYTYRHISSERAR 854
Οy	975	GTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG
qq	854	gerproalaargGlnGluSerSerArgThrSerSerArgArgArgArgGlyArgSerAr 874
Qy	1035	TCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCG 1091
qq	874	JIJIIIII JLysArgSerArgSerArgThrSerProAlaProTr
Qγ	1092	TAAGAACGGCAAGAGTG
οg	894	gSerArg-SerArgAlaSerProAlaThrHisArgArgSerArgSerArgThrProLeuI 914
۷ <u>۶</u>	1134	TCTCGAAAAGGCTTATAAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTGAGCGA 1193 1-111-111-111-111-111-111-111-111-111-

Oy Bb	1194 GA	. 060382 ID 060382 AC 060382;
Qy Db	1224 TTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAA 1283 	DT 01-AUG-1 DT 01-DEC-2 DE KIAA0324
Qy Db	1284 ATCGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG	
oy.	1344 CATGCTCGATATTGTACGCCGCGTATCCCTGCCG	OX NCBI_Tax RN [1] RP SEQUENCE RA Ricke D.
Oy Dp	1379ACAAGCTCCCCGATATATTCAAGAATGTAATCGACAGAAATTCAAAGGCGACACGAA 1436 	
Oy Dp	1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTT 1490	
oy Op	1491 CCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGC 1535 ::!	
Q D	1536 TATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589 	FT NON_TER SQ SEQUENCE Alignment Sco
Oy Dp	1590 CGCTATTCAGGCCGATGCCCAATGCCTATGAGAAGGCCAAGCGTCTTT 1649 :::	Pred. No.: Score: Percent Simila Best Local Sin
oy B	1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCAC 1709	Query Match: DB: US-10-008-355
δ q	1710 CATGCGTATGAGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAA 1769 	Qy 27 TCT Db 611 Ser
O _Y	1770 CTATCATACGACAGGCGAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGC 1829 1115 erSerAspargSer	Qy 87 GCTC ::: Db 624 Seri
Qy Dp	1830 CGTACAGGAGAATATCCTCGACCTCTTCCGCACAAAACTATGGTCGCTATGCCGAGAA 1889 	Oy 147 CCC Db 644 Pro
Oy Dp	1890 CGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGGGGTAACTCCGGTAG 1949 ::::: ::: ::: :::	Qy 207 CGG' Db 645
Oy Dp	1950 CCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCATGGGAACTGGGAAGC 2009 :: 1159 sp	Qy 267 CTG
oy Op	2010 TATGAGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGA 2063 	Qy 327 TTT Db 668 Seri
Oy Dp	2064CATCCGCTACGTTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCT 2114	Qy. 381 GTA: Db 688 Glus
Oy Dp	2115 CATCCAAGACTGATCTA 2138 	Oy 441 TGA Db 702

RESULT 9

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TCCTCAACGAACTCAATCAGGAGAATCTGGATCGGAATGCGTGAGCTCGGCTTTACGCT 146
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                                                                                                                                                                                                                                                                                         DEFROM N.A. Bruce D., Mundt M., Doggett N., Munk C., Saunders E., D.O., Bruce D., Muckingham J., Chasteen L., Thompson S., D. D., Jones M., Buckingham J., Chasteen L., Longmire J., White S., T.L., Bryant J., Tesmer J., Meincke L., Longmire J., White S., Tatum O., Campbell C., Fawcett J., Deaven L.; Campbell C., Fawcett J., Deaven L.; cring of Human Chromosome 16pl3 3."; ted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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------ArgAlaGlnSerGlySerAsp-----
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uSerSerProGluHisProProLysSer-----ArgThrAlaArg-----
                                                                                                                                                                 ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Euthheria; Primates; Catarrhini; Hominidae; Homo.
«XID=9606;
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Scale Sequence Analysis and Annotation with the Sequence
Ison Analysis (SCAN) System.";
ted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
ACC04493; AACO8453.1;
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PRT; 1791 AA.
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1998 (TrEMBLrel. 07,
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---ÀAAAGTTTGCCAAGGC 1535 GGAGGGATGCCAACTTCAC 1709 ||||:::::: |TII| |ArgSerLeuThrArgSerP 1104 ------ArgArgS 1038 AGANGGGCAAGCGTCTTT 1649 ||||||| |trgargargsera AGGACGGTGCTGGTACAA 1769 ||||::: |TrgSerAlaSerGlySerS 1116 TTARGAGCGATGAGTTTGC 1829 ||||::: :: | --ArgSerAlaThrProp 1126 ATGGTCGCTATGCCGAGAA 1889 |||| -------ProValA 1140 SCGTAATAGCTGCTCG 1589 rcgargcaactgggaagc 2009 rata; Euteleostomi; nidae; Homo. mplete cds."; databases. 123 CRC64; te) date)

Sun May 25 15:40:19 2003

		86 1591	146 1611	206	1612	266 1619	326 1635	380	1655	440	497	1688	. → <	1708	1725	629	σ	1757	749	1768	60	1781	869	29	æ
Length: 2752 Matches: 184 Conservative: 81 Mismatches: 276 Indels: 229 Gaps: 35	(1-2752)	CGGAGCACCCTGCTGTTGGGGTGCTTCAGGGGTAGCCAAAGCCGACAAAGGCATGTG	GCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT	CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT 		CACAGTGTCCGATCAGGGCCTGATCTTTACCAACCACCA :::	CTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGG	TTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAA	ProSerProGluGlyS	GTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGACAGCTCAAGGGTATCAC ::: ::: ::: J ::: GluSerSerProGluHisProProLysSerArgThrAlaArg	GGCCAAAA			SerProGluLeuThrArgLysAlaArgLeuSerArgArgSerArg	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTT	TCAGCGTATTCC	::: SerAlaSerSerProArgThrLysThrThrSer	CGTGTATGCCGGTGCCGACCACCGCCGAATACAGCAAGGACATAAACCCTATAA	sPro	ACAAGGCTGACGACTATGCCATGA(rArgSerArgArgGluLys	CATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT	GAAAACGAGAACATCCTCGTATCGAAGTTCGCGGTATCAAGGAAGG	::: SerSerGlnSerThrSerArgArgArgGlnArg
. No.: 0.0535 31.55.00 31.428 Local Similarity: 34.428 Local Similarity: 23.908 4.088	3-355-1 (1-2139) x Q9UQ35	TCT Ser	-	-	2 Pro	CGGTGGCGGATGTACCGGTAT	-	7 TTTCGTTTCTCGCACGA	gSerGlySerS	1 GTATCTGCGCAAGATCGTGAAGGTAACGGA :: :: :: 6 GluSerSerProGluH1sProProLysSer	1 TGACGAGATGGAGCGTCTGCGCA		-	y ArgserserArgserserProGl	SerAlaSerSerSerProGluT	9 ATTCAAGGACGTTCGTATGGTATTTGCTCC	0 CGGAGGCGATACGGACAACTGGA		0 cererarecegreceacaace	ArgArgGlyArgSerProSer	_		_	0 CGAAAACGAGAACAATCCTCGTA	- «
Pred. No. Score: Percent Sest Loca Query Mat	10-008	27 1579	87 1592	4	1612	207	267	327	1636	381	44]	1670	49	1689	0	579	630	1743	069	1758	75	1769	810	870	1786
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Oy 9:	30 AGCCATGAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAA 974
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18	23 gSerProAlaArgGlnGluSerSerArgThrSerSerArgArgArgArgGlyArgSerAr 1843
Qy 103 Db 184	35 TCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCACACTGGATCCG 1091
Qy 109	2 TAAGAAC
Db 18(::: SerArg-SerArgAlaSerProAlaThrHisArgArgSerArgSerArgThrProLeuI 1883
Qy 113	34 TCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGA 1193
Db 186	 83 leSerArgArgArgSerArgThrSerProValSerArgArgArgSerArgSerA 1903
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12	4 TTTTGCACAGTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAA 128
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Qy 128 Db 193	84 ATCGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG
0y 134	44 CATGCTCGATATTGTACGCCGGCGTATCCCTGCCG
Db 195	::: hThrArgArgArgSerArgSerArgThrProProValThr
Qy 137	AA 143
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Qy 14:	37 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTT 1490
Db 199	٩rg
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Qy 153	36 TATCGAGAAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589
Db 202	26 leArgArgArgSerArgSerArgThrProLeuLeuProArg
Qy 159	90 CGCTATTCAGGCCGATGCGATGGCCAATGCCTTTGAGAAGGCCAAGCGTCTTT 1649
Db 204	0
Qy 165	50 CTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCAC 1709
Db 205	57 rgThrProArgThrAlaArgGlyLys
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Qy 177	0 CTATCATACGACAGGCGTATTGGAGAAGCAGGATC:::
Db 208	4
Qy 183	30 CGTACAGGAGAATATCCTCGACCTCTTCCGCACAAAACTATGGTCGCTATGCCGAGAA 1889
Dp 208	94 roAlaThrArgAsnHisSerGlySerArgThrPro
Qy 189	90 CGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAG 1949

:::	358	Db 289 SerThrLeuPheGlyGlyV	Oy 376G Db 309 AsnSerSerGluThrPheV	Qy 418 GAAGGACAGCTCAAGGGTA' Db 328 HisSerSerLysSerS	Oy 478 TGCCAAGAACTGGCCAAAAA 111 111 Db 348 -AlaLenAshProThr:	Qy 538 TTCTATTCCAACACGAAT:	Qy '598 GTATTTGCTCCTCCCAGCT		Db 393 yAlaThrSerValThr	Qy 718 GCCGAATACAGCAAGGACA.::111:::Db 412 eValSerThrSerThrLeu	757	Qy 817 TTCCCGGGCAGTACGGATC	Db 452 eSerThrSerValLys	Qy 877 GAGAACAATCCTCGTATCG	Db 460 rAlaSerValAlaSerSer	937 AGCGCAGATCAGGCT	478	QY 997 TGGAAGAATTCGATCGGTA Db 486	Qy 1057 CGTGCCGAGGAAAGAGCAT	Db 486 rSerSerAlaSerSer	Qy 1117 GGCGATGTATTGTCTTCTC	uValSerSerThr	1	514	Qy 1237 GCCAACGCATTGGCTACAA	Db 519	OV 1297 AAGTACAAAGACTACT
	1950 CCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTTCGATGGCAACTGGAAGC 2009	2128 sp	2010 TATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCAATCAGCGTGGA 2063 11	2064CATCCGCTACGTTCTCTTCATGACAAATGGGGTCAGTGCCCCGTCT 2114	2115 CATCCAAGAGCTGAACTTGATCTA 2138	2T 11 55 Q9C105 PRELIMINARY; PRT; 1236 AA.	2001 (TrEMBLrel. 17, 2001 (TrEMBLrel. 17, 2002 (TrEMBLrel. 21,	Putative glucoamylase I (alpha-1,4-glucan glucosidase), extracellular starch-degrading enzyme, by similarity to S. cerevisiae STA1, contains chitinase family signature.	SPAPBIET 04C	Eukaryota; Fungi; Ascomyocta; Schizosaccharomyoetes; Schizosaccharomyoetales; Schizosaccharomyoetaceae; Schizosaccharomyoes.	NCBI_TaxID=4896; [1]	Wood V., Kajandream M.A., Barrell B.G., Seeger K., Harris D.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. -!- SIMTLARITY: BELONGS TO CHTTINASE CLASS IT (FAMTLY 18 OF CLYCOSY).	HYDROLASES). Ll; AL590605; CAC36921.1;	InterPro; IPR001223; Glyco_hydro_18. InterPro; IPR001917; NHtransf_2.	Pfam; PF00704; Glyco_hydro_18; 1. PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.	Glycosidase; Hydrolase. SEQUENCE 1236 AA; 123387 MW; 5A2D33A30BB7CDDB CRC64;	Scores:	0.0455 154.50 35.92%	<pre>imilarity: 20.42% Mismatches: 4.04% Indels: 3 Gans.</pre>	5-1 (1-2139) x Q9C105 (1-1236)	166 AGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGT 225		226	:::::::	259 AACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTG 318		T
op qa	Qy 1	Op 7	0y 2	oy da	Oy O	55		DE SO								SQ	Align	Pred. Score: Percen	Best Local S Query Match: DB:	us-10	Qy	op Op	Qy	Db	Οy	QQ	

qq	::: 269 SerAsı	: ::: ::: ::: ::: ::: nGlyPhelleSerProLysAsnLeuThrArgAspLeuLeuAsnTyrLysAlaAsn 288
ΟY	358	CGATTCCGGGTCTTT
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Οy	1	GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTA 4
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Qy	478 TGCCA	CAAGAACTGGCCAAAAAAGAAAATGCAGACGAGAACCAACC
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Qy	538 TTCTA	CTATTCCAACAACGAATACTTCCTCATGGTCTACGATGTATTCAAGGACGTTCGTATG 597
qq	· 🖳	leSerThrIleSerGlnAspHisThrLysThrValThrS
Qy	598 GTATT	AACTGGATGTGG 65
QQ	382	\neg
Οy	658 CCGCG	CGCGTCACACGGGCGACTTCAGCGTATTCCGCGTATGCCGGTGCCGACAACGGGCCG 717
qq	393 yAL	laThrSerValThrThrThrLysThrAspPheAspThrValThrThrTl 412
δy	718 GCCGA	GCAAGGACAATAAACCCTATAAGCCCGT
Dp	412 eValSe	::: ::: SerThrSerThrLeulleSerAlaSerAspSerThrSerI].elleValSerSerTy 432
Qy	757 TACTTO	CTACAAGGCTGACGACTATGCCATGACCATCGG
QQ	432 rvals	rThrArgValGlnThrThrThrValSerSe
Οy	817 TTCCCG	3GCAGTACGGATCGCTACCTCACTTCTTG
Db	452 eserThr	ServalLysGlnProT
Qy	877 GAGAAG	CAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATGTG
QQ	460 rAlas	AlaSerSerValSerValProSerSerSerS
Οy	937 AGCGC	AAATATGC
Dp	478	oglnSerSerThrProIleSe
ΟŊ	997 TGGAA	GGAAGAATICGAICGGIAIGAACCGCGGICTCGCTCGTCTTGACGIGAIAGGICGIAAG 1056
QQ	486	
Qγ	1057 cerec	CTGGATCCGTAAGAACGGCAAGAGTGCTG
QQ	486 rSerSer	erSerAlaSerSerProGlnSerThrLeuSerThrSerSerGluValValSerGl 506
Qy	1117 GGCGA	GGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGGA
qq	506 uVals	erSerThrLeuLeuSer513
δy	1177 ATGACTT	ATTTGAGCGAGACGCTCTTCGGTG
Dp	514	AlailePr
QY	1237 GCCAAC	CGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCÀAATCGCTTGACGAC 1296
Dp	519	519
οy	1297 AAGTA	AAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTGCCGCCATGCTGCTCGATATT 1356

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                                                                   AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT 1473
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 -SerThrSerSerThrProSerSerIleIleSerSerProMetThrSerValLe
                      GTACGCCGGCGTATCCCTGCCGACAGCTCCCCGATA - - TATTCAAGAATGTAATCGAC
                                   1474 CCTTATAGCGACAAGTTCCATGCCATGCTCAAG-----TCCATGGA
                                                                                                                            GGGCAAGCGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGTTTGCCGAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                              Escande F., Aubert J.P., Porchet N., Buisine M.P.; "Human mucin gene MUC5AC: organization of its 5'-region and central
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                                                                       repetitive region.";
Biochem. J. 358:763-772(2001).
EMBL. AJ298317: CAC83674.1; -
InterPro: IPR001209; Ribosomal.514.
InterPro: IPR001209; TIL. Cysrich.
InterPro: IPR001907; VWF_C.
InterPro: IPR001846; VWF_D.
Pfam: PF001826; TIL; 2.
Pfam: PF001846; VWC; 3.
SWART; SW00214; VWC; 3.
MEDLINE-21426417; PubMed-11535137; Escande F., Aubert J.P., Porchet N.
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STRAIN-YORKSHITECHESTER WHITE/HAMPSHIRE CROSS; TISSUE-GASTRIC MUCOSA;
MEDLINE-94102478; PubMed-7506218;
Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras M., Specian R.D.,
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ysMetCysLeuAsnIleGluValArgValLeuCysCysGluThrFroLysGlyCysProV 2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ACTICACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGC 1760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998 CAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAG 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGGACATCCGCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCAT 2117
                                                                                                                                                            .......CysSerArgGlu 2187
                                                                                                                                                                                                                          CTGGTACAACTATCATACGACAGGCAAGGCGTATTGG---AGAAGCAGGATCCTAAGAG 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGG 1937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1818 CGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGG
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                                                                                               TATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTAT
                                                                                                                                                                                                                                                                                           2269 hrTyrAlaHisThrThrSerThrThrSerAlaProThrAlaArgThrThrSer-----
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Sus.
||| |||::::||| ||| 2165 CysArgAlaLysSerHisProGluValSerIleGluHisLeuGlyGlnValValGln
                                                                                                                                                                                                                                                                                                                                                           1656 CGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCA----
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Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 308:89-96(1995)
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2339 hrProSer 2341
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a)		127	187 28	247	307	367	52	427	487	65 547 77	607	667	700	745	805	865
c mucin: isolation and characterization of a cDNA clone. tandem repeat."; clogy 106:200-200(1994). 11. AAC48526.1; 528 528 528 528 528 528 528 528 528 528	: 0.0716 Length: 528 149.00 Matches: 154 17: 34.22% Conservative: 91 arity: 21.51% Indea: 243 6 Gaps: 28	355-1 (1-2139) x Q29071 (1-528) AAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGC :::: ::::::::::::::::::::::::::::::	ACAGTTTCGACAAGCCGTCCATTG ::: SerSerSerSerVal	TGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCC :::	TGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC :	ACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGG		GTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAAAGGTAGAAGGTAGAAGGACAGC (AGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC	ProproileserserThr	TTCGTATGGTATTTGCTC :::	CTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGGTCACA	CGGGCGACTTCAGCGTATTCCGCGTGTATGCCG	SerSerGlySerValProThrThrSerAlThrSerValGlnSerSerSerSer	CCA	
nt J.T. gastri a nove coenter ullo28	Scores milari Simila h:	-008-355-1 68 AAGCCGA									8 ACAACGA 					
RA LAMOR RT "P19 RT With RL Gasti DR EMBL, FT NON 7 SC SEQUE	Alignment & Pred. No.: Score: Percent Sin Best Local Query Match DB:	US-10-00	12	Oy 188 Db 29	Oy 248 Db 42	Qy 308	Db 52	Qy 368 Db 53	4	DD 60 Qy 488 Db 66	Oy 540 Db 70	Qy 608 Db 85	Oy 668 Db 99	Oy 701 Db 119	Qy 746 Db 139	Qy 806

QQ	155	SerProProlleSerSerThrValSerValGlnProSer167
QY	866	TATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG
Q Ω	168	reserSerAlaProThrThrSerAlaThrSerValGlnProSerSerSe
ΟŅ	926	GATCAGGCTACCCGTATCAAATATGC
Ob	187	SerPropro1leSerSerThrValSerValGlnThrSerSerSerSer 203
δδ	98	AATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTCACGTGA 10
QO (lProThrThrSerThrThrSerValGlnProSer 215
Oy Dp	1046	TAGGTCGTAAGGGTCGAGGAAAGACCATTCGCAGACTGGATCCGTAAGAACGGCAAGA 1105
Qy	1106	GTCTTCTCTCGAAAAGGCTTATAAGGAAGGAGCCAAGG 11
qq	233	:: SerSerSerThrProlleProSerThrThrSerValGlnProSerSerSerSerAla 252
ç ç	1166	CCAACCGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT 1225
ò	~	GTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAAT 12
qq	267	8
Οy	ã	CTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCA 13
qq	283	SerAlaProThrThrSerAlaThrSerValGlnProSerSerSerSerProPro 301
Qy	1346	TGCTCGATATTCAAGACCCGGCGTATCCTGCCGACAAGCTCCCCGATATATTCAAGAATG 1405
Qy	1406	GACAAGAAATTCAAAGGGGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGA 1.
qq	313	33
oy.	· 6	GTGGTTCCTTATAGGGACAAGTTCCATGCCATGGTCATGGACAAGGAAAAGT 15
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QY, Db	1526	TTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTG 1585 ::: SerProPro11eSerSerThr11e354
Qy	1586	CTCGCGCTATTCAGGCCGATGCCGATGCCTATGCCATTGAGAAGGGCAAGCGTC 1645
QQ	355	.::::: :::! SerValGlnProSerSerSer 361
Οy	1646	TTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACT 1705
QQ	362	3
Οy	1706	CACC
QQ	380	39
0y	1760	1
QQ	400	
QY	1820	-AGAATATCCTCGACCTCTTCGCCACCAAAACT 18
qq	412	1GlnProSerSerSerSerValF
οy		CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACACGACATCA 19
qq	432	SerAlaThrSerValGinThrSerSerSerSerSerThrProlleProSerThrThrSer 451

QY 1931	Qy	199 GTTATCTTC
Db 452 valGlnProSerSerSerSerAlaProThrThrSerAlaThrSerValGlnProSer 471	qa	291 ThrValGlnArgLeuLysArgGlnPhe
QY 1958 TCGATAAGAACGGCCGTCTGATCGGTCTTCGATGGCAACTGGGAAGCTATGAGTG 2017	QY	241 CAGGGCTGATCTTTACCAACCA(::
Oy 2018 GTGACATCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTC 2077 :::!	Qy	298 ACGGTGGATCACGACTATCTCCGCGAI ::: 317 ThrPheaspTrpGluTyrArgTh
OY 2078 TCTTCATGATGACAAATGGGGTCAGTGCCCCGGTCTCAAGAGC 2125 :: ::	Qy	352 GAGCTTCCGATTCCGGTCTTTCCGTC
RESULT 14 QBWZX1 ID QBWZX1 PRELIMINARY; PRT; 1037 AA.	QY	412 AAGGTAGAAGGACAGCTCAAGGGTATC ::: 345 ArgSerGluGlyAsp
AC Q8W2X1; DT 01-MAR-2002 (TrEMBLrel. 20, Created) DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Related to DNA repair endonuclease rad2.	δλ Ga	472 GAGGTATGCCAAGAACTGGCCAAAAA
B7N14.040. Neurospora crassa. Eukaryota; Fungi; Ascc	Qy Dp	532 GAGCCTTCTATTCCAACAACGAATAC ::: 11
NCBI_TaxID=5141; [1] SEQUENCE FROM N.A.	Qy dd	592 CGTATGGTATTTGCTCCTCCCAGCTCT
	S & d	
	מט עס קר	391
InterPro; IPR000513 InterPro; IPR002950 InterPro; IPR003903 InterPro; IPR001532	oy l	TCCATGCAAGGCTACAA
Pfam; PF02809; UIM; Pfam; PF00867; XPG_1 Pfam: PF00752: XPG_N	Qy	
SMAR	qq	434 GlnGlyGlySerSerAlaLysProPhe
Endo	QZ Dp	835 CGCTACCTCACTTCTTGGGGTGTGGAA ::: 454 GluThrValAlaLysLeuGlyValPro
Alignment Scores: Alignment Scores: 0.139 Length: 1037 Score: 147.00 Matches: 152 Percent Similarity: 31.96% Conservative: 80	QY	895 GAAGTTCGCGGTATCAAGCAAGGCAT(
Ly: 20.94% Mismatches: 3.85% Indels: 3 Gaps:	Qy	
	qa ^ò	476 GluLeuLysAlaAlaAsnLysGlyTh: 1015 ATGAACCGGGTCTCGCTCGTTTGA(
OY 58 GGGGTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAA 99	qa	
CTCAATCAGGAGAATCTGGATGAGTGAGCTCGGCTTTACGCTCCCG	QV P	1075 TTCGCAGACTGGATCCGTAAGAACGG :::::::: 501 LeuGluLysTyrValLysValThrLy
	Qy	1135 CTCGAAAAGGCTTATAAGGAAGGAGCGC.::: 521 -ThrSerAspTyrLeuSerLeuAspS
	da Qy	

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qa	291 ThrvalGinArgLeuLysArgGinPheProGlyLysGinAspValAspVal 307	
oy 4	1 CAGGGCCTGATCTTTACCAACCACTGCGGATACGGTGCTÀTCCAGAGCCAAAGC 29	
a	oo stusiyreaniyyairikevalArgelu si	
Qy Db	298 ACGGIGGATCACGACTATCTGCGGATGGTTTCGTTTCTCGCACGATGGGTGAG 351 317 Thrbhasoftroftutvr	
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A A	332 GAGCITCCGGTTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGAC 411	
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S 6	412 ARGSTRANGERICANGEGIATURACTEGRAGATEGRAGGIGGIATUGGCARAGGIAGG 471 11:: 11:1	
Qy	ACGAGAACGAACTCTGCATCGT	
qq	360AlaPheVal 366AlaPheVal 366	
ΟŊ	532 GAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTT 591	
Dρ	367 LysalaIleLysSerArgArgThrHisPheSerThrAspalaThrProGluLeu 384	
Qy	592 CGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGG 651	
Dp	385 ArgileSerTyrValPro 390	
Οy	TATTCCGCGTGTATGCCGGTGCC	
qq	391	
Qγ	712 CGGCCGGCCGATACAGCAAGACAATAAACCCTATAAAGCCCGTTTACTTCGCTGCCGTA 771	
Dp	il	
Qy	772 TCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACG 831	
QQ	419 SerAspAspGluPheAspAlaGluAspGluThrProGlySerThr 433	
Qy	832 GAT	
QQ	434 GlnGlyGlySerSerAlaLysProPheAspProPheLysProAspLeuAlaTrpllePro 453	
δλ	835 CGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC 894	
QQ	454 GluThrValAlaLysLeuGlyValProLeuThrValGlu	
Qy	GCCATGAGCG	
qq	467LysGlnArgAlaLys 475	
Qy	955 CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAAACTATTGGAAGAATTCGATCGGT 1014	4
qq	476 GluLeuLysAlaAlaAsnLysGlyThrArgLysAlaGlnThrThrLysGlnThrGlyGly 495	
Qy	1015 ATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCA 1074	4
QQ	496 MetproAlaGlyAla 500	
ΟŊ	1075 TTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCT 1134	4
qq	ValThrLysGlySerAlaThrAlaGlyThrValThrLysSe	
Qy	1135 CTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAG 1194	4
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ulysthrthtthrestlysclythrthtlysalsSer	3 3	AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACG 136	
CGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATTCATTC	· 8	:: ::: ::: uLysThrThrTserLysGlyThrThrLysAlaSer	
ANGGGGACACGAGGAGTGTGCATATCGACAGGAGTGTGCTTCCTATATG	λō	363 CGGCGTATCCCTGCCGACAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTC 142	
AAAGGGGAACGAAGGAACTATGCATATTGACAAGAGTGTGCTTCTATATGC	වූ	SerAlaArgThrSe 58	-
GACAAGTTCCATGCCATGCATGCATGCATGCAAGAAAGTTTGCCAAGAAAGTTTGCCAAGAAAGTTTGCCCAAGTTCCAAGAAAGTTTGCCAAGTTCCAAGAAAGTTTGCCGCT ### Comparisor of the	Oy Op	423 AAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGC 148	-
aThriserArgProProSerGlyAsnProTrpSerLeuAlaGlySerGlnAlaSerThrLy GCTATCGAGAAAGATCCGCGCGCGCT SILENING SILGHTLYSASNIIIeAlaSer ATTCAGGCCGATGCGATGCCATGCCATGGAAGGCCTAGTTCT- ATTCAGGCCGATGCGATGCCATGCCATGCCATGGAAGGCCAACTTTTCT- ATTCAGGCCGATGCGATGCCATGCCATGCCATGAGAAGGCCAACTTTTCT- ATTCAGGCCGATGCGATGCCAATGCCTATGCAAAGGCAAGCGTTTTTCT- TTGCCGCTTTGCGTGAGATGCCAATGCCTATGCAAGGCAAGCGCAACTTCACC SGLUPICIE SILENING THE STATE SERVENCE SERVEN	γo.	483 GACAAGTICCAIGCTCCAAGTCCAIGGACAAGGAAAAGTITGCCAAG 153	
GCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCGCGCT slieliii: slieliii: slieliii: slieliii: slieliii slieliii slieliii slieliii slieliii slieliii slieliii scarcaraccaraccaraccaraccaraccaraccarac	g	aThrSerArgProProSerGlyAsnProTrpSerLeuAlaGlySerGlnAlaSerThrLy	
ATTCAGGCCGATGCCAATGCCTATGCCATTGAGAGGGCAAGCGTTTTTTTT	Oý Dp	534 GCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCCGCGCT 159 ::::::::: :::::::::: 610 slleThrLysasnileAlaser	
-TTGCCGGTTTGCCGAGAGTGTACCCGGACGTCTGCCGAGCGACGACTTCACC	Οy	594 ATTCAGGCCGATGCGATGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTCT	
-TTGCCGGTTTGCGTCAGATCTACCCCGGACCTGCTCTGCCGAGCGATGCCAACTTCACC	QQ	:: 	
ATGCGTATGACCTACCGCTCCATCAAGGGATATGAACCGCAGGACGGTCCT OLCU	φ Ω	-TTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACC	
### ### ##############################	ογ	ATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCT	
-GGTACAACTATCGACGGGAGGGCGTATTGGAGAAGCAGGATCCTAAG [:::::	q	oLeuGludsnAspArgLeuPheSerProAspProPh	
AGGGATGAGTTTGCCGTACAGGAGATATCCTCGACCTTTCCGCACCAAAACTATGGT	oy Ob	-GGTACAACTATCATACGACAGGCAAGGCGGTATTGGAGAAGCAGGATCCTAAG 181	
gThrThrSeraspProThrArgHisProSerGlnArgSerMetargAspGiugluProVa 699 CGCTATGCCGAGACGGTCAGCTCATATCGCTTTCCTATCGAACAACGACATC 192 LAGGTTPALGSERGInSerSerAlaLeuAlaSerSerProArgLysGlyProAlaPheG1 719 ACGGGCGGTAACTCCGTAGCCCGTATTCGATA	γά	816 AGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTTCCGCACCAAAAACTATGGT	<u> </u>
CGCTATGCCGAGAACGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATC 192	q	gThrThrSerAspProThrArgHisProSerGlnArgSerMetArgAspGluGluProVa	
ARGGCGCGTAACTCCGTAGTACCATACCATACCATACCGTACGTA	γĊ	CGCTATGCCGAGAACGGTCAGCTCTATCGATTCAATCGAACAACGACATC 192	
ACGGCGGTAACTCCCGTAGTCGATA	g G	lArgTrpArgSerGlnSerSerAlaLeuAlaSerSerProArgLySGlyProAlaPheGl	
YLYSASPLYSTHIPTOTHILYSGINARGSETILELGUASPPHEGLYTPINGERTHITH 739	ογ	930 ACGGCGGTAACTCCGGTAGCCCCGTATTCGATA	
rLysGluGlnAlaGlySerArgLeuPheGlyArgThrGlnSerAlaValLeuPr 757 GATGGCAACTGGGAAG 2008 GATGGCAACTGGGAAG 2008 oSerThrThrGlyLys 762 PRELIMINARY; PRT; 1368 AA. 2. PRELIMINARY; PRT; 1368 AA. 7. 7. 7. 7. 7. 7. 7. 7. 7.	q	yrysAspLysThrProThrLysGlnArgSerlleLeuAspPheGlyTyrProSerThrTh	
rLysGluGlnAlaGlySerArgLeuPheGlyArgThrGlnSerAlaValLeuPr 75 GATGCCAACTGGGAG 2008	ò	AGAACGGCCGTCTGATCGTTTTC 199	
GATGGCAACTGGGAAG 2008	q	rLysGluGlnAlaGlySerArgLeuPheGlyArgThrGlnSerAlaValLeuPr 75	
2; PRELIMINARY; PRT; 1368 AA. 2; N-2001 (TrEMBLrel. 17, Created) N-2001 (TrEMBLrel. 17, Last sequence update) C-2001 (TrEMBLrel. 19, Last annotation updat hetical protein SPy1046.	Sy Op	993 GATGGCAACTGGGAAG 200 757 oSerThrThrGlyLys 762	
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SEQUENCE FROM N.A.
STRAILVE-ST30. ARCC.700294 / SEROTYPE M1;
STRAILVE-ST30. ARCC.700294 / SEROTYPE M1;
MEDLINE-ST30. ARCShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AR006549; AAR3336.1; -
Hypothetical protein: Complete proteome.
SEQUENCE 1368 AA; 158440 MW; 07004F0B5965762F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTC 162
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| AsnGluGluAsnGluAspIleLeuGluAspIleValLeuThrLeuThrLeuPheGlu--- 627
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|TyArgLeuSerArgLysLeuIleAsnGlyIleArgAspLysGlnSerGlyLysThrIle 679
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Streptococcus pyogenes.

Bacteria: Firmfoutes; Bacillus/Clostridium group; Lactobacillales; Streptococcacaes; Streptococcacaes; Streptococcus.

CEL_TaxID=1314;
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δy	844	GAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGC	
qq	857		
οy	904		
QQ	877	LysLysMetLysAsnTyrTrpArgGlnLeuLeuAsnAlaLysLeuIleThrGlnArgLys 896	
Οy	964	TATGCCAGCAAGTATGCTCAGAGTGCTAATTGGAAGAATTCGATCGGTATGAACGC 1023	
qq	897		
ΟŊ	1024	GGTCTCGCTCGTGACGTGATAGGTCGTAAGCGTGCCGAGGAAGAGCA 1074	
QQ	907	SerGluLeuAspLysAlaGlyPheIleLysArgGlnLeuValGluThr	
οy	1075	TTCGCAGACTGGATC 1104	
qq	927	IleThrLysHisValalaGlnIleLeuAspSerArgMetAsnThrLysTyrAspGluAsn 946	
δλ	1104	1104	
Op	947	AspLysLeulleArgGluValLysVallleThrLeuLysSerLysLeuValSerAspPhe 966	
ΟŊ	1104	1104	
qq	296	ArgLysAspPheGlnPheTyrLysValArgGluIleAsnAsnTyrHisHisAlaHisAsp 986	
δλ	1105	AGTGCTGTCTATGGCGATGTATTGTCTTCTCTCTCGAAAAG 1143	
DÞ	987	AlaTyrLeuAsnalaValGlyThrAlaLeuIleLysLysTyrProLysLeuGluSer 1006	
δy	1144	GCTTATAAGGAAGGA	
Db	1007	::: GlubheValTyrGlyAspTyrLysValTyrAspValArgLysMetIleAlaLysSerGlu 1026	
οy	1171	CGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCA 1230	
qq	1027	GlnGluIleGlyLysAlaThrAlaLySTyrPhePheTyrSerAsnIleMetAsnPhePhe 1046	
٥y	1231	CAGTITGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCG 1287	
QQ	1047	LysThrGlulleThrLeuAlaAsnGlyGlulleArgLysArgProLeulleGluThrAsn 1066	
ΟŊ	1288	TCCCCTCGCTCGAC	
qq	1067	GlyGluThrGlyGluIleValTrpAspLySGlyArgAspPheAlaThrValArg 1084	
Qy	1330	AAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGT	
qq	1085	LysValLeuSerMetProGlnValAsnIleValLysLysThrGluValGlnThrGlyGly 1104	
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837GAGAATATCTCGACTCTTCCG 298 ArgAspLysProlleArgGluGlnAlaGluAsnIlelleHisLeuPheTh 870 TATGGT	His 1297
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870 TATGGT	Asn 1317
	-CGCTATGCC 1884
1111 1318 LeuGlyAlaProAlaAlaPheLysTyrPheAspThrThrIleAspArgLysArgTyrThr	Thr 1337
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1338 SerThrLysGluValLeuAspAlaThrLeuIleHisGlnSerIleThrGly 13	

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Page 1

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ALIGNMENTS

Nectria haematococca mpVI retrotransposon Nht2, complete sequence. AY038360 Nectria haematococca mpVI.

Nectria haematococca mpVI

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Pungi; Ascomycota; Nectria.

I (bases 1 to 5888)

Shiflett,A.M., Enkerli,J. and Covert,S.F.

Nht2, a copia LTR retrofransposon from a conditionally dispensable chromosome in Nectria haematococca RESULT 1
AV038360
LOCUS
DEFINITION
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ORGANISM REFERENCE AUTHORS TITLE

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165743)
                                       2 (bases 1 to 5898)
Shiflett, A.M., Enkerli, J. and Covert, S.F.
Direct Submission
Submitted (06-JUN-2001) Forest Resources, University of Georgia,
Brooks Drive, Athens, GA 30602-2152, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                <3984. .>5537
/note="similar to reverse trancriptase and RNase H
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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    5898
    note="degenerate copia-like retrotransposon"
/transposon="Nht2"

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                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 15% of reads
Chemistry: Dye-terminator; 15% of reads
Chemistry: Dye-terminator; Big Dye; 84% of reads
Consensus quality: 165711 bases at least Q40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                             1. .5898
/organism="Nectria haematococca mpVI"
/isolate="156 30-6"
/db_xref="taxon:70791"
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Homo sapiens chromosome 1 clone RP11-543D5,
PROGRESS ***, in ordered pieces
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5894. .5898
5894. .3898
7.note="3" duplicated target site"
/rpt_type=direct
                                                                                                                                                                                                                                                                     /note="5' duplicated target site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 21; DB (100.0%; Pred. No. 12; ive 0; Mismatches
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Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                    'note="mpVI"
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                source
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                                                        AUTHORS
TITLE
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JOURNAL
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AL691459
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KEYWORDS
SOURCE
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 166143)
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Direct Submission
Submitted (11-NOV-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 09-MAY-2001
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Submitted (28-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166143)
Sulston, J.E. and Waterston, R.
Consensus quality: 165743 bases at least Q30 Consensus quality: 165743 bases at least Q20 Insert size: 165743; sum-of-contigs Insert size: 179024; 7.48 error; agarose-fp Quality coverage: 11.08x in Q20 bases; sum-of-contigs Quality coverage: 10.63x in Q20 bases; agarose-fp
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HOMO Sapiens BAC clone RP11-543D5 from 1, complete sequence.
AC013447
                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
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Joshu,C., Stoneking,T., Gregory,S. and Burkett,M.
The sequence of Homo sapiens BAC clone RPII-543D5
Unpublished
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Pred. No. 12;
0; Mismatches
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39965 c 40507 g 43666
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/organism="Homo sapiens"
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/rpt_family="MER1_type"
20958. .21229
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/rpt_family="L2"
11774. 11894
/rpt_family="MIR"
12407. 12617
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21618. .21660
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19931, 1900
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15240, 15467
/rpt_family="MIR"
15520, 15634
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21230. .21277
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11463. .11526
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17826. 17960
/rpt_family="L1"
18236. 18379
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9532. 19756
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10946. .11080
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/rpt_family="MIR"
13849. .13950
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7300. .17592
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20328. .20518
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                       /rpt_family="CR1"
5897. .6961
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7348. .7465
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10546. .10648
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20075. .20213
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11081. .11462
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21449. .21587
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10649. .10945
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.6457. .16677
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22345. .22655
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23309. .23379
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15812. 150
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20638. .20
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18993. .19
      repeat_region
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(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence fidelity of RP11-543D5 from base position 100749 to 101626 can not be guaranteed. This region is made up of a variable GT run where there are single M13 and PCR only regions. Location/Qualifiers
                                      Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 28, 2000 this sequence version replaced gi:7631057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-689L22. Actual start of
this clone is at base position 1 of RP11-543D5; actual end is at
base position 166143 of RP11-543D5.
                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                        Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                           Center project name: H_NH0543D05
                                                                                                                                                                                                        Summary Statistics
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/db_xref="taxon:9606"
/chromosome="2"
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/clone_lib="RPCI-11"
79. .574
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4783. .4857
/rpt_family="MIR"
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/rpt_family="L2"
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      Waterston, R.
Direct Submission
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Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission

Submitted (18-SEP-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

### A foases 1 to 200368)

Kaul, R.K., Olson, M.V., James, R.A., Rouse, G., Wu, Z.,

Searphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
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Submitted (31-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 31, 2002 this sequence version replaced gi:15638689.
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Sequencing vector: plasmid: LO8752; 62% of reads
Chemistry: Dye-terminator ET; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199860 bases at least Q40
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Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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Center clone name: RP11-330M19 (sc0667)
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Mismatches
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                           all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing
                                                                                                                                                            Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                           follows unless otherwise noted:
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Consensus quality: 200007 bases at least Q30 consensus quality: 200368 bases at least Q20 Insert size: 200368; sum-of-contigs quality coverage: 9.5x in Q20 bases; sum-of-contigs
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/db_xref="G1:9106968"
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                                                                                                               /translation="MMEEARATAPQGGLAASDPQRITDAPKKTGLRKRKYPTTGSASI
IVLRHVLTQRQQKRKASP"
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YYSPAHLSEAASSVAGASGQASLRAAPASLSSSRSLVSGMRTYAVLETESAPTLSGCV
SSDRSCRCFNTDGYQIDMSVVECRRLLASPLPFNVYHAYVTSSSSAAAVSSSPSSSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="similar to SPIP03626 (percent identity: 36 %/query Alignment coverage: 88.0 %/subject alignment coverage: 105.0 %): identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLNLVTGAPGNGKTLYAVDWLIRQIEIDKSLVKSGAVPRSFYTD
IEGFDVEAVRRLTGYVVQSAPEDWRTTPQGSVIVYDEAHRMFPAGRPGRSDDPRVCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                        /note="similar to GI|479340 (percent identity: 36 %/query alignment coverage: 87.8 %/subject alignment coverage: 90.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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/db_xrefe"GI:9106966"
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/protein_id="AAF84682.1"
   /protein_id="AAF84678.1"
/baxref="G1:9106963"
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/gene="XF1875"
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1351. .1662
/gene="XF1874"
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941. .1288
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MKETLKLTTESKWYPVVVGSSLIAAGATAATLFIKLFH"
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Alvarenga,R., Alves,L.M., Araya,J.E., Bala,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R., Buenco,M.R., Camargo,L.E., Carraro,D.M., Carrer,H., Colauto,N.B., Colombo,C. Costa,F.F., Costa,M.C., Costa-Neto,C.M., Carrer,H., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J., Ferreira,V.C., Froinme,M., Fulan,L.R., Fraga,J.S., Franca,S.C., Franco,M.C., Froinme,M., Fulan,L.R., Hobelsel,J.D., Junquelra,M.H., Gomes,S.L., Gruber,A.,
                                                                                                                                                                                                                                                                                                                                                  The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide
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/db_xref="G1:9106962"
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/gene="XF1871"
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SYLLDTDGQQLVRSDPSTYNNUTDSQTGAVLLTPEIVSALKRLRRSLEDELKASHAP
DQQPSSGGASSPPSSGTAMPSTCSRAASVVODFIDWVKSDEFLKPIVPDDVPYVDKL
PQAKTWSSGLGGGACPSPTIPIEFSGYKTSVEISYQPFCDFAALMRPVVIVATILA
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similarity; putative; ORF located using Glimmer/RBSfinder"
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SSVISDGVSTSATFEARSTALVNGVRYYTVPVDISASTLGSLAKVAVRRGMAFYNVYS
                                                                                                                                                                    MLSGLINGAGWVIDELTHEVMSGPALKEIPVGTVAWWWQRPGDGHVFYSVTPQGLIAP
                                                                                                                                                                                                                                                                                                                        //gene="xF1878"
//force="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAQQLMSLYCTQYDVEARTCSQQAWMVPPSLLPPISYEDVRILL PHIVMCFLVAWGFHFLFTVVRD"
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Hepatocellular Carcinoma Pathogenesis 1
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA, chromosome 4q22-q24, clone:343A4,
Complete sequence.
AP001860
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/db_xref="GI:9106970"
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44;
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Pred. No.
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Homo sapiens
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100.0%; PIE
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                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                    /gene="XF1878"
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                                                                                                                                                                                                                                                      AYIAGGFRGVKNV
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Best Local Similarity
Matches 20; Conserva
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AUTHORS
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Direct Submission Submitted (07-NOV-2001) Department of Genetics, Washington Submitted (07-NOV-2001) Department of Genetics, Massouri 63108, USA
Submitted (24-APR-2000) Shih-Feng Tsai, National Yang-Ming University, Institute of Genetics: 155 Li-Rong St. Section 2, Peitou, Tailpei, Tamain 11221, Republic of China (E-mail:ympetsai@ym.edu.tw, UKL:http://genome.ym.edu.tw/, Tel:886-2-28267043, Fax:886-2-28264930) On Feb 22, 2001 this sequence version replaced gi:7649705. Quality: the expected Phred/Phrap calculated error rate (per 10 kb) is 0.0019; Estimated total number of errors is 0.0167.
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Direct Submission
Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 129240)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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VanBrunt,A. and Meyer.R.
The sequence of Homo sapiens BAC clone RP11-289C17
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Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
/chromosome="4"
/map="4q22-q24"
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16281 c 16491 g 24306
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa.K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswall Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                            Mapping information for this clone was provided by Dr. John D. Werberson. Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match to EST AI791382 (NID:95339098) oh0lall.y5"
273. .756
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                                                                                                                                                         This sequence was finished as follows unless otherwise noted:
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7note-"similar to Homo sapiens EST AV650986
(NID:99872000)"
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(NID:913050347)"
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NEIGHBORING SEQUENCE INFORMATION:
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/db_xref="taxon:9606"
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25. .309
/rpt_family="Alu"
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1871. .2198
/rpt_family="L1"
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rpt_family="(A)n"
310. .1593
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/rpt_family="L1"
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4681. .5216
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Anote-"aimilar to Homo sapiens EST BG576912
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(NID:913279885)"
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                                /rpt_family="AT_rich"
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(NID:913047851)"
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/rpt_family="L1"
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contig of 605 bp in length
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contig of 743 bp in length
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of 1242 bp in length
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37214
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Direct Submission

Univert Submission

Submitted (01-0CT-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Mar 20, 2000 this sequence version replaced gi:6984326.

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 130 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1000 this procession number will

* 1000 this planeth
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SM Drosophila melanogaster.

Bukaryota; Mathropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 131813)

S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hinkle,A., Hoskins,R.A., Houston,R.A., Hummasti,S.R., Karra,K.,
Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,
Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,
Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.

Sequencing of Drosophila melanogaster

L Unpublished

L Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster chromosome 2 clone BACR09L20 (D1140)
RPCI-98 09.L.20 map 39A-39A strain y; cn bw sp, *** SEQUENCING IN
AC011067
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                     Score 20; DB 9; Length 129240;
Pred. No. 44;
4865. .5343
/note="similar to Homo sapiens EST BE779572
(NID:910200770)"
                                             4870. 5387 /
/note="similar to Homo sapiens EST BG283401
(NID:913033252)"
                                                                                                                                        4874. .5379
/note="similar to Homo sapiens EST AW991862
                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                              (NID:98251932)"
4875. .5383
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AC011067
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KEYWORDS
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unknown length
g of 809 bp in length
"mknown length"
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unknown length
of 548 bp in length
unknown length
of 635 bp in length
unknown length
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bp in length
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of 2663 bp in length
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of 1548 bp in length
                                                                                                                                                    unknown length
of 2609 bp in length
unknown length
of 1744 bp in length
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of 3297 bp in length
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of 3430 bp in length
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of 3385 bp in length
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of 4221 bp in length
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unknown length
of 862 bp in length
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unknown length
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unknown length
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gap of unknown length
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unknown lens
of 741 bp in lens
n length
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of 1649 r
                           unknown ]
of 2053 b
                                          unknown l
of 1950 b
                                                                                                                                 unknown of 1257 k
                 1504
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92749
92829
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Raturs, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Bavies, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Carron, T., Bowie, S., Biteva, M., Brown, H., Bryard, N. C., Carron, T., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T., Chen, G., Chen, R., Cher, G., Chen, G., Chen, R., Che, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., David, R., David, R., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinhi, H. H., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Durbin, K. J., Earnhart, C., Edgar, D., Eragar, D., Eragar, D., Erards, C., Coyle, M. D., Forter, P., Hanle, S., Hamilton, K., Farntart, C., Harris, K., Hark, M. Hale, S., Hamilton, K., Harrandez, O., Hodgson, M., Ganner, T., Hale, S., Hamilton, K., Harrandez, O., Hodgson, M., Garner, T., Hale, S., Hamilton, K., Harrandez, O., Hodgson, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Lucier, A., Lucier, K. J., Harla, M., Loulseqed, H., Li, J., Li, L., Li, Z., Lichterago, O., Lieu, C., Liu, J., Liu, W., Loulseqed, H., Locado, R., Martin, R., Martin, R., Martindale, A., Martinca, E., Massey, E., Mawhiney, E., Martin, R., Wartin, R., Warti
                                                                                                                                                                                                                                                                                                                                                                                                      ACLIAU223
Rattus norvegicus clone CH230-307M22, *** SEQUENCING IN PROGRESS
***, 50 unordered pleces.
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Direct Submission
Submitted (05-MAY-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                           ö
                                                                                                                     Length 131813;
                                                                                                                                                                           0; Indels
93491: gap of unknown length
94063: contig of 572 bp in length
94143: gap of unknown length
                                                                                                                  Score 20; DB 2;
Pred. No. 44;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                     0;
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                                                                                                                     0.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat.
Rattus norvegicus
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Best Local Simi
Matches 20;
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SOURCE
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COMMENT

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                                                                                                                                                                                                                                                     contig of 1439 b
gap of unknown 1
contig of 2700 b
gap of unknown 1
contig of 2700 b
gap of unknown 1
contig of 2994 b
gap of unknown 1
contig of 1352 b
gap of unknown 1
contig of 3352 b
gap of unknown 1
contig of 3352 b
gap of unknown 1
contig of 3340 b
gap of unknown 1
contig of 3355 b
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contig of 5030 b
gap of unknown 1
contig of 5048 b
gap of unknown 1
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NOTE: This is a "working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                     Direct Submission Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 136241)
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Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 73 contigs. The true order of the pieces is not known and their order in this sequence record is
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On Jul 9, 2002 this sequence version replaced gi:17942055
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                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                       Center clone name: CH230-8E13
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MURLY, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alstrocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, R., Blankenburg, K., Bonin, D., Barbaria, J., Benton, J., Binage, R., Blankenburg, K., Bonin, D., Barbaria, C., Burch, P., Burkert, C., Burrell, K.L., Byrd, N.C., Carron, P., Burkert, C., Burrell, K.L., Byrd, N.C., Chen, Z., Chowd, Y., Chavez, D., Charler, M. Carron, T.E., Ding, T., Byrd, N.C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., J., Drager, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Drager, H., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Eddards, C.C., Elhaj, C., Escotto, M., Eallay, T., Fragudo, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Harris, K., Juna, Y., Jula, Y., Johlet, S., Joudah, S., Ordah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Lucker, K., Martin, R., Martin, 
                                                                                                                                                                                          HTG 10-JUL-2002
                                                                                                                                                                                                                       *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-8E13,
                            AC095129.3 GI:21716997
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AUTHORS
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                                                                                                                                                                                                                                                                                                      VERSION
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Direct Submission

L Submitted (16-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Nov 8, 2000 this sequence version replaced gi:11064146.

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                    PRI 06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insert of clone RP11-19664 The true right end of clone RP13-104H2 is at 71449 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30;) an attempt was made to resolve all sequencing problems; such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-19664 is from For further details see
AL391294 152120 bp DNA linear PRI 06-DEC-200
Human DNA sequence from clone RP11-196G4 on chromosome X Contains
part of a novel gene and a CpG island, complete sequence.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152120)
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/note="17 copies 2 mer ac 98% conserved"
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/note="LIM1 repeat: matches -1389. .-744 of consensus"
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/note="MBR5A repeat: matches 1. .184 of consensus"
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//note="MER9 repeat: matches 1. .511 of consensus"
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/note="75_copies 2 mer tt 58% conserved"
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/note="23 copies 2 mer tt 87% conserved"
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/db_xref="taxon:9606"
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1. .1563
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/note="L1M1 repeat: matches -1186. .-1037 of consensus"

repeat_region repeat_region

Db 31654 TGCAGACGAGAACCAACTCT 31635

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RESULT 12 AL391294/c

.2714 of consensus"

/note="LlM1 repeat: matches -523. comptement(8868. .9026) /note="match: GSS: Em:AZ392746" 8952. .9312

> misc_feature misc_feature

us-10-008-355-1.oli.rge

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AC019024 160279 bp DNA linear HTG 14-MAR-2002
Homo sapiens chromosome 11 clone RP11-478E10 map 11, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34392. .34463

/note="12 copies 6 mer ttatta 68% conserved"

34500. .34936

/note="LIPAR repeat: matches 5724. .6163 of consensus"

35012. .37203

/note="LIPAL2 repeat: matches -355. .1833 of consensus"

37383. .37682
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38407. .39569
38407. .39569
7.0014-1.1PAL2 repeat: matches 1323. .1554 of consensus"
39571. .12509
39571. .41509
7.0014-1.1PAL5 repeat: matches 4193. .6148 of consensus"
41502. .42355
7.0014-1.1. repeat: matches 3785. .4644 of consensus"
42366. .48504
7.0014-1.1PAL4 repeat: matches 1. .6141 of consensus"
42366. .48504
7.0014-1.1PAL4 repeat: matches 1. .6141 of consensus"
49131. .49187
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/note="LIPA8 repeat: matches 5696. .6161 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LIP repeat: matches 1818. .4658 of consensus" 34390. .34461 34701 and conserved" 34392. .34463
                                                                                                            /note="remain repeat: matches 29. .123 of consensus" 28186. .28209
/note="12_copies 2 mer ac 100% conserved"
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/note="THE1C-internal repeat: matches 1524. .1576 of
                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 5. .305 of consensus" 29427. .30036
/note="LIPA8 repeat: matches 10. .602 of consensus"
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                                                                                                                                                                                    28331. .28775
/note="MLT2A repeat: matches 9. .453 of consensus"
29122. .29426
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1M4 repeat: matches -2. .556 of consensus"
11629. .34385.
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                                                                     matches 1. .371 of consensus"
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/note="LIMD2 repeat: matches 5575. 6116 of
31104. 31624
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AC019024.5 GI:19424608 '
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens.
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Mismatches
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//gener_balagod4.1
//groduct="Dalagod4.1
//note="match: cDNAs: Em:AKO24111 Em:AKO01535 Em:AL050030
match: EST9: Em:AL252657 Em:BE673995 Em:AA947819
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Em:BF17877 Em:AA603412 Em:AA263316
Em:AA83692 Em:AA86540 Em:AA878779 Em:AA262381
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21236. .21293
21236. .21293
// (note="MLTIAZ repeat: matches 85. .142 of consensus"
21550. .21678
// (note="MLTIAZ repeat: matches 220. .349 of consensus"
21681. .2476
// (note="LiPBZ repeat: matches 3013. .6152 of consensus"
21804. .21855
// (note="Sequence from overlapping clone AL359775. Assembly confirmed by restriction digest"
24754. .25642
// (note="LiPP repeat: matches 1560. .2455 of consensus"
25634. .26219
// (note="LiPP repeat: matches 8. .416 of consensus"
25634. .26219
                                                                                                                                                                               /note="Aluba repeat: matches 138. .289 of consensus" 9180. .12619
//note="LiMA2 repeat: matches 2325. .5786 of consensus" 12644. "LiMA3 repeat: matches 3768. .6152 of consensus" 14961. .15487
//note="LiMA2 repeat: matches 5769. .6303 of consensus" complement(15532. 17999)
//gene="bA19664.1"
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"note="LIMD1 repeat: matches 5566. .5825 of consensus"
16518. .27573
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/note="LIMEc repeat: matches 358. 1420 of consensus"
27597. 27650
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                                     /note="match: GSS: Em:AQ552982 Em:AQ568449"
8971. 9159
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complement(8971. .9176)
                                                                                         /note="match: STS: Em:Af002096"
                                                                                                                 complement(9021. .9179)
/note="match: STS: Em:G09176"
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15801. .16081
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Drosophila melanogaster, chromosome 2L, region 39A-39A, BAC clone BACR24F17, complete sequence.
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Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodsson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalall,M., Kruse,D., Lip., Mattel,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Wurphy,B., Nelson,C., Nelson,K.A., Nunnoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                    is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is available and the accession number will be preserved.
                 Insert size: 161000; agarose-fp Insert size: 160079; sum-of-contigs Quality coverage: 19.1 in 020 bases; agarose-fp Quality coverage: 19.5 in 020.

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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77957 79239: contig of 1283 bp in length
Consensus quality: 159947 bases at least Q20
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Pred. No. 45;
0; Mismatches
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/note="assembly_fragment
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/db_xref="taxon:9606"
/chromosome="11"
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                                                                                                                                                                                                                                                                                                               This sequence will be replaced
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AC009253.16 GI:16798933
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Best Local Similarity 100.0
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S (Dases I to 1002/2)

Anderson, S., Barna, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, M., Bastien, V., Bloom, T., Boguslavkly, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Garo, S., Gerde, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S.
Ginde, S., Gorde, S., Goyette, M., Tilev, I., Dinson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Norbu, C., Norman, C. H., O'Connor, T., Nguyen, C., Nicol, R.,
Oliver, J., Peterson, K., Phunkhang, P., Petere, N., Pollara, V.,
Seaman, S., Severy, P., Spencer, B., Santos, R., Schubers, S., Schupback, R., Travls, N., Triglio, J., Vassiliev, H.,
Viel, R., Wo, A., Wilson, B., Wiyan, D., Ye, W.J., Young, G.,
Direct Submission
                                                                                                                                                                                                     Submitted (29-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 160279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Street, 320 Charles Street, Cambridge, MA 02141, USA ON MAI 44, 2002 this sequence version replaced gi:19387766. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-478E10 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Nov 8, 2001 this sequence version replaced gi:7264755.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                               Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Cissiolak,L., Doyle,C.W., Farfani,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Maxda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sequeira,A., Sair,R., Sair,B., Sair,R., Man,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Bunay, C., Burch, P., Burkett, C., Burchilk, L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chowdhry, I., Christopoulos, C.,
                       Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 2L, region 39A-39A
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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1. 160282

/organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="21"
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delandy, R.J., Delandy, R.J., Delandy, R.J., Dinh, H.H., Douthwaite, K.J., Drapper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagy, M., Ford, J., Foster, P., Frantz, P., Gabis, A., Garcia, A., Garner, T., Garza, N., Hamilton, K., Harris, C., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Harris, C., Krartovic, J., Kelly, S., Khan, U., King, L., Korvah, J., Kovan, L., Karlsson, E., Kallys, J., Khan, U., King, L., Korvah, S., Karlsson, C., Liu, J., Liu, M., Lida, Martin, R., Pickers, M., Poten, R., Pote, A., Pace, A., Payton, B., Peery, J., Pickers, R., Pace, A., Payton, B., Peery, J., Pickers, R., Pace, A., Payton, B., Peery, J., Pickers, R., Pace, A., Payton, B., Thomas, R., Tang, H., Sotter, S., Savery, G., Scherr, S., Sott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sotalk, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tang, H., Tang, M., Wang, S., Warren, R., Walliano, R., Wallis, R., Wallians, R., Wallians, R., Wallian, R., Wallian, R., Wa
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NOTE: This is a "working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
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Submitted (13-001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Maylor Plaza, Houston, TX 77030, USA
Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
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Sequenciary Statistics
Sequenciary Statistics
Sequenciary Vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 116803 bases at least Q40
Consensus quality: 121625 bases at least Q40
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Contact: hgsc-help@bcm.tmc.edu
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Gaps ó, 2; Length 163706; 0; Indels DB . Pred. No. 45 Mismatches Score 20; Pred. No. Query Match 0.9%; Sco Best Local Similarity 100.0%; P. Matches 20; Conservative 0; CCAAGGCCAACCGTGAGATG 1179 0.9%; 1160

Search completed: May 23, 2003, Job time : 5892 secs

Db 136347 CCAAGGCCAACCGTGAGATG 136366

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5.1.4_p5_4578 Compugen Ltd.

version : - 2003 (

GenCore Copyright (c) 1993

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Run on:

Sequence 253, App Sequence 657, App Sequence 657, App Sequence 657, App Sequence 4571, App Sequence 1856, App Sequence 126, App Sequence 2414, App Sequence 2414, App Sequence 2414, App Sequence 25073, A Sequence 852, App Sequence 852, App Sequence 852, App Sequence 98, App Sequence 26, App Sequence 106, App Sequence 106, App Sequence 166, App Seq Sequence 12, Appl Sequence 87, Appl 2 US-10-044-090-253 US-10-046-915-657 US-09-918-178-657 US-09-923-876-4571 US-09-918-995-18569 US-09-918-995-18569 US-09-918-995-18569 US-09-918-995-18569 US-09-918-995-3910 US-09-918-995-3910 US-09-918-995-3928 US-09-918-995-3928 US-09-919-580-8450 US-09-919-580-857 US-09-917-8600A-857 US-09-918-3-156-US-09-883-152-26 US-09-883-152-26 US-09-883-152-26 US-09-883-152-26 US-09-883-152-26 US-09-883-152-26 US-09-883-152-26 US-09-983-152-26 US-09-983-152-26 US-09-983-152-26 US-09-983-152-26 US-09-983-152-26 US-09-452-599-166 US-09-974-300-4593 US-09-887-527-12 US-10-001-857-87 7557 2564 2664 2864 2885 3373 349 349 4402 4413 4413 606 0000

ALIGNMENTS

RESULT 1 US-10-008-355-1 Sequence 1, Application US/10008355 Patent No. US20020164/59A1 GENERAL INFORMATION: APPLICANT: Travis, James APPLICANT: Potempa, Jan S APPLICANT: Botempa, Jan S APPLICANT: Botempa, Jan S TITLE OF INVENTION: Dipeptidyleptidases And Methods Of Use FILE REFERENCE: 235.00440101 CURRENT PAPLICATION NUMBER: US/10/008,355 CURRENT FILING DATE: 2000-11-08 PRIOR FILING DATE: 2000-11-08 NUMBER OF SEQ ID NOS: 26 SOFTWARE: PatentIn Version 3.0 SEQ ID NO 1 LENGTH: 2139 TYPE: DNA ORGANISM: Porphyromonas gingivalis	Query Match 100.0%; Score 2139; DB 9; Length 2139; Best Local Similarity 100.0%; Pred. No. 0; Matches 2139; Conservative 0; Mismatches 0; Indels 0; Gaps	Qy 1 ATGCAAATGAAATTAAAAGTATTCTTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG 60	Qy 61 GTAGCCAAAGCCGACAAAGGCATĞTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT 120	Qy 121 CGAATGCGTGGGCTTTACGCTCCGTTGGATTCGCTCTACAGTTTCGACAGCCG 180	Qy 181 TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT 240
	1.1 A	App App Ap	Ap Ap Ap	A A A A A A	Ap 11: 11: 11:

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(without alignments) 14634.553 Million cell updates/sec 1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa May 23, 2003, 07:01:32; Search time 193 Seconds 828747 segs, 660231138 residues using sw model OLIGO_NUC Gapop 60.0 , Gapext 60.0 US-10-008-355-1 2139 nucleic search, 0 score: Scoring table: Word size :

Title: Perfect sc Sequence:

Searched:

2139

Post-processing: Listing first 45 summaries

Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published_Applications_NN:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NRW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
1	2139	100.0	2139	6	US-10-008-355-1	Sequence 1, Appli
2	19	6.0	490	σ	US-09-918-995-37887	Sequence 37887, A
m	19	0.9	502	σ	US-09-918-995-37842	Sequence 37842, A
4	19	6.0	4163	10	US-09-954-456-528	Sequence 528, App
Ŋ	18	0.8	203	10	US-09-960-352-10103	
9 υ	18	0.8	252	10	US-09-974-300-7766	Sequence 7766, Ap
7	18	0.8	355	10	US-09-960-352-12702	Sequence 12702, A
8	18	0.8	408	10	US-09-960-352-9104	•
6	18	0.8	410	10	US-09-960-352-10777	Sequence 10777, A
10	18	0.8	417	10	US-09-960-352-5137	Sequence 5137, Ap
11	18	0.8	418	10	US-09-960-352-11256	Sequence 11256, A
12	18	0.8		10	US-09-960-352-12448	Sequence 12448, A
c 13	18	0.8		10	US-09-864-761-6022	Sequence 6022, Ap
14	18	0.8	479	10	US-09-960-352-14538	Sequence 14538, A
15	18	0.8	499	σ	US-09-918-995-1375	Sequence 1375, Ap
16	18	0.8	2699	8	US-08-834-666A-3	Sequence 3, Appli
17	18	0.8		œ	US-08-834-666A-1	Sequence 1, Appli
18	18	0.8	2915	œ	US-08-834-666A-5	Sequence 5, Appli
19	18	0.8	3995	10	US-09-919-497-9	Sequence 9, Appli

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δ	0	GTGGATCACGACTATCTGCGCATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG 36	Oy Dp
9 2	361	GFGGAFCACCATCTGCGCGAFGGFTTCGFTTCFCGCGCGCGTGGGGFGAGGGG ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGG	Qγ
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oy Op	421	GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGC 480 	QY Db
Oy Dp	481	CAAGAACTGGCCAAAAAAGAAAATGCAGACGAACCAACTCTGCATCGTAGAGCCTTTC 540	oy ob
Oy Dp	541	TATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA 600	Oy Db
δ d	601	TTIGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCG 660	oy Db
Qy Db	661	CGTCACACGGGCGACTTCAGCGTATTCCGCGTGTTATGCCGGTGCCGACAACCGGCCGG	do o
o d	721	GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA 780	Oy Dp
9 9	781	GGCTACAAGGCTGACGACTATGCCATGGCTTTCCCGGGCAGTACGGATCGCTAC 840	Oy Db
Oy Dp	841	CTCACTTCTTGGGGTGTGGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT 900	Oy Dp
Q Q	901	CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC 960	oy Db
Oy Db	961	AAATATGCCAGCAAGTATGCTCAGAGTGCTAATTGGAAGAATTCGATCGGTATGAAC 1020 	do .
oy Op	1021	CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080	oy D
Qy Dp	1081	GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA 1140	ωs
Qy Dp	1141	AAGGCTTATAAGGAAGGACCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTC 1200 	
Oy Db	1201	TTCGGTGGTACCGAGGTGGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCT 1260	
O.y D.b	1261	GATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCG 1320 	
٥y	1321	CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTM	 w

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1321 CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC 1380
                                                                                                     1621 TATGCCATTGAGAAGGCAAGCGTTTTTTTTTTTGCCGGTTTGCGTGAGATGTACCCCGGA 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1441 TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG 1500
                                                                                                                                                                                                                                                                                    1501 CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG 1560
                                                                                                                                                                                                                                                                                                                                                                                      1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCAATGCC 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1621 TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1741 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAG 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1861 ACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAAC 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                 1981 GGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGAT
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US-09-918-995-37887
US-09-918-995-37887
US-09-918-995-37887
Sequence 37887, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.;
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFRERENT SOUTH-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/215,076
PRIOR PAPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOUTHWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2101 CAGTGCCCCCGTCTCATCCAAGAGCTGAAGTTGATCTAA 2139
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APPLICANT: Tao, which will be a specific and a spec
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1D Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-02
CURRENT APPLICATION NUMBER: 05/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 43-LIB34-066-Q1-E1-C12
US-09-960-352-10103
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24;
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7;
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                                                                                PRIOR APPLICATION NUMBER: US/UN/LUNCTED PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19;
                                                              FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10103, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7766, Application US/09974300 Patent No. US20020146721A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.98;
      FILING DATE: 2000-09-26
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Best Local Similarity
Matches 18; Conserv
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US-09-960-352-10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-954-456-528
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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TITLE OF INVENTION: Sets
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                                                                                                                                                                                                                                            Length 490;
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                       Mismatches
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CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT PELLON DATE: 2001-09-18
PRIOR PELLON DATE: 2001-09-18
PRIOR PELLON DATE: 2000-09-18
PRIOR PELLON NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR PELLING DATE: 2000-09-25
PRIOR PELLING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
                                                                                                                                                                                                                                         Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 528, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
                                                                                                                                                                                                                0.9%; SCOL.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1) ... (505)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-37842
                                                                                                                ; LCCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-37887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CAGGGCCTGATCTTTACCA 259
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                                                                                                                                                                                                                                                                                                                                                                                           274 CAGGGCCTGATCTTTACCA 292
                                                                                                                                                                                                                                      Query Match 0.9
Best Local Similarity 100.
Matches 19; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                          NAME/KEY: misc_feature
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Best Local Similarity
Matches 19; Conserv
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10777
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEC ID NOS: 15112
SEC ID NO 5137
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (383)
COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: 46-LIB34-016-Q1-E1-D6
US-09-960-352-10777
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CTHER INFORMATION: Clone ID: 22-LIB34-030-01-E1-F5
US-09-960-352-5137
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100.0%; Pred. No. 25;
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100.0%; Pred. No. 25;
ive 0; Mismatches 0
                                                                                                                                                      ; Sequence 10777, Application US/09960352
patent No. US20020137139A1
; GENERAL INFORMATION:
APPLICANT: Warren, Wesley.C.
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                        1160 CCAAGGCCAACCGTGAGA 1177
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
Matches 18; Conserv
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US-09-960-352-10777
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US-09-960-352-5137
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APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND PAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12702
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APPLICANT: Tao, Nengbing
APPLICANT: Byat, John C.
APPLICANT: Hao, Nengbing
APPLICANT: Byat, John C.
APPLICANT: Hyperican Nengbing
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND EAT DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB34-010-Q1-E1-F10
US-09-960-352-12702
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100.0%; Pred. No. 25;
tive 0; Mismatches 0,
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NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7766
LENGTH: 252
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Pred. No.
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100.0%; Pre
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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Matches 18; Conservative
                                                                          ; TYPE: DNA; ORGANISM: Bacillus clausitus-09-974-300-7766
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Matches 18; Conserv
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Matches 18; Conserv
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US-09-960-352-9104
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LENGTH: 408
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Score 18; DB 10; Length 466;
Pred. No. 25;
0; Mismatches 0; Indels
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N HELA, SIGNAL = 1.9
N HEART, SIGNAL = 1.8
N FETAL LIVER, SIGNAL =
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                                                                                      PRIOR PLLING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR PAPLICATION NUMBER: US 09/632,366
PRIOR PLLING DATE: 2000-09-04
PRIOR PLLING DATE: 2000-09-27
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-130
PRIOR PLLING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-30
                                                  : US 60/180,312
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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                                                                         PRIOR FILING DATE: 2000-02-04
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                                                PRIOR APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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US-09-864-761-6022
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12448, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPRENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                             APPLICANT: Tac., Nengbing
APPLICANT: Tac., Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DAIE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11256
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; OTHER INFORMATION: Clone ID: 48-LIB34-016-Q1-E1-D8
US-09-960-352-11256
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Pred. No.
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100.0%; Pred. No.
                    Sequence 11256, Application US/09960352 Patent No. US20020137139A1
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                                                                 GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
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NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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Matches 18; Conserv
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US-09-864-761-6022/c
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US-09-960-352-12448
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US-09-960-352-11256
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FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14538
LENGTH: 479
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                        TYPE: DNA POSANIAM: BOS taurus CTPER INFORMATION: CLONE ID: 62-LIB3058-022-01-K1-H6 US-09-960-352-14538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1375
LENGTH: 499
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LCCATION: (1)...(499)
CTHER INFORMATION: n = A,T,C or G
US-09-918-995-1375
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Best Local Similarity 100.C
Matches 18; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 18; Conserva
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796 GACTATGCCATGACCATC 813

Gaps

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Search completed: May 23, 2003, 09:58:00 Job time: 210 secs

Sun May 25 15:40:21 2003

Lung cancer relate Human garp homolog Human ASTHIJ 5 ge Human ASTHIJ 5 ge Human ASTHIJ 5 ge Haemophilus influe Streptococcus poly Bacillus clausii g Human gene signatu Human gene signatu Human peres Hongan brain express Human brain express Human penome deriv Arabidopsis thalia Arabidopsis thalia Human colon cancer Human secreted pro H. Pylori call env H. Pylori bacteria H. Pylori bacteria H. Pylori bacteria

10 19 0.9 4163 24 ABL65218 Human garp homolog	39 18 0.8 2007 18 AAV25118 H. Pylori 44 18 0.8 2070 21 AAZ88408 H. Pylori 42 0.8 2070 21 AAZ88408 H. Pylori 18 0.8 2114 21 AAA87667 H. Pylori 44 18 0.8 2125 21 AAZ88405 H. Pylori 45 18 0.8 2125 21 AAZ88406 H. Pylori 19 0.8 2226 21 AAZ88406 H. Pylori 24 3635 AAL43635 Standard; DNA; 2139 BP. AAL43635 Standard; DNA; 2139 BP. AAL43635 Standard; DNA; 2139 BP. Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding se Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleav DPP-7 inhibitor identification; periodontal disease; gingivitis;	XX VS Porphyromonas gingivalis. XX XX XY XY XX XY Yoroduct= "Porphyromonas gingivalis DPP-7" PN W0200238742-A2.	
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: May 23, 2003, 04:44:52; Search time 328 Seconds (without alignments) 14686.050 Million cell updates/sec Title: US-10-008-355-1 Perfect score: 2139 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 2139 Scoring table: OLGG_NUC Gapop 60.0, Gapext 60.0 Searched: 2185239 seqs, 1125999159 residues Word size: 0 Total number of hits satisfying chosen parameters: 4370478 Minimum DB seq length: 2000000000 Post-processing: Listing first 45 summaries	N_Geneseq_101002:* 1: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:* 2: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 3: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:* 4: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:* 5: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:* 7: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 8: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 9: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 10: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:* 11: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 12: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 13: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 14: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 15: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 16: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 17: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 18: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 19: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 10: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 11: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 12: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 13: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 14: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 15: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 16: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 20: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 21: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 22: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 23: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 24: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 24: SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:* 24: SIDS2/gcgdata/geneseq/geneseq-embl/NA2001.DAT:*	the number of results predicted by chance to have than or equal to the score of the result being p d by analysis of the total score distribution. SUMMARIES CHARACTER DESCRIPTION DESCRIPTION	2139 24 AAL43635 Porph 315 23 ABL037551 Droso 948 23 ABL03799 Liste 1431 24 ABQ70337 Liste 2252 23 ABL27548 Droso 2315 23 ABL27550 Droso 2324 23 ABL27550 Droso 2316 23 ABL03759 Droso 2316 23 ABL03759 Droso 2316 23 ABL03759 Droso

The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amiddlytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for electing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidase-7 (DPP-7) enzyme of the invention. οĘ Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas ginglvalis 4; 65pp; English 2002-490075/52 P-PSDB; AA015205 Claim 11; Fig

Sequence 2139 BP; 544 A; 543 C; 565 G; 487 T; 0 other;

0 240 300 300 360 360 120 180 420 420 480 480 120 099 9 9 Gaps 1 ATGCAAATGAAATTAAAAAGTATTCTTCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG 1 ATGCAAATGAAATTAAAAAGTATTCTTCGGAGCAGCCGCCTGTTGGGTGCTTCAGGG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT CAGGGCCTGATCTTTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCCAAAGCTCAGGAGGTATGC CAAGAACTGGCCAAAAAAAAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTC DB 24; Length 2139; ; 0 Indels .; 0 100.0%; Score 2139; 100.0%; Pred. No. 0; Mismatches ö Local Similarity 100 nes 2139; Conservative Query Match Matches 61 61 121 121 181 181 241 241 301 301 481 361 361 421 421 481 541 541 501 601 à 8 g Qy Db 9 q ò a õ g ò à ò ò QQ ò q ò g ò

1620 CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGATTCGCA 1741 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAG GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA AAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAAC CGCGGTCTCGCTCGTTTGACGTGATAGCTCGTAAGCGTGCCCGAGGAAAGAGAGATTCGCA GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA AAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTC CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG 1441 TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA GGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTAC CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT CTCACTTCTTGGGGTGTGGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT TTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCT 1321 CTCGACCGTAAGGTGCTGCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGAC AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAAGCGACACGAAGAAG 1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA CGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGA 1021 1261 1321 1381 781 1081 1081 1141 1141 1381 1621 661 901 901 196 1021 1201 1261 1441 1501 1561 1681 721 721 841 961 1201 QQ οy qq οy g δy g δ a Qγ q ò Dp οy g Qγ g ò Ω ò Q Ω q QΥ Q δ g οy QQ δ g οy qq δy Ωp ò

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1741 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCGAAGGCGTATTGGAG 1800
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                                                                                                                                                             AACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATC 1980
                                                                                                                                                                                        1921 AACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATC 1980
                                                                                                                                                                                                                                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                   AAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC
                                                                                                                     1861 ACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell.signalling and cell-cell
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red. No. 24;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO
                                                                    23; Length 315
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                                        Sequence 315 BP; 68 A; 103 C; 83 G; 61 T; 0 other;
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Mismatches
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Pred. No.
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100.0%; Pre
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                                                                                                                         262 CACCACTGCGGATACGGTG 280
                                                                                                                                        314 CACCACTGCGGATACGGTG 296
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                        ABL03799 standard; cDNA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    Drosophila;
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ABL03799
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ABQ70337 RESULT

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of inscetticides, therapeutics and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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The sequence data for this patent dld not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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Pred. No. 25;
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100.0%; Pre-
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ID ABL27550 standard; DNA; 2315
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2000US-0614150.
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11-JUL-2000; 2000US-0614150.
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                Orosophila melanogaster.
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Best Local Similarity
Matches 19; Conserv
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic sequences from Listeria species, useful for detection, atment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                        Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and pathogenicity of Listeria (potential therapeutic agents), alk treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
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pharmaceutical; gene; ds.
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24;
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                                                                                                                                                                    Listeria monocytogenes 4b contig DNA sequence #279.
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                                                  ABQ70337 standard; DNA; 1431 BP.
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(CNRS ) CNRS CENT NAT RECH SCI
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antibodies and modulators
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                                                                                                                                                                                                                           infection; ds
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Matches

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insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                                                                                                 (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                          ed nucleic acid detection reagent for detecting 1000~\mathrm{or} more Drosophila and for elucidating cell signalling and cell-cell
                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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cal; gene; ds.
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                                                                                 SEQ ID NO 34123; 21pp + Sequence Listing; English
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Pred. No.
Myers EW;
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2000US-0614150.
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Matches 19; Conservative
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Adams M,
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                   WPI; 2001-656860/75
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interactions
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Venter JC,
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                     sequences (ABLO1840-ABL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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(ABL16176-ABL30511), expressed DNA
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red. No. 25;
Mismatches 0: TrAP1
                                                                                                                                                                                                                                      Length 2324;
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discloses genomic DNA sequences (ABL16176-ABL30511), eysequences (ABL01840-ABL16175) and the encoded proteins
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red. No. 25;
Mismatches 0;
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11-JUL-2000; 2000US-0614150.
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Matches 19; Conservative
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P-PSDB; ABB59735.
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method (M1) for screening for an
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            Lung cancer related gene sequence SEQ ID NO:3555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 3555; 44pp; English
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2000US-234052P.
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Weaver 2;
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                                                                                                                                                  WO200194629-A2.
                                                                                                                       Homo sapiens
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Soppet DR,
                                                                                          gene; ds.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 \text{ or more} genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
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                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 5876
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100.0%; Pred. No. 25;
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                                                                                                                    ABL03798 standard; cDNA; 3006 BP
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Conservative 0;
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11-JUL-2000; 2000US-0614150.
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           485 AACTGGCCAAAAAAAAA
                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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P-PSDB; ABB59695.
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Best Local Similarity
Matches 19; Conserv
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ID ABL6
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AC ABL6
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Horrigan S;

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agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (5) selected from 847 sequences (given in ABL5064 to ABL7010), or is at least 95% identical to (5), where a change in expression is indicative of anti-neoplastic activity. (1) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, coscophageal, ovarian, kidney, prostate or pancreatic cancer, cachingma, carcinoma, clear cell carcinoma, neuroendocrine infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine Human; cytokine; cell proliferation; cell differentiation; growth factor; hematopoiasis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; mayeloid cell disorder; sathma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiarhmatic; antiarhmitic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. Gaps Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -; 0 0.9%; Score 19; DB 24; Length 4163; 100.0%; Pred. No. 25; tive 0; Mismatches 0; Indels (0; Indels Sequence 4163 BP; 836 A; 1303 C; 1112 G; 912 T; 0 other; bone disorder; osteoporosis; vascular growth disorder; Human garp homologue-encoding cDNA, SEQ ID NO:807. carcinoma, papillary carcinoma and Wilm's tumour. ABA09031 standard; cDNA; 4428 BP. 3135 CAGGGCCTGATCTTTACCA 3153 Drmanac RT; 241 CAGGGCCTGATCTTTACCA 259 05-FEB-2001; 2001WO-US03800. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875. (first entry) 19; Conservative WPI; 2001-457740/49. Best Local Similarity (HYSE-) HYSEQ INC. Tang YT, Liu C, P-PSDB; ABB11787 WO200157188-A2. Homo sapiens. 11-JAN-2002 09-AUG-2001 ABA09031; Query Match RESULT 11 ABA09031/c Matches ολ

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of fadertifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby cylvipeptides of the invention have homology to known proteins, thereby cylving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; including cytokine, cell proliferation or cell differentiation activities; sem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; chemically activity; activin or inhibin related activities; chemocactic or chemokinetic activities; hemostatic, thrombotic or thrombolytic activities; receptor or lighand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treathing or ameliocating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell aborders), chronic inflammantary conditions (e.g., asthma or arthritis), conditions and any entire activities and any entire activities and any entire activities and activities or metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischemata, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, inclisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
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Pred. No. 25;
0; Mismatches 0; Indels (
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                                               Claim 1; Page 713-715; 1963pp; English.
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100.0%; Pre-
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ches 19; Conserv
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\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{\times}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N}}{\mathsf{N}}\overset{\mathsf{N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splicing of transcripts has no effect on the open reading frame of ASTH1J, as the exons involved are all 5' to the start codon in exon b. In contrast, alternative splicing of ASTH1 transcripts results in 3 different ASTH1 isoforms. The invention also encompasses mouse asthly protein. The ASTH1 nucleic acids are useful as diagnostics to identify a hereditary predisposition to asthma, as probes for identifying ASTH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J antibodies are useful in the identification of individuals predisposed to development of asthma, and for modulation of gene activity in vivo for
                                                                                                                                               The invention relates to the ASTHI locus on the short arm of human chromosome (11p). This locus comprises the ASTHI and ASTHI genes, which are associated with a genetic predisposition to asthma and bronchial hyperreactivity. The ASTHII and ASTHII genes are oriented in opposite directions with the ASTHII and ASTHII genes are oriented in expression and common sequence motifs. They are both expressed in trachea, lung and several other tissues. ASTHII and ASTHII are novel implicated in the activation of avariety of genes including the TCRA gene and cytokine genes known to be important in the activity of asthma. Both ASTHII and ASTHII mRNAs are alternatively spliced, Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related genes, for identifying expression of the gene in a biological specimen, and for generating genetically modified non-human animals or site specific gene modifications in cell lines. The encoded ASTH1 proteins are useful as immunogens to raise specific antibodies; in drug screening for compositions that mimic or modulate activity or expression of ASTH11 and/or ASTH13 (including altered forms of these proteins); and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic. The ASTH1 genes or fragments thereof, encoded proteins
     for e.g. screening compositions that modulate expression ASTH1 proteins or as diagnostics for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prophylactic and therapeutic purposes. The intact ASTH11 or ASTH13 proteins or active fragments thereof may be used to modulate or reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72928 BP; 20041 A; 15101 C; 16036 G; 21750 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchial hyperreactivity. The present sequence represents the non-transcribed region upstream of the human ASTH1J gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 21; Length 72928;
Pred. No. 27;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
                                                                                                     Claim 7; Column 49-112; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42063 standard; DNA; 1830121 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9
Best Local Similarity 100.
Matches 19; Conservative
                                                 predisposition to asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae
     TH1 protein, function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9633276-A1
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21-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42063;
     ASTH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42063/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pp
     δ
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0
                                                                                                                                                                                                                                                                                                                                          The invention identifies a genetic locus ASTH1, associated with asthma, mapped to human chromosome 11p. ASTH11 and ASTH1J are genes present within the locus, located close to each other on human chromosome 11p, and have similar patterns of expression, and common sequence motifs. The ASTH1 genes and fragments, encoded protein, genomic regulatory regions and anti-ASTH1 antibodies are useful in the identification of individuals predisposed to development of asthma, and for the modulation of gene activity in vivo for prophylactic and therapeutic purposes. The ASTH1 protein is useful as an immunogen to raise specific antibodies, in drug screening for compositions that minic or modulate ASTH1 activity or expression, including altered forms of ASTH1 protein, and as a therapeutic. The present sequence represents a human ASTH1 genomic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids other than naturally occurring chromosomes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72928 BP; 20042 A; 15100 C; 16036 G; 21750 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 72928;
                                                                                                                                                                                                                          Mammalian asthma related genes, useful for diagnosis of a predisposition to development of asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTH1 locus; ASTH1J; human; chromosome 11p; asthma;
                                                                                                     Carey AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardon L,
                                                                                                  Cardon L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 19;
Best Local Similarity 100.0%; Pred. No.
Matches 19; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                   Claim 15; Page 75-96; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA80253 standard; DNA; 72928 BP
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                                                                                                  Brooks-Wilson AR, Buckler A,
Galvin M, Miller A, North M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1625 CCATTGAGAAGGCCAAGCG 1643
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Brooks-Wilson AR, Carey AH;
98WO-US01260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0009913
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                                                 (AXYS-) AXYS PHARM INC
                                                                                                                                                                         WPI; 1999-479058/40.
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21-JAN-1998;
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This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence in a computer readable form, it is possible to identify genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to requiate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFs can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                        Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleic acid fragments by homology searching
                                                                                                                                                                                                                                                                             Claim 1; Page 77.2-77.1091; 1291pp; English
                                          (HUMA-) HUMAN GENOME SCI INC.
95US-0476102.
                                                              UNIV JOHNS HOPKINS
                                                                                                         Fleischmann RD,
                                                                                                                                               WPI; 1996-485782/48.
07-JUN-1995;
                                                                                                         Adams MD,
                                                              (UYJO)
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White 0;

Venter JC,

Smith HO,

ö Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other; Gaps 0.9%; Score 19; DB 17; Length 1830121; ilarity 100.0%; Pred. No. 29; Conservative 0; Mismatches 0; Indels 0; Local Similarity nes 19; Conserv Query Match Matches

1138 GAAAAGGCTTATAAGGAAG 1156 δ

ABN69869 standard; DNA; 228 (first entry) 01-JUL-2002 ABN69869;

Streptococcus polynucleotide SEQ ID NO 7651.

27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640.

(GENO-) INST GENOMIC RES

Grandi G, Margarit Ros YI, Masignani V, rettelin H; relford J,

Fraser C;

WPI; 2002-352536/38. P-PSDB; ABP29238.

```
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5813 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6604.ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a streptococcus mapped. (1) is used to detect of the disease caused by Used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity charactering.
New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein
                                                                                                            Claim 7; Page 3903; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins
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Sequence 228 BP; 85 A; 23 C; 46 G; 74 T; 0 other;

Gaps . 0 Score 18; DB 24; Length 228; Pred. No. 80; Indels 0 100.0%; Prec. 0.8%; Best Local Similarity 100 Matches 18; Conservative Query Match

7 ATGAAATTAAAAAGTATT 24 21 4 ATGAAATTAAAAAGTATT Db Óλ

completed: May 23, 2003, 07:31:39 le : 2006 secs Job time Search

; 0

Db 1428299 GAAAAGGCTTATAAGGAAG 1428281

RESULT 15

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

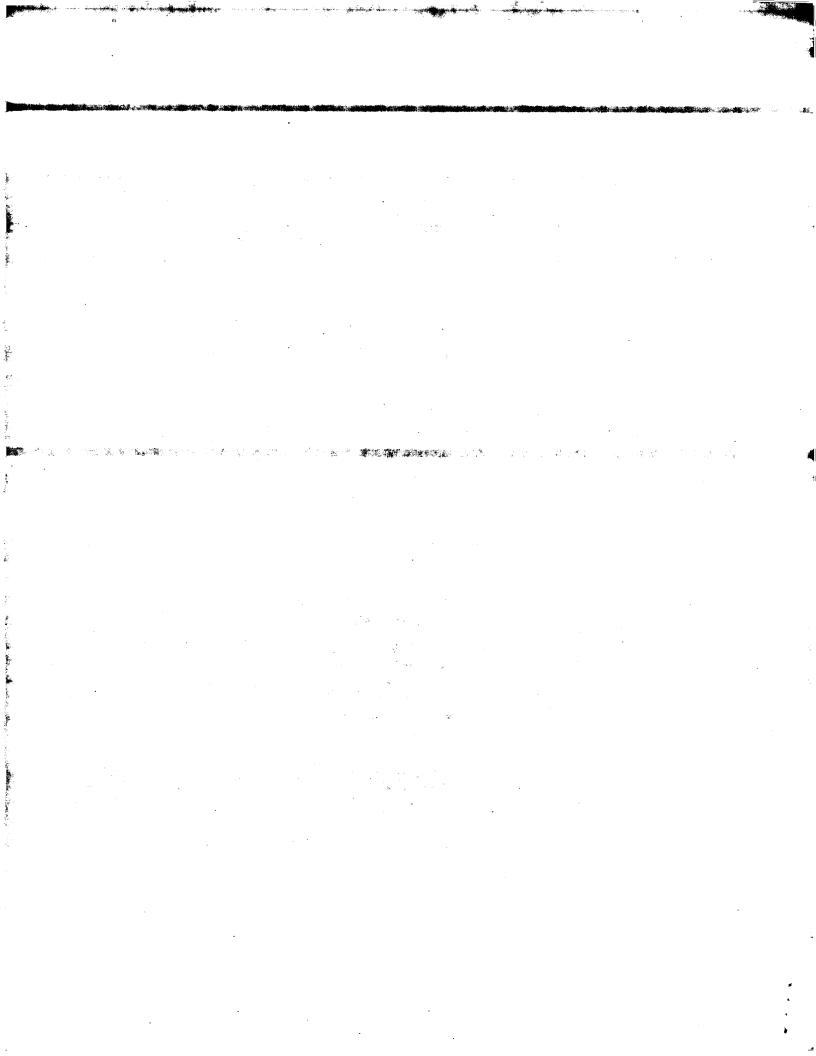
Streptococcus pyogenes

WO200234771-A2

02-MAY-2002.

29-OCT-2001; 2001WO-GB04789.

(CHIR-) CHIRON SPA



Page

		28	16	0.7	1330 2	US-08-405-496A-22
	GenCore version 5.1.4_p5_4578	29	16	0.7	1330 4	US-08-915-136-22
	Copyright (c) 1993 - 2003 Compugen Ltd.	30	16	0.7	1347 2	US-08-959-749-1
		31	16	0.7	1347 4	US-09-351-497-1
		32	16	0.7	1359 4	US-09-134-001C-1336
OM nucleic - nu	OM nucleic - nucleic search, using sw model	33	16	0.7	1402 1	US-08-480-604A-25
		34	16	0.7	1402 2	US-08-405-496A-25
Run on:	May 23, 2003, 05:20:28 ; Search time 62 Seconds	35	16	0.7	1402 4	US-08-915-136-25
	(without alignments)	c 36	16	0.7	1491 4	US-08-740-223A-21
	10580.348 Million cell updates/sec	c 37	16	0.7	1491 4	US-09-709-188-21
		c 38	16	0.7	1500 4	US-08-740-223A-23
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Sequence;	1 atgcaaatgaaattaaaaaagaagagctgaagttgatctaa 2139	c 41	16	0.7	1812 1	US-08-328-322-18
		c 42	16	0.7	1829 1	US-08-201-118-8
Scoring table: OLIGO_NUC	OLIGO_NUC .	c 43	16	0.7	1829	US-08-238-821B-8
	Gapop 60.0 , Gapext 60.0 .	C 44	16	0.7	1829	. PCT-US95-05744-8
		c 45	16	0.7	1964 1	US-08-328-322-9
Searched:	441362 segs, 153338381 residues					

ALIGNMENTS

Sequence Seq

Sequence Seq

APPLICANT: ROSS, Bruce C. TITLE OF INVESTMENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF CORRESPONDENCE ADDRESSE: ADDRESSE: OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: REGISTRATION NUMBER: 32,430
REFREROCA/COCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-813-5600 US/09/221,017B PCT/AU98/01023 Sequence 726, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION: ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto TELEFAX: 650-494-0792 TELEX: 706141 INFORMATION FOR SEQ ID NO: 726: PP1546 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUBER:
FILING DATE:
FILING DATE: 30-JAN-1998 PP2911 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP291
FILING DATE: 09-APR-1998 IBM Compatible 23-DEC-1998 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION: 1974 base pairs NAME: Monroy, Gladys H REGISTRATION NUMBER: 32 SEQUENCE CHARACTERISTICS: COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette PRIOR APPLICATION DATA: APPLICATION NUMBER: 1 TYPE: nucleic acid STRANDEDNESS: double APPLICATION NUMBER: FILING DATE: US-09-221-017B-726 COMPUTER:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

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882724

Post-processing: Listing first 45 summaries

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DNA (genomic)
NO
                                                                                   70.1%;
99.8%;
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1021 GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGA
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TITLE OF INVEWTION: P. GINGIVALIS
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
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Sequence 382, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
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APPLICATION DATA:
APPLICATION NUMBER: US/no/^^^
                                                                                                       SOFTWARE: PASLSED for Windows Version 2.0 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/N9/nno ... FILING name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: SI
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1625 CCATTGAGAAGGGCAAGCG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-JAN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                21-JAN-1998
                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 72928 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA
US-09-009-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.9
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
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                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 755 PAGI CITY: Palo Alto
 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-221-017B-382
                                                     94301
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                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTERG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%; Score 92; DB 4; 99.3%; Pred. No. 1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
                                                                                                                                                        PROGRADICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31.DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PC7/AU98/01023
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                        MBER: US/09/221,017B
23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 CGAATGCGTGAGCTCGGCTTTAC 508
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                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1...561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circular
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: bourELEFAX: bourer 706141
                                                                                                                                             CLASSIFICATION:
                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-221-017B-12
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US-09-009-913-1/c
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SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                          APPLICANT: PARSER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: US-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFRENCE/DOCKET NUMBER: 850586.90012
TELECOMNUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414)277-5591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 166, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francols J.
APPLICANT: OUELETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: PROBES AND AMPLIE;
TITLE OF INVENTION: PROBES AND AMPLIE;
TITLE OF INVENTION: ANTIBIOTIC RESIST;
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 EAST WISCONSIN AVENUE CITY: MILWAUKEE STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11.5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 1325 ACCGTAAGGTGCTGCCCG 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-743-637B-166
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ESULT 6
S-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WITTE, Owen R.
APPLICANT: WINTE, Owen R.
APPLICANT: WINTE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UPBRECULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATCHIN VOS: 2.
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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                               NAME: MONTOY, Gladys
REGISTRATION NUMBER: 32,430
REGISTRATION NUMBER: 27340-20021.00
RELEPHONE: 650-813-5600
TELEPHONE: 650494-0792
TELERA: 660494-0792
TELERA: 660494-0792
TELERA: 660494-0792
TELERA: 660494-0792
TELERA: 660494-0792
TELERA: 660494-0792
TELERA: 600411
TENERA: 600411
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 18;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: PORYPHYROMONAS GINGIVALIS
            FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09103840A; Patent No. 6294328
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tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1325 ACCGTAAGGTGCTGCCCG 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        636 CGATACGGACAACTGGAT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: 1...1317
US-09-221-017B-382
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Matches 18; Conservative
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Matches 18; Conserv
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LENGTH: 4403765
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US-09-103-840A-2
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DB 4; Length 4411529; 13;

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GENERAL INFORMATION:
APPLICANT: Department of Veterans Affairs
APPLICANT: Department of Veterans Affairs
TITLE OF INVENTION: factor releted protein
FILE REFERENCE: 107999.00106
CURRENT APPLICATION NUMBER: US/09/570,454
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/134,200
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
AITLE OF INVENTION: PLANT REGULATORY PROTEINS III
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Boulevard
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO AU96/00383
FILING DATE: 21-01N-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION NUMBER: AU PN3779/95
FILING DATE: 23-01N-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/997,251
23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Scc.
100.0%; Pre
0;
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; Patent No. 6271440
                   RESULT 9
US-09-570-454-1/c
Sequence 1, Application US/09570454
; Patent No. 6399743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1255 CCAATGCCTATGCCATT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1613 CCAATGCCTATGCCATT 1629
                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus norvegicus US-09-570-454-1
                                                                                                                                                                                                                                                                                                            Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Winner, Ellen P.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ns
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                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BERGERON, Michel G.
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: NOY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                        0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                           Score 17; DB 2;
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB;
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 166, Application US/08526840B Patent No. 6001564
                                                                                                                                              0.8%; Scc.
100.0%; Pre
0;
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TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 166: SEQUENCE CHARACTERISTICS: LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prative 0;
                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-166
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SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                           Query Match 0.89
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                               37 GCCCTGCTGTTGGGTGC 53
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Best Local Similarity
Matches 17; Conserva
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US-08-526-840B-166
                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-526-840B-166
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ADDRESSEE: No. 58663930 No. 5866393disk of No. 5866393th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
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APPLICANT: Fuglsang, Claus
APPLICANT: Halkier, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Oxenboll, Karen M.
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Haloperoxidases from Curvularia
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                               DB 1; Length 2692; 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2822;
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MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC COMPOSITION
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/679,405
FILING DATE: JULY 9, 1996
CLASSIFICATION TOWNER: US/08/679,405
FILING DATE: JULY 9, 1996
FILING DATE: JULY 14, 1995
PRIOR APPLICATION NUMBER: 08/600,534
FILING DATE: JULY 14, 1995
PRIOR APPLICATION NUMBER: 08/600,534
FILING DATE: FEBURATION:
AMME: LAMBINIS, Ellas J.
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ IDO: 1:
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00.0%; Pred. No. 46;
ve 0; Mismatches
                                                              Pred. No. 46;
Mismatches
                                  Score 17;
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                                     0.00.
100.0%; Pro
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100.0%; Pr
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                                                                                                                                                     1394 TATTCAAGAATGTAATC 1410
                                                                                                                                                                                        1809 TATTCAAGAÄTGTAATC 1793
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LENGTH: 2822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                               Query Match 0.8%
Best Local Similarity 100.C
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New COUNTRY: U. ZIP: 10174
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; LOCATION:
US-08-679-405-1
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US-08-679-405-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUTHRIE, ELLEN P.
TITLE OF INVENTION: ISOLATED DNA ENCODING THE SphI
TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR PRODUCING
TITLE OF INVENTION: THE SAME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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POSITION 703/ENDS AT 1653. 'RESTRICTION
ENDONUCLEASE STARTS AT POSITION 1703/ENDS AT 2410"
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STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DUS
SOUTHWERN PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 1920820
FILING DATE: 1920820
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLLAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: 42078
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 523-3400
TELEPAN
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 0.8%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 45; Matches 17; Conservative 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/07932454A Patent No. 5262318
                            LENGTH: 2352 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: OFF SELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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1703..2410
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396..2054
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OTHER INFORMATION: COTHER INFORMATION: FOTHER INFORMATION: FOTHER INFORMATION: FOTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-932-454A-2/C
                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-997-251-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOS
STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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US-07-932-454A-2
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CURRENT APPLICATION DATA:
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STRANDEDNESS: single
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NUMBER OF SEQUENCES:
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SOFTWARE: Patent
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 9. CLASSIFICATION:
                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS ; LOCATION: 477 PCT-US96-11458-1
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                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: No. 59654180 No. 5965418disk of No. 5965418th America, Inc. 405 Lexington Avenue, Suite 6400
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Verruculosa and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                           Haloperoxidases from Curvularia
Verruculosa and Nucleic Acids Encoding Same
21
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

FOR APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORPUSADE: COMPUTABLE COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9611458 GENERAL INFORMATION:
                                                         Sequence 1, Application US/08842799 Patent No. 5965418 GENERAL INFORMATION:
                                                                                                                                                      APPLICANT: Fuglsang, Claus
APPLICANT: Halkier, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Chery, Joel
TITLE OF INVENTION: Haloperoxid
TITLE OF INVENTION: Verruculosa
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8%; Soc
Best Local Similarity 100.0%; P:
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10174
COMPUTER READABLE FORM:
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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: U.S.A.
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MOLECULE TYPE:
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; LOCATION:
US-08-842-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                         US-08-842-799-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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Length 2822;
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Patent No. 5773267
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 17; DB 5;
100.0%; Pred. No. 46;
E: Novo Nordisk of North America, 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN STREET: 90 PARK AVENUE CITY: NEW YORK COUNTRY: U.S.A.
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 4441.204-WO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US96/11458
FILING DATE: 9-JUL-1996
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,194
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,534
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 867-0123
TELEFRAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2822 base pairs
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Query Match 0.8%; Score 17; DB 1; Length 49272; Best Local Similarity 100.0%; Pred. No. 47; Matches 17; Conservative 0; Mismatches 0; Indels 0
HELDING DATE: WARCH 7, 1996
ATTORNEY FAGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REPRENENCE/COCKET NUMBER: 96700/402
TELEPAN: (212) 697-5995
TELEPAN: (212) 697-5995
TELEPAN: (212) 286-082
TELEPAN: (212) 897-595
TELEPAN: (212) 897-51
TELEPAN: (212
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Search completed: May 23, 2003, 10:27:15 Job time : 6285 secs

Db 46900 GCTACCTCTTGG 46916 836 GCTACCTCACTTCTTGG 852

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Gaps

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Sun May 25 15:40:22 2003

20 0.9 410 12 BG158262 BG158262 EM1.9_F06 20 0.9 410 10 AM199497 BG809317 21725 BM 20 0.9 463 14 BG413467 BG413470 BG809317 21725 BM 20 0.9 473 14 BG413467 BG413470 AM19949 217929 BM 20 0.9 473 14 BG413470 BG619917 217929 BM 20 0.9 579 12 BF654953 BG819994 BG819994 217929 BM 20 0.9 579 12 BF654953 BG819994 BG819994 217929 BM 20 0.9 579 13 B187557 BG819994 BG819994 217929 BM 20 0.9 579 13 B187557 BG819994 BG819994 217929 BM 20 0.9 570 13 B187557 BM02939 BM2391 CCKECLEL 10 BE1 BM 20 0.9 581 13 BM02939 BM2311 BM02939 BM321169 CCKECLEL 10 BE1 BM02939 BM321169 CCKECLEL 10 BE1 BM02939 BM321169 CCKECLEL 10 CCKECLEL 10 CCKECLEL 10 CCKECLEL 10 CCKECLEL 10 CCKECLE 10 CCKECLEL 10 CCKECLER 10	Mahairas, G.G., Wallace, J.C., Steller, A., Shaker, R., Furlong, Hood, L. Sequence-tagged connectors: A scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 9380589 Contact: Mahairas GG, Wallace High Throughput Sequencing Certification of Wallace High Throughput Sequencing Certification of Wallace High Throughput Sequencing Certification of Wallace Mane Avenue North, Stell Queen Anne Avenue North,
C C C C C C C C C C C C C C C C C C C	REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT
compugen Ltd. Compugen Ltd. arch time 2048 Seconds (without alignments) 16915.110 Million cell updates/secaagagctgaagttgatctaa 2139 meters: 32308132	results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES SUMMARIES A0820052 A0820052 A0820052 A0820052 A0820052 A0820052 A0820052 A0820052 A0820052 A0820053 A088100 BM553311 AW200173 AW881153 AW881153 AW881153
GenCore version 5 cch, using sw model cch, using sw model 169 1-355-1 1tgaaattaaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag 1tgaaattaaaag	27: em_gss_rod:* is the number of ater than or equal rived by analysis * Query Autch Length DB 1.0 444 17 1.0 800 17 1.0 800 17 1.0 1061 13 0.9 223 10 0.9 223 10
Copyris OW nucleic - nucleic sear Run on: May 23, 7 Title: US-10-006 Perfect score: 2139 Sequence: 1 atgcaae Scoring table: OLIGO_NUC Searched: 0.151006 Word size: 0 Total number of hits sati Minimum DB seq length: 0 Maximum DB seq length: 0 Post-processing: Listing Database: EST:* Database: EST:* 1: em_est 2: em_est 3: em_est 4: em_est 4: em_est 5: em_est 7: em_e	Pred. No. score gree and is deland i

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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1928924 Schneider fetal brain 00004 Homo sapiens CDNa clone IMAGE:2518932 5' similar to 9b:X63432_cds1 ACTIN, CYTOPLASMIC 1
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1 (bases I to 591)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Conpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissum_type="frontal lobe"
/tissum_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript SK (Stratagene);
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 846 row: O column: 19
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 444.
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco.
High quality sequence stop: 329.
Location/Qualifiers
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0
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 17; Length 444; Pred. No. 20;
                                                                                                                                                                                                                                                                                /clone="Plate=846 Col=19 Row=0"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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/clone="InA66:2518932"
/clone_lib="Schneider fetal brain 00004"
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                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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KEYWORDS
SOURCE
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumirku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimppanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                 Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-081L22.R.
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0
                                                                                                                                              The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 03-NOV-2001
                                                                                                  and 3' adaptor sequence:
5'-GAGAGAGACTCGAGTTTTTTTTTTTTTTTT.3'. The library wa size-selected for >0.5 kb inserts and has an average size-selected for >0.5 kb inserts and has an average enrichment size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy). " I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG084100 800 bp DNA linear GSS 03-NOV-2007
Pan troglodytes DNA, clone: PTB-081L22.R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 21; DB 9; Length 591;
100.0%; Pred: No. 21;
iive 0; Mismatches 0; Indels
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male"
148 q 254 t
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Pred. No..22;
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-081L22.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1160 CCAAGGCCAACCGTGAGATGA 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 CCAAGGCCAACCGTGAGATGA 429
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                              sedneuce:
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Matches 21; Conservative
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ORIGIN
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AG084100
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Other_ESTS: dal2e08.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seg primer: -40RP from Gibco
High quality sequence stop: 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Lissue_Lype="nocyte (stages 5 and 6)"
/Lissue_Lype="nocyte (stages 5 and 6)"
/Lib_host="Top-10 F"
/Lib_host="Top-
                                                                                                                        1 (bases 1 to 223)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW881153 23-MAY-20 CVO-070033-170400-197-c10 CVO-070033-170400-197-c10 CVO-033 HOMO SAPIEDS CDNA, MRNA SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 223; 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnoc003015"
/clone_lib="Xenopus laevis occyte"
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100.0%; Pred. No.
Live 0; Mismatci
                                                                                                                                                                                                                                                                                     WashU Xenopus EST project, 1999
Unpublished (1999)
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Best Local Similarity 100°.
Matches 20°, Conservative
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      Xenopus laevis
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COMMENT
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                                                                                                                                                                                                                                                                                         EST 20-FEB-2002
                                                                                                                                                                                                                                                                                  BM553311 1061 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6542482 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5742946
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      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12761 row: o column: 11
High quality sequence stop: 682.
High quality sequence stop: 682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1061)
NIH wGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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   Mismatches
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/clone="INAGE:5742946"
/clone_lib="NIH_MGC_119"
/tissue_type="medulia"
/lab_host="DH108"
   ;
0
                                                                                           575 GAATACTTCCTCATCGTCTAC 595
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                                                          553 GAATACTTCCTCATCGTCTAC 573
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100.0%;
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Best Local Similarity 100.0
Matches 21; Conservative
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21; Conservative
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AW200173
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COMMENT

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SOURCE

ORIGIN

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REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_axref="taxon:4558"
/clone_lib="Embryo | (EMI)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea: Pipidae:
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea: Pipidae:
1 (bases 1 to 410)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Clifton,S., Johnson,S.L., Miderwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
                           Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library constructed by Bruce Blumberg
Library normalized by Jihan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -400P from Gibco
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XENOPUS_SOURCE_ID:xlnoc003o15 3' similar to SW:CLN3_CANFA Q29611
CLN3 PROTEIN. ;, mRNA sequence.
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Fax: 314 286 1810
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61;
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/db_xref="texoron:8355"
/clone="xeNoPUS_SOURCE_ID:xlnoc003015"
/clone_lib="Xenopus laevis oocyte"
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WashU Xenopus EST project, 1999
Washington University School of Medicine
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69 c 110 g 10 t
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100.0%; Pred. No.
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Location/Qualifiers
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High quality sequence start: 5
High quality sequence stop: 116
POLYA-No.
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100.0%; Pre-
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  Fax: 706 583 0210
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/db_xref="taxon:9606"
/clone_lib="corous3"
/dev_stage="Adult"
/note="Organ: ovary; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

86 a 30 c 57 g 84 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-OT0033-170 Seq primer: puc 18 forward
                        1 (bases 1 to 257)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Bagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deolivelar,P.S., Bucher,P., Jongeneel,C.Y., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
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EM1_9_F06.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
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Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
An EST database from Sorghum: developing embryos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                   sequence tags
Proc. Ntl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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100.0%; Pred. No. 61;
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Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  rel: +55-11-2704922
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Query Match Best Local

Matches

q ð

BASE COUNT

BG158262/c DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

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TITLE JOURNAL

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EST 22-MAY-2002
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
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/cultivar="8400"
/db_xref="taxon:29329"
/clone="GA_E60058F03r"
/clone="GA_E60058F03r"
/clone="Lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
    /note="vector: pcMv SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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Eukaryota, viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Magnoliophyta; eudicotyledom;; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
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Clemson University Genomics Institute
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Pred, No.
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Seq primer: TAATACGACTCACTATAGGG
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High quality sequence stop: 464
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                                                                                                                                                                                    ilarity 100.0%; P. Conservative 0;
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144 c 6
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BQ412487.1 GI:21100174
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ (bases 1 to 419)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Sasas, E., Wary, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Lagereid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
/tissue_type="oocyte (stages 5 and 6)"
/lab_host="Top-10 F'"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA.
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
                                                                                                                                                                                to biotinylated driver (prepared from the same library by excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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21180013
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0.9%; Score 20; DB 10; Length 410;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 20; Conservative 0; Mismatches 0; Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                            Collection (XGC) library.
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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PCR PRimers
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BE809917.1 GI:10241029
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SOURCE
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Contact: Smith TPL
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SOURCE
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1 (base 1 to 473)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Neckown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                       Gossypium arboreum:

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:

Rosidae: eurosids II: Malvales: Malvaceae; Gossypium.

I (bases 1 to 472)

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 25-APR-2001
GA_Ed0058F03f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ed0058F03f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:29729"
/clone="GA_Ed0058F03f"
/clone="Iib="GAGOSSypium arboreum 7-10 dpa fiber library"
/tlssue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: xho!"
80 c 131 g 124 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                     Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gossypium arboreum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
Total High Quality bases = 216
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 3
High quality sequence stop: 446.
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BQ403470.1 GI:21091157
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                                                                                                          Gossypium arboreum.
                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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Matches 20; Conservative
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.909004.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 220.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as59q06.xl Barstead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2333050 3' similar to SW:Y281_HUMAN Q92556 HYPOTHETICAL
PROTEIN KIAA0281 ;; mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4390
Fax: 402 762 4390
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68;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2333050"
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Pred. No.
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/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTACG
Plate: 74 row: G column: 8
Plate: 74 row: G sogner: 8
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
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100.0%;
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Contact: Wilson RK
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Best Local Similarity 100.
Matches 20; Conservative
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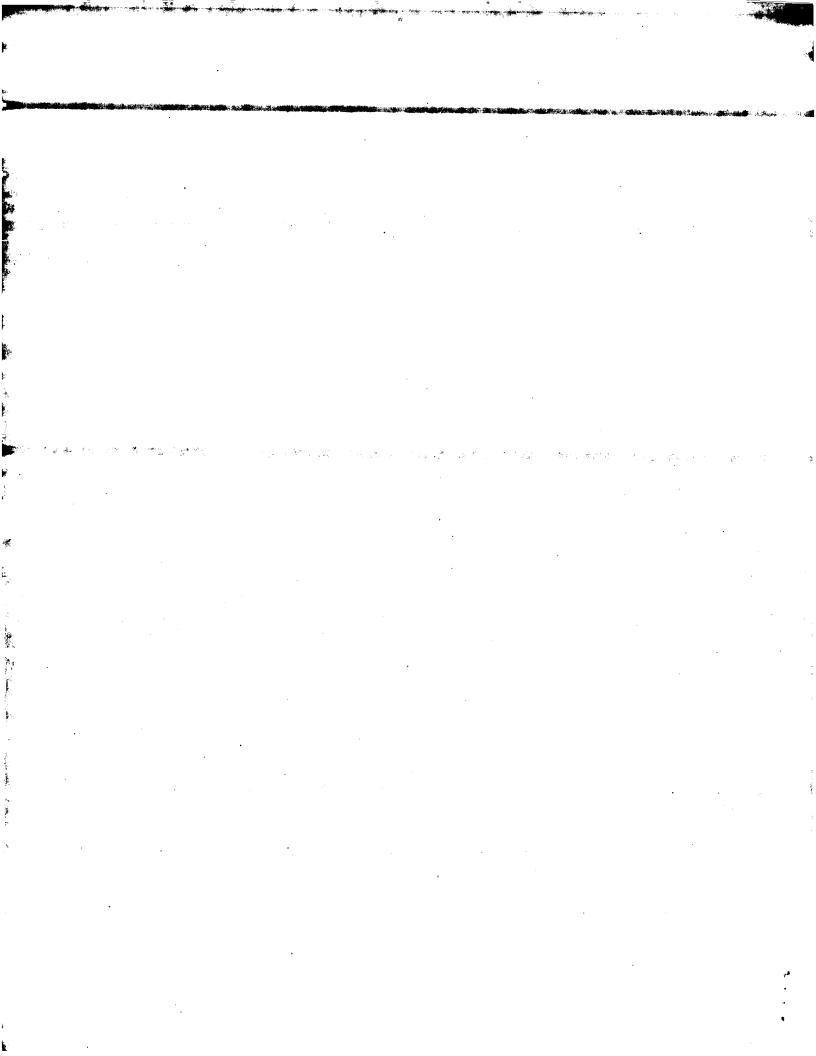
Length 519;

DB 12; 70;

us-10-008-355-1.oli.rst

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Pred. No.
                                    Score 20;
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1. .523
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Job time : 2065 secs
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100.0%; Pre-
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Bovidae; Bovinae; Bos
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Best Local Similarity 100.(
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                                                    Best Local Similarity 100. Matches 20; Conservative
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                                      Query Match
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                                             Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the minscore 18 and -minmatch 12 options.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                     Length 509
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/clone_lib="Barstead colon HPLRB7"
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
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69;
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                                   /dev_stage="adult, age 25"
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/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Location/Qualifiers
1. .519
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 75 row: D column: 10
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
vv0.980904 e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, E., Wary, J.E., White, J., Cho, J., Pahrenkrung, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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469747 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI847597
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Fax: 402 762 4390
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/clone_lib="MARC 2BOV"
/tissue_type="pooled"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 94 row: D column: 18
seq primer: ATTTAGGGGACACTATAG.
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Sequence 19, 984 2 US-08-449-645A-19 Sequence 19, 984 2 US-08-702-367A-19 Sequence 19, 1.3 984 2 US-08-702-367A-19 Sequence 19, 984 2 US-08-702-367A-19 Sequence 19, 116 1 US-09-086-201-8 Sequence 19, 98 1.1 116 1 US-09-086-201-8 Sequence 2, 98 1.1 116 1 US-09-086-201-8 Sequence 2, 98 1.1 396 4 US-08-860-656B-3 Sequence 2, 98 1.1 396 4 US-08-455-35-10 Sequence 10, 1170 4 US-08-455-35-10 Sequence 10, 1170 4 US-08-602-999A-8 Sequence 2, 1170 4 US-08-602-999A-8 Sequence 2, 1170 4 US-08-860-656B-10 Sequence 10, 1170 4 US-08-860-656B-10 Sequence 10, 1170 4 US-08-860-656B-10 Sequence 10, 1170 4 US-08-860-656B-10 Sequence 5, 1170 1170 1170 1170 1170 1170 1170 117	42 7 1.0 102 2 US-08-820-754-24 Sequence 44 7 1.0 102 3 US-08-956-652-24 Sequence 45 7 1.0 102 3 US-08-956-652-24 Sequence 46 7 1.0 102 3 US-08-956-652-24 Sequence 508-523-373-22 Sequence 22, Application US/08523373 SERET SEQUENCES: 24 CORRESPONDENCE ADDRESS: 24 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: BURNS, DANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: STREET: 699 Prince Street CITY: Alexandria STREET: BM PC compatible COMPUTER: IBM PC compatible OPERATION UNMER: US/08/523,373 FILING DATE: 05-58P-1994 APPLICATION NUMBER: JP 6-296028 FILING DATE: 07-SPEP-1994 ATTORNEY/AGENT INFORMATION: NAME: MACHIN DATA: APPLICATION NUMBER: 35 607 STRING DATE: 07-SPEP-1994 ATTORNEY/AGENT INFORMATION: NAME: MACHIN DATA: APPLICATION NUMBER: 36 607 REFERENCE/DOCKET NUMBER: 36 607 REFERENCE/DOCKET NUMBER: 301050-251 TELECOMMUNICATION INFORMATION:
Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 13:03:17; Search time 30 Seconds (without alignments) 4195.709 Million cell updates/sec 712 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 2139 Scoring table: OLIGO Xgapop 60.0, Xgapext 60.0 Ygapop 60.0, Yappext 60.0 Ygapop 60.0, Yappext 60.0 Fgapop 60.0, Pappext 7.0 Delop 6.0, Pappext 7.0 Searched: 262574 seqs, 29422922 residues Word size: 1 Total number of hits satisfying chosen parameters: 438908 Minimum DB seq length: 2000000000	Command line parameters:

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APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: 24
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 619 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUSTEM: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                     213
0 0
0 0
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994.
ATTORNEY/AGENT INFORMATION:
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; Sequence 23, Application US/08523373
; Patent No. 6037145
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
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   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: FNGTH: 213 amino acids
                                                                                                                                                                                                 0.351
10.00
100.008
100.008
1.408
703-836-6620
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amino acid
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                                                                                                                                MOLECULE TYPE: peptide
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ZIP: 22314-3187
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Best Local Similarity:
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US-08-523-373-23
TELEPHONE:
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PROCESS FOR PRODUCTION OF PROTEIN 24
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                                      Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
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   Length:
Matches:
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                                                                                              Gaps:
                                                                                                                                                                                        165 ThrGlyGlyAsnSerGlySerProValPhe 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               Sequence 24, Application US/08523373
Patent No. 6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FNUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
0.351
10.00
100.00%
100.00%
1.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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10.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 699 Princ
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22314-3187
                                    Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                             US-08-523-373-24
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GENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                          TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS VB
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
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Mismatches:
Indels:
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                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             имвек: US/08/657,192
03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION UNBER: 1P 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                      Sequence 3, Application US/08657192
Patent No. 5747321
GENERAL INFORMATION:
APPLICANT: YABUTA, MASAYUK!
APPLICANT: OHSUYE, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08523373 Patent No. 6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
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100.00%
100.00%
1.40%
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                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                   CITY: Alexandria
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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RESULT 4
US-08-657-192-3
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US-08-523-373-5
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APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
UNMER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                       SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/523,373 FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
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Mismatches:
Indels:
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Alexandria
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                                                                                                                                                                                                                                                                                                                                                       001560-251
                                                                                                     05-SEP-1995
                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                   NAME: Meuth, Donna M. REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
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10.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 344 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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ZIP: 22314-3187
COMPUTER READABLE FORM:
                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity:
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CLASSIFICATION:
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                                         MEDIUM TYPE:
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STREET: 69
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us-10-008-355-1.olin2p.rai

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GENERAL INFORMATION:
APPLICANT: YABUTA, Masayuki
APPLICANT: OBSUYE, RAZUMITO
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
STATE: Virginia
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY, FAGENT INFORMATION: NAME: Meuth, Donna M. REGISTRATION NUMBER: 36,607
REFERENCE/COKET NUMBER: 001560-251
TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION SEC 10 NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086,
FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08657192 Patent No. 5747321
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                                                                                                                                                                                                                                                                                                                                not relevant
                                                                                                                                                                                                                                                                                    LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .408
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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DB:
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APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                        289 ThrGlyGlyAsnSerGlySerProValPhe 298
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCHWARE: PATENTIN Release #1.0, Ve)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIETCATION NUMBER: UP 6-28695
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: UP 6-296028
FILING DATE: 07-NOV-1994
APPLICATION NUMBER: UP 6-296028
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08523373 Patent No. 6037145
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REGISTRATION NUMBER: 36,607
REFERENCE-DOCKET NUMBER: 0(
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 2214-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                      0.315
10.00
100.00%
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: 532 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                     single
                                                      inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexandria
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STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                 STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                      MOLECULE TYPE:
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                                                                                     US-08-657-192-9
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                             JS-08-523-373-7
                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                Score:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTONNEY/AGENT INFORMATION: APPLICANT: YABUTA, Masayuki
APPLICANT: ORSUVE, Mazuhiro
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: PROTEASES 537 110 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-008-355-1 (1-2139) x US-08-657-192-15 (1-537) Mismatches: Indels: US-10-008-355-1 (1-2139) x US-08-523-373-7 (1-532) TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS ALTITLE OF INVENTION: PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS
STREET: P.O. BOX 1404 1930 ACGGCGGTAACTCCGGTAGCCCCGTATTC 1959 1930 ACGGCGCTAACTCCGGTAGCCCCGTATTC 1959 289 ThrGlyGlyAsnSerGlySerProValPhe 298 NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620 US-08-657-192-15 ; Sequence 15, Application US/08657192 ; Patent No. 5747321 0.314 10.00 100.008 100.008 1.408 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 1 Best Local Similarity: 100.00% Query Match: 1.40% 537 amino acids CITY: Alexandria STATE: Virginia COUNTRY: United States SEQUENCE CHARACTERISTICS single protein ZIP: 22313-1404 COMPUTER READABLE FORM: linear GENERAL INFORMATION: Percent Similarity: Best Local Similarity: STRANDEDNESS: MOLECULE TYPE: Alignment Scores: US-08-657-192-15 Query Match: οχ

Sequence 3729, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14 APPLICANT: HIBBS, Margaret L.
APPLICANT: SCOTT, Bernadette M.
APPLICANT: BONADONNA, Lisa
APPLICANT: HULETT, Mark D.
TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN.
NUMBER OF SEQUENCES: 136 0000 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-008-355-1 (1-2139) x US-08-332-562A-67 (1-15) APPLICATION NUMBER: US/08/332,562A
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/896,457
FILING DATE: 27-MAY-1992
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 54270/119/GRHA
TELECOMMUNICATION: E: Foley & Lardner 3000 K Street, N.W., Suite 500 1930 ACGGGGGTAACTCCGGTAGCCCCGTA 1956 5 ThrGlyGlyAsnSerGlySerProval 13 Floppy disk 100.00% 100.00% 1.26% (202)672-5399 LENGTH: 15 amino acids INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS COUNTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: single NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: CITY: Washington STATE: D.C. TYPE: amino acid linear Percent Similarity: Best Local Similarity: 904136 STRANDEDNESS: MEDIUM TYPE: RESULT 11 US-09-134-001C-3729 TELEPHONE: TELEFAX: (ADDRESSEE: JS-08-332-562A-67 Alignment Scores: Pred. No.: TOPOLOGY: Query Match Score:

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TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                984
9
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION: APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS, APPLICANT: T.; KROMEK, LAWRENCE, F.; VANDE WOUDE, APPLICANT: GEORGE, F.
                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                        1933 GGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                           261 GlyGlyAsnSerGlySerProValPhe 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
                                                      ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3729
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345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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100.00%
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
NUMBER OF SEQ ID NOS:
SEQ ID NO 3729
LENGTH: 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                               Percent Similarity:
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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Pred. No.:
                                                                                                                            Alignment Scores
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US-08-673-789-9
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US-08-449-645A-19
Sequence 19, Application US/08449645A
Sequence 19, Application US/08449645A
Sequence 19, Application US/08449645A
SEMERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Ainases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   984
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
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     Mismatches:
Indels:
                                                                             US-10-008-355-1 (1-2139) x US-08-673-789-9 (1-984)
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                                                                                                                                                                                                                                                                                                                                                                                           Amgen Patent Operations/RBW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                       25 CTTCTCGGAGCAGCCCTGCTGTTGGGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 CTTCTCGGAGCAGCCCTGCTGTTGGGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-702-367A-19; Sequence 19, Application US/08702367A; Sequence 10, Application US/08702367A; Detent No. 5981246; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1840 behavilland brive
CITY: Thousand Oaks
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
Best Local Similarity: 100.00%
Query Match: 1.26%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Query Match:
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Pred. No.:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COMPUTER: USA
2.1P: 913.0
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: Release #1.0, Version #1.25
                                                                          CAPTE: 913.0

CAPTE: 913.0

CAPTE: 913.0

CAPTE: FISHER FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTONEY/AGENT INPORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 984 anino acids

TYPE: anino acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-008-355-1 (1-2139) x US-08-702-367A-19 (1-984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
1.26%
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APPLICATION NUMBER: PCFILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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Thousand Oaks
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
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                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-04681-19
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                                              COUNTRY:
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PCT-US95-04681-19
Alignment Scores: 2.68
Pred. No.: 9.00
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	2.68	Length:	984
	9.00	Matches:	φ
Percent Similarity:	100.00%	Conservative:	0
ilarity:	100.00%	Mismatches:	0
	1.26%	Indels:	0
	2	Gaps:	0

US-10-008-355-1 (1-2139) x PCT-US95-04681-19 (1-984)

Search completed: May 16, 2003, 13:17:28 Job time : 44 secs

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Result Query No. Score Match Length DB	712 100.0 52 7.3 52 21 2.9 26 10 1.4 52	10 1.4 213 1. 10 1.4 214 1. 10 1.4 215 1. 10 1.4 336 1.	10 1.4 344 1 10 1.4 344 1 10 1.4 357 1 10 1.4 352 1 10 1.4 532 1 10 1.4 532 1	10 1.4 537 9 1.3 76 9 1.3 76	9 1.3 282 9 1.3 311 8 1.1 27	22 8 1.1 55 23 8 1.1 73 24 8 1.1 75	25 8 1.1 88 33 9 1.1 88	28 8 1.1 116 33 8 8 1.1 116 33 8 8 1.1 116 33 8 8 1.1 116 33 8 8 1.1 116 34 8 8 1.1 115 22 8 8 1.1 12 23 8 1.1 23 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 1.1 335 8 1.1 335 8 1.1 340 8 1.1 340 8 1.1 340 8 1.1 395 	RESULT 1 AAO15205 ID AAO15205 standard Drotein	AA015205;	XX DT 05-SEP-2002 (first entry)	DE Porphyromonas gingivalis di XX XX Dipeptidylpeptidase-7; DPP- KW DPP-7 inhibitor identificat KW DPP-7 inhibitor identificat		PN W0200238742-A2. XX PD 16-MAY-2002.
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 12:38:22 ; Search time 113.5 Seconds (without alignments) 5022.433 Million cell updates/sec	Title: US-10-008-355-1 Perfect score: 712 Sequence: 1 atgcaaatgaaattaaaagaagagctgaagttgatctaa 2139	Scoring table: OLIGO		word size: 1 Total number of hits satisfying chosen parameters: 1687582	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	Command line parameters: -MODEL-frame+.n2p model -DEV=xlp -Q-/cgn2_1/USPTO_spool/US10008355/runat_16052003_110425_9716/app_query.fasta_1.2311 -Q-/cgn2_1/USPTO_spool/US10008355/runat_16052003_110425_9716/app_query.fasta_1.2311 -DB=A_Geneseq_101002 -QFMT=fastan -SUFFIX=olin2p.rag -MINMAYCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORESquality -THR_MIN1 -ALIGN=15 -MODE-LOCAL -USER-US10008355_GCGN_1 -1153_Grunat_16052003_110425_9716 -NCPU=6 -USER-US10008355_GCGN_1 -1.153_Grunat_16052003_110425_9716 -NCPU=6 -VGAPOP=0 -VGAPOR=30 -THREADS=1 -XGAPOP=6 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7 -VGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7	Database: A_Geneseq_101002:* 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* 1: /SIDS2/gcgdata/geneseqg/geneseqp-emb1/AA1981.DAT:* 3: /SIDS2/gcgdata/geneseqg-emb1/AA1981.DAT:* 4: /SIDS2/gcgdata/geneseqg-emb1/AA1983.DAT:* 5: /SIDS2/gcgdata/geneseqg-emb1/AA1984.DAT:* 6: /SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:* 7: /SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:* 8: /SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:* 9: /SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:* 9: /SIDS2/gcgdata/geneseqg-emb1/AA1986.DAT:*	10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* 11: /SEDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* 12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*	13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:* 14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*	<pre>15: /SIDSL/gagata/geneseq/geneseqp-emol/AAL994.DAT:* 16: /SIDS2/gagdata/geneseq/geneseqp-emol/AA1995.DAT:* 17: /SIDS2/acadata/geneseq/geneseqp-emol/AA1996.DAT:*</pre>	 18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:* 19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* 20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* 21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* 22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* 	/SIDS2/gcgdata/geneseg/gethe number of results predi	than or equal 1 by analysis

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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and N-sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontilis). The present amino acid sequence represents the porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme of the
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DPP-7 inhibitor identification; periodontal disease; gingivitis;
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal and of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the
                                                                                                                                                                                                                                                                             N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingiyalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the (c-terminal region of the Porphyromonas gingivalis dipeptidase-7 (DPP-7) enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1990 TTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PheAspGlyAsnTrpGluAlaMetSerGlyAspTleGluPheGluProAspLeuGlnArg
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the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; ,
DPP-7 inhibitor identification; periodontal disease; gingivitis;
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                         English.
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52.00
100.008
100.008
7.308
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                                                                         Fig 5; 65pp;
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Best Local Similarity:
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                                                                            Example 6;
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and of the second amino acid from the useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the N-terminal region of the Porphyromonas gingivalis dipeptidase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; active site; DPP-7 inhibitor identification; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 ATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAATGGAATGCGTGAGCTCGGCTTT 141
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Matches:
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                                                                   Example 6; Page 30; 65pp; English.
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21.00
100.00%
100.00%
2.95%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                   (DPP-7) enzyme
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DB:
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Purphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an alighatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-7 inctein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis (document).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidase-7 (DBP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N·terminal end of a target peptide.
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                                                The invention comprises the amino acid and coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis; V8 endopeptidease.
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Mismatches:
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Matches:
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              5; Page 32; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA015207 standard; Protein; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2001; 2001WO-US46782
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10.00
100.00$
100.00$
1.40$
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Best Local Similarity:
                                                                                                                                                                                                                                                                                          10 AA;
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                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                            enzyme
                Claim
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substituent on the alpha-carbon atom of the second amino acid from the V-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivals (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Staphylococcus aureus V8 endopeptidase enzyme.
The DPP-7 target peptide has an aliphatic or aromatic residue as a
88888888888
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52 AA; Sequence

000000 Conservative: Mismatches: Indels: Length: Matches: Gaps: 0.618 .100.00 100.008 100.008 1.408 Best Local Similarity: Query Match: Percent Similarity Alignment Scores: .. ⊗ Score:

US-10-008-355-1 (1-2139) x AAO15207 (1-52)

1930 ACGGCCGTAACTCCGGTAGCCCCGTATTC 1959 g

1 ThrGlyGlyAsnSerGlySerProValPhe 10

RESULT 6 AAR91042

AAR91042 standard; Peptide; 213 AAR91042;

AA

mature protease (aa1-2:13). (first entry) 23-MAY-1996

Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.

Staphylococcus aureus strain V8 (ATCC 27733)

EP700995-A2

13-MAR-1996

95EP-0306235 06-SEP-1995;

94JP-0296028 94JP-0238595 07-NOV-1994; 07-SEP-1994;

(SUNR) SUNTORY LTD.

Ohsuye K, Yabuta M;

WPI; 1996-141021/15

Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide

Example 8; Fig 14a; 44pp; English

A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli Omp7 protease to yield active VB protease. Extension of the C-terminal end of the VB moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of THE STATE OF THE S

213 10 0 0 0 Conservative: Mismatches: Length: Matches: Indels: 0.542 10.00 100.00\$ 100.00\$ 1.40\$ 213 AA; Best Local Similarity: the host cells. Percent Similarity: Alignment Scores: Sequence Query Match: . No. : Score: Pred

US-10-008-355-1 (1-2139) x AAR91042 (1-213)

AAR91043 RESULT

ΑA AAR91043 standard; Peptide; 214

AAR91043;

(first entry) 23-MAY-1996

V8 mature protease (aal-214).

Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.

Staphylococcus aureus strain V8 (ATCC 27733).

EP700995-A2

13-MAR-1996

95EP-0306235 06-SEP-1995; 94JP-0296028 94JP-0238595 07-NOV-1994; 07-SEP-1994;

(SUNR) SUNTORY LTD.

Ohsuye K, Yabuta M;

WPI; 1996-141021/15

Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide

Example 8; Fig 14b; 44pp; English.

A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli Ompr protease to yield active VB protease. Extension of the C-terminal end of the VB moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of the host cells.

AA; 214 Sequence

0.541 Alignment Scores: Pred. No.: Score:

Length: Matches:

9

Percent Similarity: Best Local Similarity:

Query Match: DB:

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The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
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Matches:
Conservative:
Mismatches:
Indels:
   1930 ACGGCCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1.68
7.label Signal_peptide
69.336
/label Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                     165 ThrGlyGlyAsnSerGlySerProValPhe 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ThrGlyGlyAsnSerGlySerProvalPhe 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 15-16; 25pp; Japanese.
                                                                                                                                                                                                                                           Protease; PCR; amplify; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-355-1 (1-2139) x AAR29644 (1-336)
                                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91033 standard; Protein; 344 AA.
                                                                                                     AAR29644 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91JP-0024633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.519
10.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                           Protease from S. Aureus
                                                                                                                                                                                                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-304938/37.
N-PSDB; AAQ27988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                  JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                       11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1992
                                                                                                                                         AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91033;
                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                         AAR29644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91033
                                                                       RESULT
                                                                                                                          A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli Ompt protease to yield active VB protease. Extension of the C-terminal end of the W moteaty of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodn. of recombinant polypeptide(s) \cdot using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                              recombinant protein; fusion protein; beta-galactosidase;
Escherichia col1; transposon Tn903;
aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
10
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
   Conservative:
                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus strain V8 (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
Gaps:
                                                                                                                     1930 ACGGCCGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                         US-10-008-355-1 (1-2139) x AAR91043 (1-214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-008-355-1 (1-2139) x AAR91044 (1-215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 14c; 44pp; English
                                                                                                                                                                                                                       AAR91044 standard; Peptide; 215
                                                                                                                                                                                                                                                                                                                             mature protease (aa1-215).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94JP-0296028.
100.00%
100.00%
1.40%
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.40%
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohsuye K, Yabuta M;
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(SUNR) SUNTORY LTD.

06-SEP-1995; 07-NOV-1994; 07-SEP-1994;

EP700995-A2 13-MAR-1996

Linker peptide; V8

23-MAY-1996

AAR91044;

AAR9104 RESULT

WPI; 1996-141021/15

215 AA;

Sequence

Alignment Scores:

Percent Similarity: Best Local Similarity:

Query Match: DB:

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proteolytic activity; fusion protein; beta-galactosidase; urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                         344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                              31-MAY-1996;
                                                                                                                                                                                  02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                        EP745669-A2
                                                                                                                                            04-DEC-1996
                   Chimeric
Chimeric
                                                                                                                                                                                                                        Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                         Region
                                                                           Region
                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR26842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X E X B X S X B X
 Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification;
                                                                                                                                                                                                                                                                                                 Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                            comprising
                                                                                                                                                                                                                                                                                                                                                         Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature VB protease without or with the repeat region. The constructs were inserted into vector p69784DhCT(G)R6, yielding pVBRPT(-) and pVBRPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                       "mature V8 protease without the repeat region"
                           V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli.
                                                      Chimeric Escherichia coll;
Chimeric Staphylococcus aureus strain V8 (ATCC 27733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
10
0
0
0
                                                                                           1..124
//note= "beta-galactosidase region"
125..34
/note= "mature V8 protease without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
         Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by pV8RPT(-) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-008-355-1 (1-2139) x AAR91033 (1-344)
                                                                                                                                                                                                                                                                                                                                        Example 2; Page 12-13; 44pp; English.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW22218 standard; Protein; 344 AA
                                                                                                                                                                                          95EP-0306235
                                                                                                                                                                                                            94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.518
10.00
100.00
100.008
1.408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                           Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                         (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                              WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-1997
                                                                                                                                                                                                            07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                          06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                    EP700995-A2
                                                                                                                                                                       13-MAR-1996
                                                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22218;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                             Region
                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
AAW22218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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sequence. The coding sequence was then used to generate mutants of the V8 protease which retain their levels of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated VB prodeases lacking 48 (AAW2218), 56 (AAW2219) or 53 (AAW22220) anino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, VMIS and/or R14YK. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus VB protease lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, downstream of the E. coli beta-galactosidase. The S. aureus portion of the chimaera was amplified by the primers AAT73254-5 from wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to new mutant Staphylococcus aureus V8 proteases
                                                                                                                                                                                                                                                 /note= "truncated S. aureus V8 protease portion"
                                                                                                                                  /note= "E. coli beta-galactosidase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus V8 protease mutants - with increased resistance to denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344
100
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                       "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1930 ACGGCCGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 ThrGlyGlyAsnSerGlySerProValPhe 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-008-355-1 (1-2139) x AAW22218 (1-344)
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 13-14; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease from S. Aureus ATCC12600

    Escherichia coli.
    Staphylococcus aureus.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR26842 standard; Protein; 357
                                                                                                                                                                                                                                                                                                                                                                                                                      96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.518
10.00
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100.00%
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                                                                                                                                                            101..120
/note= "s;
125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.40%
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
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1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
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                                                                                                                                                                                                                                                                 Example 2; Page 14-15; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR91035 standard; Protein; 532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "R6 linker"
104..105
  region"
                                                                         95EP-0306235
                                                                                                               94JP-0238595
                                                                                                94JP-0296028
                                                                                                                                                                                                                                                                                                                                                                                                                              0.512
10.00
100.008
100.008
1.408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                Ohsuye K, Yabuta M;
                                                                                                                                       (SUNR ) SUNTORY LTD
                                                                                                                                                                                        WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                            392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                          06-SEP-1995;
                                                                                                   07-NOV-1994;
                                                                                                             07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   Aliqnment Scores:
                          EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-1996
                                                 13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric E
Chimeric S
Chimeric S
Chimeric t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR91035;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91035
 The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                       Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125..392
/note= "mature V8 protease including the repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant protein; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus strain V8 (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
10
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "beta-galactosidase region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 ThrGlyGlyAsnSerGlySerProValPhe 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 13-15; 25pp; Japanese.
Protease; PCR; amplify; Staphylococcus
                                                          1.68
/label= Signal_peptide
69.358
/label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-008-355-1 (1-2139) x AAR26842 (1-357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion protein; beta-galactosidase;
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR91034 standard; Protein; 392 AA.
                                                                                                                                                                           91JP-0024633.
                                                                                                                                                                                                    90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.516
10.00
100.00$
100.00$
1.40$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                           SHIO ) SHIONOGI & CO LTD.
                        Staphylococcus aureus
                                                                                                                                                                                                                                                    WPI; 1992-304938/37.
N-PSDB; AAQ27987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                         JP04211370-A
                                                                                                                                                                        19-FEB-1991;
                                                                                                                                                                                                  20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                  03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                            Peptide
                                                                                    Protein
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Region
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AAR91034

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Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                       Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mauure V8 protease without or with the repeat region. The constructs were inserted into vector pG9784DhCT(G)R6, yielding pV8RPT(-) and pV8RPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic;
Staphylococcus aureus strain V8 (ATCC 27733);
transposon Tn903.
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/note= "beta-galactosidase region"
101..120
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Matches:
Conservative:
Mismatches:
Indels:
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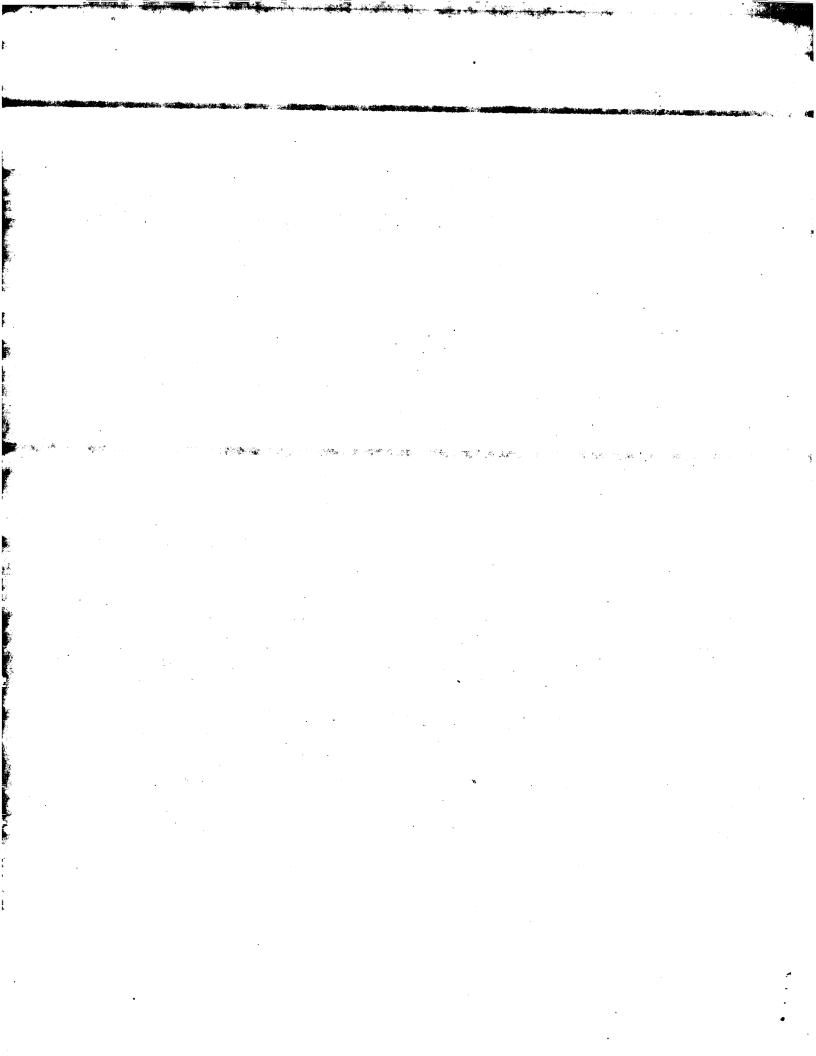
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us-10-008-355-1.olin2p.rag

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    Staphylococcus aureus.

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                                                                                                                                                                           31-MAY-1996;
                                                                                                                                                                                               02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                     EP745669-A2
                                                                                                                                                        04-DEC-1996
 Chimeric
                             Region
                                                                                      Region
                                                                                                         Region
                                                Region
                                                                   Region
 Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                             A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta-galactosidase and and Tn903 aminodylvoside 3'-phosphotransferase, respectively), B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker peptide (AAR91032). The fusion protein is expressed in inactive form in E. coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e. OmpT protease, to allow recovery of VB protease.
                                                                                                                                                                                                                                                      Prodn. of recombinant polypeptide(s) – using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                 /note= "R6 linke.
339.340
/note= "cleavage site for OmpT protease"
/note= "aminoglycoside 3'phosphotransferase
region"
"cleavage site for OmpT protease"
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000
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Matches:
Conservative:
Mismatches:
                  "V8 protease region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 ThrGlyGlyAsnSerGlySerProvalPhe 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-008-355-1 (1-2139) x AAR91035 (1-532)
                                                                                                                                                                                                                                                                                            Example 3; Page 16-18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by pV8D construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW22219 standard; Protein; 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Escherichia coli,
                                                                                                                                            95EP-0306235
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94JP-0238595
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/note=
125..33
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                                                                                                                                                                                             (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                   WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                              532 AA;
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                                               Cleavage-site
                                                                                                                                                                07-NOV-1994;
07-SEP-1994;
                                                                                                                                              06-SEP-1995;
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                                                                                                      EP700995-A2
                                                                                                                           13-MAR-1996
                                                                                                                                                                                                                                                                           polypeptide
                                                                                                                                                                                                                 Ohsuye K,
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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          Region
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The invention relates to new mutant Staphylococcus aureus VB proteases which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated VB proteases lacking 48 (AAM2218), 56 (AAM22219) or 53 (AAM22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus VB protease lacking the prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, downstream of the E. coli beta-galactosidase. Also included downstream of the VB protease fragment is a second R6 linker and a fragment of the aminoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the VBRPT(-) sequence (see AAW22218) by using a natural EcoRV site which removed a further 8 amino acid from the C-terminus. This truncated VB protease, designated VBD, retains its level of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                /note="R6 linker sequence"
361..532
/note= "aminoglucoside 3'-phosphotransferase portion"
                                                                                                                                                                               aureus V8 protease portion"
                                        /note= "E. coli beta-galactosidase portion"
101..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus V8 protease mutants - with increased
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                                                                                                                 "R6 linker sequence"
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Job time: 123.5 secs
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 16-17; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96EP-0303939
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337..36
                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-013693/02
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Query Match:
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Perfect score:

Sequence:

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Scoring table:

Word size:

Searched:

Appli , Appl Appli , Appli

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Sequence 17, Appl
Sequence 51, Appl
Sequence 10510, A
Sequence 44, Appl
Sequence 18, Appl
Sequence 3, Appl
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Sequence 4, Appli
Sequence 2, Appli
Sequence 89, Appl
Sequence 36591, A
Sequence 38691, A
Sequence 57, Appl
Sequence 39413, A
Sequence 368, Appl
Sequence 368, Appl
Sequence 368, Appl
Sequence 368, Appl
Sequence 16, Appl
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Sequence 189, Ap
Sequence 324, Appl
Sequence 324, Appl
Sequence 5217, Ap
Sequence 1913, Ap
Sequence 1970, Ap
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Sequence 1694, Ap
Sequence 961, App
Sequence 29, App1
Sequence 29, App1
Sequence 14523, A
             Sequence 25,
Sequence 4, A
Sequence 6, A
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APLICANT: Banbula, Agnieszka
TITLE OF INVENTOR: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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10 US-09-964-761-39470

10 US-09-964-761-39470

10 US-09-774-639-268

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10 US-09-774-639-268

10 US-09-774-800-324

10 US-09-74-800-324

10 US-09-764-817-1813

10 US-09-764-817-1813

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10 US-09-764-877-1694

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US-09-815-242-10510
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US-08-945-749-3
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US-09-848-798-154
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US-09-745-763-130
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Conservative:
Mismatches:
Indels:
                                                   US-10-008-355-6
US-10-008-355-26
US-10-008-355-9
US-10-166-087-30
US-09-510-332-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10008355
Patent No. US20020164759Al
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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4971.283 Million cell updates/sec
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Sequence 8, Al
Sequence 3, Al
Sequence 18, A
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GenCore version 5.1.4_{-}p5_{-}4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                       protein search, using frame_plus_n2p model
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US-10-008-355-3
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Match Length DB
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Database :

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DB:	O 6	
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oy Db	PC/	qa .
Oy 1 Db	CGAATGCGTGAGCTCGGCTTTACGCTCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG	Oy 1
Qy 1 Db	18 TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT 240	Qy add
Oy 2 Db	241 CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG 300 	qа
Qy 3 Db 1	301 GTGGATCACGACTATCTGCGCGATGGTTTCTCGCACGATGGGTGAGGAGCTTCCG 360 	da d
Oy 3	361 ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA 420 	do dy
Oy 4 Db 1	121 GGACAGCTCAAGGGTATCACTGACGAGGGGGGCTCTGCGCAAGCTCAGGAGGTATGC 480 	Qy
Oy 4 Db 1	481 CAAGAACTGGCCAAAAAAAAATGCAGAGAACCAACTCTGCATCGTAGAGCCTTTC 540 	da da
Qy 5 Db 1	541 TATTCCAACAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA 600 	qa .
Oy 6 Db 2	601 TTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGCGATACGGACAGCAGCAGTGGCG 660 	Qy Db
Oy 6 Db 2	661 CGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGGACAACCGGCCGG	o da
Oy 7 Db 2	721 GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCGTATCCATGCAA 780 	do .
Oy 7 Db 2	781 GGCTACAAGGCTGACGACTATGCCATGACCATCGGTTCCCGGGCAGTACGGATCGCTAC 840 	da d
Oy 8 Db 2	841 CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT 900 	À qa (
Qy 9 Db 3	901 CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCGTATC 960 	
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0y 10	021 CGCGGTCTCGCTCGTCTTGACGTGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080	

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Matches:
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            RESULT 2
US-10-008-355-8
Sequence 8, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Agnieszka
TITLE OF INVENTRON: Dipeptidylpeptidases And
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEG ID NO 8
LENGTH: 699
701. GlnCysProArgLeuIleGlnGluLeuLysLeuIle
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APPLICANT: Potempa, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TTILE OF INVENTION: Dipoptidylpoptidases And Methods Of Use;
FILE REFERENCE: 235.00440101
CURRENT FILING DATE: 2001-11-08
FRICR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 52
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APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
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                                                                           APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of U
FILE REFERENCE: 233.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 18
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Matches:
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Matches:
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Sequence 18 Application US/10008355; Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10008355; Patent No. US20020164759A1; GENERAL INFORMATION:
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US-10-008-355-7
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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SEQ ID NO 5 LENGTH: 734

TYPE: PRT

US-10-008-355-5

Pred. No.:

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Sequence 4, Application US/10008355; Patent No. US20020164759A1; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S
; APPLICANT: Banbula, Agnieszka
; TITLE OF INVENTION: Dipeptidaylpeptidases And Methods Of Use
; FILE REFERENCE: 235.00440101
; CURRENT APPLICATION NUMBER: US/10/008,355
; CORRENT FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Jan S
APPLICANT: Banbula, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipoptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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1 ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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Best Local Similarity:
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LENGTH: 732
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LENGTH: 52
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SOFTWARE:
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APPLICANT: Banbula, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidyleptidases And Methods Of Use
FILE REFERENCE: 235. 00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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212 AspAsnTrpMetTrpProArgHisThrGlyAspPheSer 224
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Conservative:
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PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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; Patent No. US20020164759A1
                                                          US-10-008-355-5; Sequence 5, Application US/10008355; Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Shewanella putrefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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RESULT

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Length:
Matches:
Conservative:
Mismatches:

Length: Matches: Conservative: Mismatches:

SEQ ID NO 25 LENGTH: 10

FEATURE:

Query Match:

Score:

Indels:

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APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US2003002278Alel Family of Taste Receptors;
FILE REFERENCE: 02307E-0980100S
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR PILING DATE: 1999-09-10
NUMBER OF SEO ID NOS: 172
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 17
                                                                                                                                Sequence 30, Application US/10166087

| Publication No. US2003007767A1
| Publication No. US20030077767A1
| GENERAL INFORMATION:
| APPLICANT: Ecopia Biosciences Inc.
| APPLICANT: Farnet, Chris
| APPLICANT: Staffa, Alfredo
| APPLICANT: Staffa, Alfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptomyces refuineus subspecies thermotolerans US-10-166-087-30
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US-09-510-332-17
   221 TrpProArgHisThrGlyAspPheSer 229
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-166-087-30
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US-09-510-332-17
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APPLICANT: Travis, James
APPLICANT: Totempa, Jan S
APPLICANT: Bothula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT PILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VERSION 3.0
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APPLICANT: Banbula, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101 US/10/008,355
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
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662 ThrGlyGlyAsnSerGlySerProValPhe 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Consensus sequence US-10-008-355-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   655 TGGCCGCGTCACACGGGCGACTTCAGC 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                       ; Sequence 26, Application US/10008355
; Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10008355; Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.14e+07
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APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                         RESULT 10
US-10-008-355-26
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LENGTH: 720
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LENGTH: 9
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QQ

Conservative:

Length: Matches:

FEATURE:

Mismatches: Indels:

Gaps:

Indels: Gaps:

Query Match:

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Pred. No.:

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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTHARE: Patentt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, NUMER: APPLICANT: Oblsen, Rari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                  APPLICANT: Mueller, Ken
APPLICANT: Hoo, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Ale1 Family of
FILE REPRENCE: 02307E-098000US
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Matches:
Conservative:
Mismatches:
Indels:
US-10-008-355-1 (1-2139) x US-09-510-332-17 (1-312)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10510, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                       1164 CTTGGCTCCTTCCTTATAAGCCTT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1164 CTTGGCTCCTTCCTTATAAGCCTT 1141
                                                              135 LeuGlySerPheLeuIleSerLeu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 51, Application US/09393634; Patent No. US20020051997A1; GENERAL INFORMATION:
                                                                                                                                                                                                                    Zuker, Charles S.
Adler, Jon Elliot
Ryba, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: human GR09
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100.00%
100.00%
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US-09-815-242-10510
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SEQ ID NO 51
LENGTH: 312
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## PRIOR FILING DATE: 2000-10-23
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-12-22
| PRIOR FILING DATE: 2000-12-16
| PRIOR FILING DATE: 2001-02-16
| PRIOR FILING DATE: 2001-02-16
| PRIOR FILING DATE: 2001-02-16
| NUMBER OF SEQ ID NOS: 14110
| SEQ ID NO 10510
| LENGTH: 659
| TYPE: PRT
| ORGANISM: Enterococcus faecalis
| TYPE: PRT
| ORGANISM: Enterococcus faecalis
| ORGANISM: Enterococcus faecalis
| Pred. No.: 8.00
| Alignment Scores: 8.00
| Pred. No.: 8.00
| Best Local Similarity: 100.00% Mismatches: 0
| Dest Local Similarity: 100.00% Mismatches: 0
| Ouery Match: 1.12% Indels: 0
| Ouery Match: 1.12% Indels: 0
| Ouery Match: 1.12% Indels: 0
| Ouery Match: 1.11% Indels: 0
| Ouery Match: 0
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	15 8 1.1 162 2 16 8 1.1 189 2 17 8 1.1 214 2 18 8 1.1 224 2
OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 13:00:32 ; Search time 79 Seconds (without alignments) 5205.861 Million cell updates/sec	.1 226 2 \$04752 .1 241 2 A69299 .1 256 2 A34770 .1 288 2 F72219 .1 332 2 \$46947
Title: US-10-008-355-1 Perfect score: 712 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 2139	8 1.1 349 2 8 1.1 382 2 8 1.1 392 2 1.1 400 2
Scoring table: OLIGO	8 1.1 401 2 D98173 8 1.1 421 2 D98173 8 1.1 421 2 C91109 8 1.1 421 2 S54010 8 1.1 425 2 S54010
Searched: 283224 seqs, 96134422 residues	8 1.1 458 2 8 1.1 479 2 8 1 1 513 2
	38 8 1.1 544 2 D64882 39 8 1.1 544 2 G99867
	8 1.1 544 2 885/51 8 1.1 563 2 89/319 8 1.1 570 2 A48836 8 1.1 586 2 S71235
Post-processing: Listing first 45 summaries	44 8 1.1 633 2 G95385 Kup2 Potassiun 45 8 1.1 637 1 YCRP acetolactate
Command line parameters:	RESULT 1 GRA627 hypothetical protein XF1887 [imported] - Xylella fastidiosa (strain 9a5c) C.Species: Xylella fastidiosa C.Species: Xylella fastidiosa C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C.Accession: GRA627 R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000 A.Title: The genome sequence of the plant pathogen Xylella fastidiosa. A.Reference number: AR5115: MIID: 20186717: PMTD: 10410347
11: 12: 12: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13	A:Note: for a complete list of authors see reference number A59328 below A;Accession: G92627 A;Status: preliminary A;Molecule type: DNA
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	A; ROSIGUGES: 1-716 < S.LM> A; Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
SUMMARIES Result Query No. Score Match Length DB ID Description	as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.F.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Butthors: Ferreira, V.C.A.; Ferro, J.A.; Fraqa, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La*
	chado, M.A.; Madelra, A.M.B.N.; Madelra, H.M.F.; Marlino, C.L.; Marques, M.V.; Martins, C.A.; Mathors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Niv., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: ad Silva, A.C.R.; da Silva, F.R.; da Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number: A59328 A;Contents: annotation C;Genetics: A;Gene: XP1887
9 1.3 984 9 1.3 1116 8 1.1 102 8 1.1 106	Alignment Scores: 0.000396 Length: 716 0.00 Score: 13.00 Matches: 13 Percent Similarity: 100.00% Conservative: 0

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A; Accession: F75381
                                                                                                                                                                                                          Alignment Scores:
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                                                                           C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                  Juliamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus
Nyllternate names: staphylococcal serine proteinase
C;Species: Staphylococcus aureus
C;Date: 04-Dec-1966 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C;Accession. Az6812; A00966
C;Accession. Az6812; A00966
C;Accession. Az6812; A00966
C;Accession. Az6812; MUID:87316953; PMID:3306605
A;Title: Nuclectide sequence of the serine protease gene of Staphylococcus aureus, strain
A;Reference number: Az6812; MUID:87316953; PMID:3306605
A;Title: Nuclectide sequence of the serine protease gene of Staphylococcus aureus, strain
A;Reference number: Az6812; MUID:87316953; PMID:3306605
A;Cross references: EMBL:Y00356; NID:946686; PIDN:CAA68434.1; PID:946687
A;Cross reference aurent v@
A;Accession: As6 534-544, 1978
A;Accession: As6 5, 534
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Sate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Sacession: G89873
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; (ma, A.; Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet, 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
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Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                  US-10-008-355-1 (1-2139) x G82627 (1-716)
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-342 <KUR>
Best Local Similarity:
Query Match:
DB: '
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C; Species: Staphylococus aureus
C; Species: Staphylococus aureus
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Accession: S21758
R; Yoshikawa, K; Tsuzuki, H.; Fujiwara, T.; Nakamura, E.; Iwamoto, H.; Matsumoto, K.;
Biochim. Biophys. Acta 1121, 221-228, 1992
A; Title: Purification, characterization and gene cloning of a novel glutamic acid-spe A; Reference number: S21758; MUID:92287954; PMID:1599945
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001999; GB:AE000513; NID:96459316; PIDN:AAF11119.1; PID:9645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable two-component sensor - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: F75881
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
A;Cross-references: GB:BA000018; PID:g13700850; PIDN:BAB42146.1; GSPDB:GN00149, A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA .
A; Residuos: 1:575 cx755
A; Residuos: 1:575 cx755
A; Cross-references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971
C; Superfamily: staphylococcal serine proteinase
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Matches:
Conservative:
Mismatches:
                                                                          A,Gene: sspA
C;Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
Gaps:
                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                    1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
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                                                                                                                                                                           0.512
10.00
100.00$
100.00$
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100.008
1.408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.51
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                                                                                                                                                                                                                              Percent Similarity:
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Alignment Scores: Pred. No.: Score: Score: Score: Score: Score: Score: Percent Similarity: D00.00%	RESULT 8 AF2363 hypothetical protein all4462 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. C;Decies: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Decies: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Date: 14-Dec-2001 #sequence of the Filamentous M: Yamada, M:; Yasuda, M:; Tabata DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:2159285; PMID:11759840 A;Accession: AF2363 A;Accession: AF2363 A;Accession: AF2363 A;Molecule type: DNA A;Residues: 1-483 < KUR> A;Accession: Seriain ary A;Molecule type: DNA A;Residues: 1-483 < KUR> A;Cross-references: GB:BA000019; PIDN:BAB76161.1; PID:g17133598; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: all4462	Alignment Scores: Pred. No.: Score: Score: Score: Percent Similarity: Percent Similarity: 100.00% Percent Similarity: 1.26% Policy Mismatches: 0 Us-10-008-355-1 (1-2139) x AF2363 (1-483) Qy 34 GCAGCCCTGCTTGGGGGCTTCAGGG 60	RESULT 9 Tyd571 probable integral membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Accession: T36771 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, July 1999 A;Reference number: 221574 A;Accession: T36771 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-684 <see> A;Cross-references: EMBL:AL096844; PIDN:CAB50875.1; GSPDB:GN00070; SCOEDB:SC128.01 A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SC128.01</see>	Alignment Scores: 5.03 Length: 634 Pred. No.: 9.00 Matches: 9 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0
Alignment Scores: 0.484 Length: 569 Pred. No.: 10.00 Matches: 10 Score: 10.00 Matches: 10 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 1.40\$ Mismatches: 0 Ouery Match: 2 Gaps: 0 US-10-008-355-1 (1-2139) x F75381 (1-569) Qy 25 CTTCTCGGAGCCCTGCTGTTGCTGCT 54	etical protein - Deinococcus radiodurans (strain R1) des: Deinococcus radiodurans 1 03-Dec-1999 #text_change 28-Jul-2000 ssion: D75483 e. 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma tth, H.O.; Venter, J.C.; Fraser, C.M. e. 286, 1571-1577, 1999 e. Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. rence number: A75250; MUID:20036896; PMID:10567266 ssion: D75483 us: pretiminary cule type: DNA dlues: 1-266 <whi> sreferences: GB:AE001928; GB:AE000513; NID:g6458421; PIDN:AAF10302.1; PID:g645843 filmental source: strain R1 tacs: DR0714 position: 1 position: 1 position: 1 position: 1 position: 1 position: 1 position: 1</whi>	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Score: Percent Similarity: 100.00%	RESULT 7 AEI710 AEI710 AFI710 Dypothetical protein homolog lin2224 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Species: District C;Accession: AEI710 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker C;Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MuID:21537279; PMID:11679669 A;Status: preliminary A;Molecule type: DNA	1-45; erence tal se 2224

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C;Accession: T04804
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hohelsel, J.; Mewes submitted to the Protein Sequence Database, February 1999
A;Reference number: 215385
                                                                                               NID:92984274; PIDN:AAC07805.1; PID:92984280; GB:AE00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T36095
R;Saunders, D.; Barris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, April 1999
A;Reference number: Z21596
A;Reference number: Z21596
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-102 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL049661; PIDN:CAB41211.1; GSPDB:GN00070; SCOEDB:SCE134.13
A;Experimental source: strain A3(2)
                 preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SCE134.13 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F10M23.150 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Streptomyces coelicolor hypothetical protein SCE134.13
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A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
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Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 ValileAspLysLysPheLysGlyAsp 337
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                                               A; Molecule type: DNA
A; Residues: 1-1116 AAQF>
A; Cross-references: GB: AEO00770; I
A; Experimental source: strain VF5
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                        Alignment Scores:
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A.Cross-references: GDB:119875; OMIM:179610
A.Cross-references: GDB:119875; OMIM:179610
A.Cross-references: GDB:119875; OMIM:179610
C.Saperfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat by C.S. Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; F:123/ODMain: signal sequence #status predicted <SIG>
F:24-984/Product: protein-tyrosine kinase receptor type eph 1 #status predicted <AMT>
F:548-568/DOMain: protein kinase homology <KIN>
F:563-685/DOMain: protein kinase homology <KIN>
F:68-646/Region: protein kinase ATP-binding motif
F:918-984/Domain: SAM homology <SAM>
F:59,338,414,478/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-984 <HIR>
A;Cross-treferences: GB:M18391; NID:g339716; PIDN:AAA36747.1; PID:g339717
A;Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398-
R;Tuzi, N.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993
A:Description: An EGFR/eph chimeric receptor possesses ligand stimulated tyrosine kinase
A;Reference number: $44280
A;Accession: $44280
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A;Residues: 286-397,'A',399-580,'QRDRATDVDREDKLWLKPYVDLQAYEDPAQGALDF',583,625-984 <TUZ>
A;Cross-references: EMBL:227409; NID:g482916; PIDN:CAA81796.1; PID:g482917
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A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: B70476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Aquifex aeolicus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C.Accession: B70476
                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 22-Oct-1999 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eph gene.
                                                                                                                                                                                                                                                                                                                                         type eph 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A novel putative tyrosine kinase receptor encoded by the A;Reference number: A34076; MUID:88070650; PMID:2825356
                                                                                                                                                                                                                                                                                                                                   protein-tyrosine kinase (EC 2.7.1.112) receptor type eph 1 M.Alternate names: receptor tyrosine kinase eph 1 C;Species: Homo sapiens (man) receptor 2.5pecies: 22-ocr 1999 #sequence_revision 22-ocr 1999 #text_cC 3.6ccssion: A34076; S44280 R:Hirai, H: Maru, Y: Hagiwara, K:; Nishida, J:; Takaku, Science 238, 177-1720, 1987 A;Title: A novel putative tyrosine kinase receptor encodec
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                 Indels:
                                                  Gaps:
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                                                                                                                                                                 28 CTCGGAGCAGCCCTGCTGGTTGGGTGCT
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Best Local Similarity:
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conserved hypothetical protein AF1964 - Archaeoglobus fulgidus

conserved hypothetical protein AF1964 - Archaeoglobus fulgidus

c) species: Archaeoglobus fulgidus

C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C; Accession: C69495

R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleatschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Characterization of the human cDNA and genomic DNA encoding CART: A cocaine- an A; Reference number: JC4669; MUID:96194810; PMID:8647455
A; Accession: JC4669
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech; Reference number: A69250; MUID:98049343; PMID:9389475
A;Recession: C69495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U20325; NID:9665578; PID:9665579
C;Comment: This protein plays a conserved functional role within the mammalian central
                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jul-2000
C;Accession: JC4669; G01648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U16826; NID:g609305; PIDN:AAB08010.1; PID:g609306 R;Douglass, J.O.
                                                                                                                                                                                                                                                                                                                                                                        cocaine-and amphetamine regulated transcript protein - human
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Mismatches:
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A;Accession: G01648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-116 <D02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                   US-10-008-355-1 (1-2139) x T04804 (1-106)
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A; Residues: 1-116 <DOU>
                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Gene 169, 241-245, 199
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A; Introns: 53/3; 81/3
Alignment Scores:
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A;Gene: CART
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <KLE>
A;Cross-references: GB:AE000967; GB:AE000782; NID:g2689290; PIDN:AAB89289.1; PID:g264
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	162	œ	0	0	0	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	62.6	8.00	100.00%	100.00%	1.13%	2
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-10-008-355-1 (1-2139) x C69495 (1-162)

1401 CTTGAATATCGGGGGGCTTGTC 1378

142 LeuGluTyrIleGlyGluLeuVal 149

Search completed: May 16, 2003, 13:16:20

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092xm6 bacteriopha
033999 chromatium
091999 chromatium
091646 leishmania
091230 caenorhabdi
094801 bacillus ha
092166 shigella fl
                                                                                              Q8ynu9 anabaena sp
Q9s282 streptomyce
Q91wb5 mus musculu
Q9x668 streptomyce
Q9s221 arabidopsis
Q28315 archaeoglob
                                                                                                                                                                                  Q8zval pyrobaculum
Q9k3j5 streptomyce
O27455 methanobact
Q9ss66 arabidopsis
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Q8tv91 methanopyru
Q39862 glycine max
Q9x246 thermotoga
                                        Ogru39 deinococcus
OgajxO staphylococ
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Q9pij8 campylobact
Q8wz66 homo sapien
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Q40600 oenothera b
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09f2u9 streptomyce
        099v45 staphylococ
004186 staphylococ
                                                                 Q9rwf5 deinococcus
Q929q0 listeria in
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Q8vv03 streptomyce
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28vlm4 escherichia
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29fbg1 staphylococ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update) |
01-UN-2002 (TrEMBLrel. 21, Last annotation update) |
Hypothetical protein Xf1887.
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Q27455
Q9SS66
Q9V4H5
Q9PIJ8
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Q8VV03
Q92TL0
Q9F2U9
Q8U7A5
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Q8TV91
Q39862
Q9X246
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Q93CA1
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Q9SZ21
Q28315
Q8ZVA1
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09KBD1
09AL66
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081NU9
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Q91WB5
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Q9FDK6
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Q8VLM4
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Q9PC94;
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-MODEL=frame+_n2p.model -DEV=x1p
-Q=CQG012_110426_9734/app_query.fasta_1.2311
-Q=CQG012_110FPQ_SPOO1/USID08355/runat_16052003_110426_9734/app_query.fasta_1.2311
-Q=CGG012_110FPQ_SPOO1/USID08355/runat_16052003_110406_0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STPRT=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HERSEIZE=500 -MINLER=0 -MAXIRP=20000000
-USER=USIO008355_@CGN_1_1_238_grunat_16052003_110426_9734 -NOEV=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -LONGIGG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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(without alignments)
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                                                                                                                                                                                                                                                                                                                                                           1343044
          GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                    frame_plus_n2p model
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, Ygapext 60.0
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, Delext 7.0
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Database

So. Result

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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
R. Krieger J.E., Kutamae E.E., Lagret F., Lambais M.R., Laite L.C.C.,
Lemos B.G.M., Lemos M.V.F., Lopes S.R., Lambais M.R., Laite L.C.C.,
Lemos B.G.M., Lemos M.V.F., Lopes C.R., Marchado J.A.,
Rachado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques N.V., Martins E.A.L., Martins E.M.F., Marsino C.L.,
Marques N.V., Martins E.A.L., Martins E.M.F., Marsino C.L.,
Marques N.V., Martins E.A.L., Martins E.M.F., Marsino C.L.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nobreage F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.R., Person D.B.,
A de Silve R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
A de Solza A.P., Tereni W.F., Silva W.A., Tsuhako M.H.,
A vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Zago M.A., Zatz M., Meddanis J., Setubal J.C.;
B Marure 406:151-159(2000).
B MERDI, AFR84693.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kodaira K.I.; "Characterization of the gene encoding glutamyl endopeptidase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus warneri.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus warneri M.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AJ293885; CAC06168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        11 protein; Complete proteome.
716 AA; 79375 MW; EAF086E2315BBDFC CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glutamyl endopeptidase.
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Matches:
Conservative:
Mismatches:
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InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; Urypsin; 1.
PRIMT; SM00020; Tryps_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
PHYDROSIES; Serine protease.
SEQUENCE 316 AA; 34296 MW; 4E997A5A11
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           MEROPS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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PECIES—S. aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease; Complete proteome.
i; 5AEF42DCE01C4B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
Serine protease, V8 protease, glutamyl endopeptidase.
SSPA OR SAV1048 OR SA0901.
             316
10
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10
0
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0
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-!- SIMILARITY: TO SERINE PROTEAȘES, TRYPSIN FAMILY.
EMBL; AP003351; BAB57210.1; -.
EMBL; AP003132; BAB42146.1; -.
MEROPS; S01.269; -.
             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                  342 AA.
                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                       1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 1PR001254; Ser_protease_Try.
InterPro; 1PR000126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
SWART; SM0020; Tryp_SPC: 1.
PROSITE; PS00674; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1930 ACGGCCGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                     231 ThrGlyGlyAsnSerGlySerProvalPhe 240
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                                                                                                                        US-10-008-355-1 (1-2139) x Q9FBG1 (1-316)
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Protease; Serine pi
SEOUENCE 342 AA; 36977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.594
10.00
100.008
100.008
           0.599
10.00
100.00%
100.00%
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                                                                         1.40%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 AA;
                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
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Alignment Scores:
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                                                                                                                                                                                                                                099V45
ID 099V45
AC 099V45;
                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aureus.
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                Pred. No.:
                                                                                                                                                                                                                   RESULT 3
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                             Score:
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1933 GGGGTAACTCCGGTAGCCCCGTATTC 1959
                                              InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003018; GAF.
InterPro; IPR004359; HIS_KIN_sig.
       EMBL; AE001999; AAF11119.1; -.
                                                                                                                                                                                                                                                                                     59182 MW;
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                                                                                                                                                        PRINTS; PR00344; BCTRLSENSOR.
                                                                                                                                                                                                                     ; HATPase_c; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
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100.008
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                                                                                                                                                                                          SMART; SM00065; GAF;
SMART; SM00387; HATPA
                                                                                                                                                                                                                                                                                          569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA;
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Best Local Similarity:
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Query Match:
                                                                                                                                                                                                                                                                 Complete proteome
SEQUENCE 569 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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SIGNAL
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         Toshikawa K., Tsuzuki H., Fujiwara T., Nakamura E., Iwamoto H., Matsumoto K., Shin M., Yoshida N., Teraoka H.;
"Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from staphylococcus aureus atcc 12600.";
Biochim. Biophys. Acta 1121:221-228(1991).
EMBL. D00705, BAAR0630.1;
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_proteas_V8.
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosy M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.E., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glutamic acid specific protease prepropeptide (EC 3.4.21.19).
Staphylococcus aureus.
                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{Rl.}";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 286:1571-1577(1999).
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Last annotation update)
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Matches:
Conservative:
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Indels:
                          357 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Protease; Serine protease.
CHAIN 69 357 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-008-355-1 (1-2139) x Q04186 (1-357)
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                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00089; trypsin; 1.
PRINTS: PR00899; VBPROTEASE.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; VB_HTS; 1.
PROSITE; PS00673; VB_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWO-component sensor, putative
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                                                                    01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.591
10.00
100.00%
100.00%
1.40%
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                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                           NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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DB:
10 004186
10 004186
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10 01-NOV-
10 
                                                 004186;
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Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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Kinase; Phosphorylation; Sensory transduction; Transferase;
                                1A6CA4F88D96A940 CEC64;
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                                                                                569
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Extracellular serine proteinase precursor (Fragment)
                                                                              Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                             217 AA
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Matches:
                                                                                                                                                     Indels:
                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                         InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-008-355-1 (1-2139) x Q9AJX0 (1-217)
                                                                                                                                                                                                       US-10-008-355-1 (1-2139) x Q9RU39 (1-569)
                                                                                                                                                                                                                                         25 CTTCTCGGAGCAGCCCTGCTGTTGGGTGCT
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00673; V8_SER; 1.
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Percent Similarity:
                                                                                                                                                                                         Hypothetical
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                                                                                                                                                                                                               SEQUENCE
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No.:
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Q9S282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Faihi H., Garcia del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Raerst U., Kreft J., Ruhn M., Kunst F., Kurapkat G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Iam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
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Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{R1.}^n\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein; Complete proteome.
266 AA; 28225 MW; F7C0ED7F231ADD3C CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin2224.
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167 GlyGlyAsnSerGlySerProvalPhe 175
                                                                                                                                                                     Created)
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STRAIN-CLIP 11262 / SEROVAR 6A;
PubMed-11679669;
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                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein DR0714.
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Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Sindoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species."; Science 294.849-852(2001).

Listlict, LIN02224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc. NCBL_TaxID=103690;
                                                                                                                                                                                       al protein; Complete proteome.
452 AA; 48806 MW; OCCOBBBBF765745A CRC64;
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483 AA; 51883 MW; 17F82B83C39E7808 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein All4462.
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EMBL; AP003596; BAB76161.1; -.
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Query Match:
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SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
       NCBI_TaxID=10090;
                                                                                                         Strausberg R.;
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"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chatter K.F., Derdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces coeliaclor A3(2).";
Nature 417:141-147(2002).
EMBL; AL096844; CAB50875.1; -.
FINITESPO: IPR00285; P_ITCh_extensn.
PINITES; PR01582; K973ANNEL.
PRINTS; PR01517; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                         Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
SCO1807 OR SCI28.01.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 10.1 kDa protein.
Mus musculus (Mouse).
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                                                                                                    Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                          NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopwood D.A.;
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Taylor K.,
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BORLEY S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliveit S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC016132, AAH16132.1;
InterPro; IPR002412; FEL_allergen.
InterPro; IPR000329; Uteroglobin.
Pfam: PF01099; Uteroglobin; 1.
Probom; Pp019935; FEL_allergen; 1.
                                                                                                                                          Hypothetical protein.
SEQUENCE 92 AA; 10080 MW; F1A7557E0F5568BB CRC64;
                                                                                                                                                                                                                               0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SC03512.
SC03512 OR SCE134.13.
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Matches:
Conservative:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL049661; CAB41211.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein.
102 AA; 10274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     25 CTTCTCGGAGCAGCCCTGCTGTTG
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Best Local Similarity:
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Dodson R.J.,
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11792869;
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Ketchum K.A.,
                                                                                                                                                                       Hypothetical
SEQUENCE 16
                                                                                                    Venter J.C.;
                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                     Pred. No.:
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Lecharny A., Chefdor F., Krivitzky M., Kreis M., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               SEQUENCE FROM N.A.
Bevan M., Lecharny A., Chefdor F., Krivitzky M., Kreis M., Hohelsel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035440; CAB36527.1; -..
EMBL; AL161565; CAB79536.1; -..
Interpro; IRR003121; SWIB.
Pfam; PF02201; SWIB; 1.
SWART; SW00151; SWIB; 1.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNI-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 12.2 kDa protein.
F10M23.150 OR AT4G26810.
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Last annotation update)
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Mismatches:
Indels:
                                 106 AA.
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Matches:
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                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 106 AA; 12209 MW;
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                                 PRELIMINARY;
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Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNell L.K., Badger J.H., Glodek A., Zhou E., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                          Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Gwinn M., Hickey E.K., Peterson J.D.
                                                                                                                                                                                                                                                                                                     ll protein; Complete proteome.
162 AA; 18024 MW; 46404F9FC3EE74AA CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Transport protein part 1, authentic frameshift.
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Matches:
Conservative:
Mismatches:
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Conservative:
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Indels:
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
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17
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Search completed: May 16, 2003, 13:13:33 Job time: 177 secs

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	31 7 1.0 127 1 Y55B_MYCPN P75047 mycoplasm 32 7 1.0 129 1 CART_RAT P49192 rattus no 33 7 1.0 136 1 SCPB_APLSP P15738 P1992 aplysia s 34 7 1.0 139 1 NUSA_HALMO P15738 halococcu 36 7 1.0 139 1 NUSA_HALMI P15739 halococcu 36 7 1.0 142 1 H2B2_LYTPI P06146 lytechliuu 37 7 1.0 142 1 NUSA_HALMI P06146 lytechliuu 37 7 1.0 142 1 NUSA_LYTPI P06146 lytechliuu 37 1.0 143 1 NUSA_SULAC P11523 sulfolobu	7 1.0 147 1 7 1.0 167 1 7 1.0 167 1 7 1.0 169 1 7 1.0 173 1 7 1.0 177 1	ALIGNMENTS	SP_	_		RX PLOCHALE TOOR NATE TOO NOT THE CONTROL OF TEAM PROCESS OF THE CONTROL OF THE C	-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52B:- DATABASE: NAME-Worthington enzyme manual; www.worthington-biochem.com/manual/P/STAP.
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 12:39:16; Search time 36.5 Seconds (without alignments) 4861.253 Million cell updates/sec	t score: ce: g table:	1: 112892 :e: 1 .mber of hits so	Minimum DB seq length: U Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries	Command line parameters: -WODEL=frame+_n2p.model -DEV=xlp -Q=/Cgn2_1/USPTO_spool/US10008355/runat_16052003_110425_9723/app_query.fasta_1.2311 -Q=/Cgn2_1/USPTO_spool/US10008355/runat_16052003_110425_9723/app_query.fasta_1.2311 -DB=SwissProt_40 -OFMT=fastan -SUFFTX=0.in2p.rsp -MINMATCH=0.1 -LOOPCL=0 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -USFRY=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USFRY=US10008355_GCGN_1_147_Efunat_16052003_110425_9723 -NCPU=6 -ICPU=3 -USFRY=URBOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7	Database: SwissProt_40:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID	1 10 1.4 336 1 STSP_STANU 2 9 1.3 1116 1 YK54_AQUAE 3 9 1.3 1116 1 YK54_AQUAE 5 8 1.1 126 1 CART_MONSE/- 6 8 1.1 124 1 TPIS_HALNI 6 8 1.1 226 1 ATP6_RAT 7 8 1.1 226 1 YDH1_HSVSC 9 8 1.1 279 1 Y939_MSTRA 10 8 1.1 279 1 Y939_MSTRA 11 8 1.1 392 1 CHSY_ECHPO 12 8 1.1 392 1 MSTR_SCHPO 13 8 1.1 392 1 MSTR_SCHPO 14 8 1.1 393 1 MSTR_SCHPO 15 8 1.1 393 1 MSTR_ASCIM 16 8 1.1 570 1 FBP3_STRPU 17 8 1.1 570 1 FBP3_STRPU 18 1.1 570 1 FBP3_STRPU 18 1.1 570 1 FBP3_STRPU 18 6 1.1 570 1 FBP3_STRPU	8 1.1 586 1 RUBA_ARATH P21238 a 8 1.1 637 1 ILV2_BRANA P14874 b 8 1.1 757 1 MUS2_THEMA Q9x105 t

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Hirah H., Maru Y., Hagiwara K., Nishida J., Takaku F.;
"A novel putative tyrosine kinase receptor encoded by the eph gene.";
Science 238:1717-1720(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPA1_HUMAN STANDARD; PRT; 976 AA.
P21709; Q15405;
01-MAY-1991 (Rel. 18, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MISSING (IN REF. 3).
N -> D (IN REF. 3).
V -> T (IN REF. 3).
D -> N (IN REF. 3).
EFN -> QFD (IN REF. 3).
ENV -> NEVN (IN REF. 3).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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PIR; A26812; PRSASK.

MEROPS; S01.269; -.

InterPro; IPR00125; Ser_proteas_V8.

InterPro; IPR00125; Ser_protease_Try.

Pfam; PF00089; trypsin; 1.

R PRINTS; PR00839; V8PROTEASE.

R PROSITE; PS00673; V8_ERR; 1.

M Hydrolase; Serine protease; Zymogen; Signal.
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Matches:
Conservative:
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Owshalimpur D., Kelley M.J.;
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EPHA1 OR EPHT1 OR EPH.
Homo sapiens (Human).
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336 AA;
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DR SMART; SM00060; FN3; 2.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00019; TYIKC; 1.

DR PROSITE; PS01010; PROTEIN KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

DR PROSITE; PS00109; SAM_DOMAIN: 1.

Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

23
                                                                                                      Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS WITH A LOW AFFINITY TO EPHRIN-A1.
                                                                                                                                                                                                                                -i- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
-RECEPTOR SUBFAMILY.
"Genomic structure of the EPHA1 receptor tyrosine kinase gene."; Mol. Cell. Probes 13:169\cdot173(1999).
                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                            tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: OVEREXPRESSED IN SEVERAL CARCINOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). CYS-RICH.
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ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD001495; Ephrin_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF101171; AAD43440.1; EMBL; AF101165; AAD43440.1; JOINED. EMBL; AF101166; AAD43440.1; JOINED. EMBL; AF101167; AAD43440.1; JOINED. EMBL; AF101169; AAD43440.1; JOINED. EMBL; AF101169; AAD43440.1; JOINED. EMBL; AF101169; AAD43440.1; JOINED.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
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InterPro; IPR001245; Tyr_kinase.
InterPro; IPR001426; Ykase_receptorv.
Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF001406; pkinase; 1.
Pfam; PF001404; EPH_lbd; 1.
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                                                     SEQUENCE OF 286-976 FROM N.A.
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HSSP; P00523; 2PTK.
                                                                       TISSUE=Placenta;
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CART_HUMAN
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                                                                                                                                      N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
A - S G (IN REF. 1).
QRDRATDVOREDKLWLKPYVDLQAYEDPAGGALDFT ->
HVTAPPMWIERTSCAEALCGTSRHTRTLHREPWTLPGGWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deckert.G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                    PHOSPHORITATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
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                        PDZ-BINDING MOTIF (POTENTIAL).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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W; 423E5FCC6C02C89C CRC64;
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PHOSPHORYLATION (AUTO-)
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                                                                                                                                                                                                                                                                                               Mismatches:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 PROTEIN KINASE
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Matches:
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Hypothetical protein;
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Best Local Similarity:
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1116 9

Length: . Matches:

2.06 9.00

Pred. No.:

Score:

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Diabetes 50:2157-2160(2001).
-:- FUNCTION: Satiety factor closely associated with the actions of leptin and neuropeptide y; this anorectic peptide inhibits both normal and starvation-induced feeding and completely blocks the feeding response induced by neuropeptide Y and requlated by leptin in the hypothalamus. It promotes neuronal development and survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perrone L.; "Mutational screening of the CART gene in obese children: identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mulff B.S., Clausen J.T., Thim L., Ribel U., Christjansen K.N., Wulff B.S., Clausen J.T., Jensen P.B., Madsen O.D., Vrang N., Larsen P.J., Hastrup S.; "Hypothalamic CART is a new anorectic peptide regulated by leptin."; Mature 393:72-76(1998).
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Halsall D.J., Keogh J.M., Wareham N.J., O'Rahilly S.;
"The CART gene and human obesity: mutational analysis and population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Douglass J.O., Daoud S.; Characterization of the human cDNA and genomic DNA encoding CART: cocaine- and amphetamine-regulated transcript."; Gene 169:241-245(1996)
                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      del Giudice E.M., Santoro N., Cirillo G., D'Urso L., Di Toro R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a mutation (Leu34Phe) associated with reduced resting energy expenditure and cosegregating with obesity phenotype in a large
                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor [Contains: CART(1-39); CART(32-89)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21371766; PubMed=11478874;
Ludvigsen S., Thim L., Blom A.M., Wulff B.S.;
"Solution structure of the satiety factor, CART, reveals new
functionality of a well-known fold.";
Biochemistry 40:9082-9088(2001).
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
     0000
     Conservative:
                        Mismatches:
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                                           Indels:
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MEDLINE=21413627; PubMed=11522684;
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MEDLINE=96194810; Pubmed=8647455;
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diabetes 49:872-875(2000).
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT THR-66.
                                                                                                                                                                                                                                     CART_HUMAN
Q16568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetics."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION
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ventrolateral part of the arcuate nucleus, in the external zone of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129/SvJ;
MEDLINE-20080750; PubMed-10612705;
Adams L.D., Gong W., Vechia S.D., Hunter R.G., Kuhar M.J.;
Adams L.D., Gong W., for function.";
Brain Res. 848:137-140(1999).
1- FUNCTION: Satiety factor closely associated with the actions of leptin and neuropeptide y; this anorectic peptide inhibits both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 602606; ...
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues; Signal; Disease mutation; Polymorphism; Obesity; 3D-structure.
strant. 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                      the median eminence, and also found in terminals in the perivorticular part of the paraventricular nucleus. INDUCTION: By leptin.

DISEASE: A defect in CART is associated with reduced resting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCAINE- AND AMPHETAMINE-REGULATED TRANSCRIPT PROTEIN.
CART(1-39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CART_MOUSE STANDARD; PRT; 129 AA.
P55388, 090x28.
15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor (Contains: CART(1-52); CART(55-102)].
                                                                                                                                      energy expenditure and cosegregates with obesity phenotype. SIMILARITY: BELONGS TO THE CART FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L -> F (IN AN OBESE PATIENT).
/FTId=VAR_012199.
S -> T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_012200.
FC396CA2C032AA83 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CART (42-89).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-116)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 CTTCTCGGAGCAGCCCTGCTGTTG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LeuLeuGlyAlaAlaLeuLeuLeu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
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Best Local Similarity:
Query Match:
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CART_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
normal and starvation-induced feeding and completely blocks the feeding response induced by neuropeptide Y and regulated by leptin in the hypothalamus (By similarity).

SUBCELLULAR LOCATION: Secreted (Potential).

ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a short form; are produced by alternative splicing.

SIMILARITY: BELONGS TO THE CART FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20504483; PubMed-11016950; MEDLINE-20504483; PubMed-11016950; MeDLINE-20504483; PubMed-11016950; Medius H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genome sequence of Halbbacterium species NRC-1.", Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                             MGD; MGT:1351330; Cart.
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                      COCAINE. AND AMPHETAMINE-REGULATED TRANSCRIPT PROTEIN.
CART(1-52) (BY SIMILARITY).
CART(65-102) (BY SIMILARITY).
CART(65-102) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSENG (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Halobacteria; Halobacteriales; NCBL_TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF148071; AAF24168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 CTTCTCGGAGCAGCCCTGCTGTTG
                                                                                                                                                                                                                                                                                                             Alternative splicing; Signal. SIGNAL 1 27
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SEQUENCE
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P22575;
01-AUG-1991 (
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YDH1_HSVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grosskopf R., Feldmann H.; "Analysis of a DNA segment from rat liver mitochondria containing the genes for the cytochrome oxidase subunits I, II, II, ArPase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                        -!- PATHWAY: Plays an important role in several metabolic pathways. -!- SUBUNIT: Homotetramer (By similarity).
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                    SUBUNIT: HOMOLEtramer (By similarity). SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
                                                                                                                                                                                                                Probom; P001005; Triophos_mrse; 1.
TIGREAMS; TIGRO0419; tim; 1.
FROSITE; PSOUTI, TIM; FALSE_NEG.
ISomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis; Pentose shunt; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete nucleotide sequence of the Rattus norvegicus mitochondrial genome: cryptic signals revealed by comparative analysis between vertebrates.";
J. Mol. Evol. 28:497-516(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gadaleta G., Pepe G., de Candia G., Quagliariello C., Sbisa
                                                                                                                                                                                                                                                                                           B6DD20B1DD85D6A4 CRC64
                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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01-CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MTATP6 OR ATP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AA
                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-008-355-1 (1-2139) x TPIS_HALN1 (1-214)
                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                       InterPro; IPR000652; Triophos_ismrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 AlaSerGlyValAlaLysAlaAsp 201
                                                                                                                                                                 EMBL, AE005037; AAC19439.1; -.
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89362487; PubMed=2504926;
                                                                                                                                                                                                                                                                   Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                       52 GCTTCAGGGGTAGCCAAAGCCGAC 75
                                                                                                                                                                                                                                                                                 85 85 B
214 AA; 20928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6, and several tRNA genes.";
Curr. Genet. 4:151-158(1981)
                                                                                                                                                                                                                                                                                                                              27.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccone C.;
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H(+)(Out).

-1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                 Mathews C.E., McGraw R.A., Berdanier C.D.;
A point mutation in the mitochondrial DNA of diabetes-prone BHE/cdb rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                               Speir J.A., Stevens J., Joly E., Butcher G.W., Wilson I.A.; "Two different, highly exposed, bulged structures for an unusually long peptide bound to rat MHC class I RTl-A(a)."; Immunity 14:81-92(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D -> N.
A -> P (IN REF. 2).
S -> L (IN REF. 2).
A -> V (IN REF. 2).
W; 6074E2CCAC2B586E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 28.7 kDa protein in DHFR 3'region (ORFI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
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SEQUENCE FROM N.A., AND VARIANT ASN-101.
STRAIN-BHE/CDB, and Sprague-Dawley; TISSUE-Liver;
MEDLINE-96118462; PubMed-8529844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 29-41.
MEDLINE=21109741; Pubmed=11163232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ndels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR01131; ATP_SYNt_6_or_A; 1. PROSITE; PS00449; ATPASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-008-355-1 (1-2139) x ATP6_RAT (1-226)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000568; ATPsynt_Asub.
Pfam; PF00119; ATP-synt_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 LeuSerMetAspLeuSerMetAla 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF115770; AAD22965.1;
PIR; SO4752; SO4752.
PDB; 1ED3; 21-JUN-00.
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100.008
1.138
                                                                                                                                                                              FASEB J. 9:1638-1642(1995)
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8.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \frac{129}{205}
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226 AA;
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Best Local Similarity:
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Query Match:
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                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNJ6_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are or estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isbsib.ch).
                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90266466; PubMed=2161148;
Biesinger B., Trimble J.J., Desrosiers R.C., Fleckenstein B.;
"The divergence between two oncogenic Herpesvirus saimiri strains in a genomic region related to the transforming phenotype."; virology 176:505-514(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AV19 / DSM 6324 / JCM 9639;
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed-11930014;
MEDLINE-21927647; PubMed-11930014;
Slesarev A.I., Machevapa K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natalle D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophylyty of archeal methanogens.",
Proc. Natl. Acad. Sci. U.S.A. 99.4644.4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E04BA49D27A59D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256
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                    Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus
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Herpesvirus saimiri (subgroup C / strain 488)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypochetical protein MK0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 ACAACGAATACTTCCTCATCGTCT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 ThrThrAsnThrSerSerSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, A34770; A34770.
Hypothetical protein.
SEQUENCE 256 AA; 28662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55264; AAA72928.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                         NCBI_TaxID-10384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-2320;
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P58851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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10 Y939_ME
10 Y939_ME
11 15-UUN-
11 15-UUN-
12 Hypothre
13 MK0939
15 MK0939
16 MK0939
17 MK0939
18 MK0939
19 MK0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE row. .....
SEQUENCE row. ....
STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Craxton M., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lidyd C., Mortlmore B., O'Callaghan M.,
Latreille P., Lightning J., Lidyd C., Mortlmore B., O'Callaghan M.,
Parsons J., Percy C., Riften L., Roopea A., Saunders D., Shownken R.
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sims M., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 38.0 kDa protein R10E11.6 in chromosome III.
R10E11.6.
Caenorhabditis elegans.
EMBL, AE010383; AAM02152.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 279 AA; 31379 MW; 49474EC38B012D85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862F7D9D3E3E2E2F CRC64;
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Matches:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                         US-10-008-355-1 (1-2139) x Y939_METKA (1-279)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1. SIMILARITY: CONTAINS 1 EH DOMAIN.
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Interpro: IPR000261; EPS15_repeat.
PROSITE: PS5031; EH; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                             301 GTGGATCACGACTATCTGCGCGAT 324
                                                                                                                                                                                                                                                                                                                                                                                                         224 ValAspHisAspTyrLeuArgAsp 231
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SEQUENCE 349 AA; 37984 MW;
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                                                                                                                                                                                                                     Best Local Similarity:
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P34550;
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SEQUENCE
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                                                  EMBL;
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02
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AMEDINE-INE-INE-INE-INE-3360,

AMEDINE-INE-INE-INE-INE-3360,

AMEDINE-INE-INE-INE-3360,

AMEDINE-INE-INE-INE-INE-3360,

AMEDINE S., Brown D., Brown S., Chillingworth T., Churcher C.M.,

AMEDINE S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G.,

AMEDING S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G.,

AMEDING S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

Andames K., Jones L., Jones M., Leather S., McDeald S., McLean J.,

Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

AMEDING S., Pearson D., Quall M.A., Rabbinowitsch E.,

AND JOY K., Chilling S., Saunders D., Seeger K., Sharp S.,

AND Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

AND Skelton J., Simmonds M., Squares R., Scharp S.,

AND Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

AND Goffeau A., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Purnelle B.,

Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

A Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.,

A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

A Daninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

A Daninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

A Daninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

A Phakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Mathre G. Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 415:871-880(2002).
-!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHIONINE AND ATP (BY SIMILARITY).

--- CATALYTIC ACTIVITY: ATP + L.methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L.methionine.

--- PATHWAY: Activated methyl cycle.
--- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Saml, a new gene coding for S-adenosylmethionine synthetase in
                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
00
                                                                                                                                                                                   382 AA
 Indels:
                                               US-10-008-355-1 (1-2139) x YNJ6_CAEEL (1-349)
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21848401; PubMed=11859360;
                                                                                                 545 CCAACAACGAATACTTCCTCATCG 568
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                  SAM1 OR SPBC14F5.05C.
                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896
                                                                                                                                                                               METK_SCHPO
060198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972
 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilti
                                                                                                                                                                 METK_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pombe
                                                                                                                                                RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHALCONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWĀY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF FLAVONDIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY OF WHICH ARE BRIGHTLY COLORED.
-i- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ardi R., Kobiler I., Jacoby B., Keen N.T., Prusky D.; "Involvement of epicatechin biosynthesis in the activation of the mechanism of resistance of avocado fruits to Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA + naringenin-chalcone + 3 CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiol. Mol. Plant Pathol. 53:269-286(1998).
-!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chalcone synthase (EC 2.3.1.74) (Naregenin-chalcone synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                     9970A9D1195C5738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
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                                                                                                                                                                                                                                                                                                                                 Transferase; One-carbon metabolism; ATP-binding. NP_BIND 123 ATP (POTENTIAL). BINDING 146 146 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                             Pfam: PF00438; S-AdoMet_synt; 1.
Pfam: PF02772; S-AdoMet_syntD2; 1.
Pfam: PF02773; S-AdoMet_syntD3; 1.
TIGRFAMS; TIGR01034; metk; 1.
PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
or send an email to license@isb-sib.ch)
                                                                                                                                           interPro; IPR002133; S-AdoMet_synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1755 CGGTGCCTGGTACAACTATCATAC 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 ArgCysLeuValGlnLeuSerTyr 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                     41831 MW;
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                                                      EMBL; AJ001705; CAA04941.1;
                                                                              AL023780; CAA19323.1;
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1.12%
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                                                                                                                   P04384; 1MXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gloeosporioides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aliqnment Scores:
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Q9ZU06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mautino M.R., Goyon C., Rosa A.L.;
"Cloning and sequence of the Ascobolus immersus S-adenosyl-L-methionine synthetase-encoding gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungl; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism; ATP-binding.
NP_BIND 127 132 ATP (POTENTIAL).
BINDING 155 ATP (POTENTIAL).
SEQUENCE 393 AA; 43010 MW; 88FBZFZF14B751C3 CRC64;
            Prodom; PD000453; N-C_Synthase; 1.
PROSITE; PS00441; CHALCONE SYWH; 1.
Flavonoid biosynthesis; Transferase. Acyltransferase.
ACT_SITE 165 BY SIMILARITY.
SEQUENCE 392 AA; 42480 MW; B08D286FB80B842E CRC64;
                                                                                                                      392
8
0
0
0
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                                                                                                                      Length:
Matches:
Conservative:
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                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                JS-10-008-355-1 (1-2139) x CHSY_PERAE (1-392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002133; S-AdoMet_synt.
                                                                                                                                                                                                                                                              1223 GTTTTGCACAGTTTGCCAACGCAT 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00438; S-AdOMEL_SYNT; I.
Pfam: PF02772; S-AdOMEL_SYNTD2: 1.
Pfam: PF02773; S-AdOMEL_SYNTD3: 1.
TIGREAMS; TIGRO1034; metK; 1.
Pfam; PF02797; Chal_stil_syntC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RN42;
MEDLINE-96200878; PubMed-8621082;
                                                                                                                                                                                                                                                                             385 ValLeuHisSerLeuProThrHis 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U21548; AAB03805.1; -. HSSP; P04384; IMXB.
                                                                                                                                                   100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                        25.4
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascobolus immersus.
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5191;
                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                       METK_ASCIM
P50304;
                                                                                                                                                                                   Query Match:
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90
                                                                                                                                                                                                                                                                                                                                          METK_ASCIM
                                                                                                                                                                                                                                                                                                                          RESULT 13
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393

Length:

25.4

.gnment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPORT IS EFFECTED BY THE OLIGOPEPTIDE PERMEASE SYSTEM.
SUBCELULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed + G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 23-32.
STRAIN=K12 / AT980;
MEDLINE=98155149; PubMed-9495761;
Park J.T., Raychaudhuri D., Li H., Normark S., Mengin-Lecreulx D.
"MppA, a periplasmic binding protein essential for import of the bacterial cell wall peptide L-alanyl-gamma-D-glutamyl-meso-
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic_murein peptide-binding protein precursor.
80000
            Conservative:
Mismatches:
                                                                                                                                                                                                   537 AA
Matches:
                                        Indels:
                                                                                  US-10-008-355-1 (1-2139) x METK_ASCIM (1-393)
                                                       Gaps:
                                                                                                                                                                                                   PRT;
                                                                                                               1755 CGGTGCCTGGTACAACTATCATAC 1778
                                                                                                                             309 ArgCysLeuValGlnLeuSerTyr 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 180:1215-1223(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
            100.00%
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                                                                                                                                                                                                     STANDARD;
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    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diaminopimelate.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                         MPPA OR B1329
                                                                                                                                                                                                   MPPA_ECOLI
P77348;
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MPPA_ECOLI
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or send an email to license@isb-sib.ch)
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8.00
100.00$
1.13$
                                                                                                                                                                         SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 7.
SMART; SM00001; EGF_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                  PROSITE; PSO0577; A PROSITE; PSO1180; C PROSITE; PSO1186; E PROSITE; PSO1187; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                          Calcium-binding.
SIGNAL 1
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290
328
366
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                                      P00740;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: EXTRACEILULAR.
DEVELOPMENTAL STAGE: LOW LEVELS IN UNFERTILIZED EGGS AND DURING EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETWEEN LATE MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES.
MISCELLANEOUS: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    embryo.";
Dev. Biol. 157:526-538(1993).
-!- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
EMBL; U88242; AAC38216.1; -.
EMBL; AE000231; AAC74411.1; ALT_INIT.
EMBL; D90772; BAA14932.1; ALT_INIT.
HSSP; P06202; 1JEV.
SWISS-2DARGE; P77348; COLI.
ESCGENE; EG13376; mppA.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
22
IGNAL.
I 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-39273088; Pubmed-8500658; Bisgrove B.W., Raff R.A.; "The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing proteins that form the apical lamina of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibropellin C precursor (Epidermal growth factor-related protein 3)
(EGF III) (Fibropellin III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR
TO AVIDIN/STREPTAVIDIN.
                                                                                                                                         PERIPLASMIC MUREIN PEPTIDE-BINDING
                                                                                                                                                             C6A17656836DC3AC CRC64;
                                                                                                                                                                                                537
0
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                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                         570 AA.
                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                              US-10-008-355-1 (1-2139) x MPPA_ECOLI (1-537)
                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                                     1892 GTCAGCTCCATATCGCTTTCCTAT 1915
                                                                                                                                                                                                                                                                                                                14 ValSerSerIleSerLeuSerTyr 21
                                                                                                                                                               537 AA; 59900 MW;
                                                                                                                                                                                               24.4
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Gastrula;
                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                      FBP3_STRPU
P49013;
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                            Query Match:
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02
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FBP3_STRPU
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(POTENTIAL)
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PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01186; EGF_A; 6.
Biotin; EGF-like domain; Repeat; Signal; Glycoprote.in;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE665E3E1C05E6EE CRC64;
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBROPELLIN C. EGF-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE 2, C
EGF-LIKE 3, C
EGF-LIKE 4, C
EGF-LIKE 5, C
EGF-LIKE 6, C
EGF-LIKE 6, C
EGF-LIKE 7, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVIDIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                              InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
Fam; PP00008; EGF; 8.
Pfam; PP00431; CUB; 1.
Pfam; PP01382; Avidin; 1.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                       œ.
                                       InterPro; IPR000152; Asx_hydroxyl InterPro; IPR000088; Avidin.
                                                                                                                                                                                                                                                                                                       SMART: SMOODI; EGF_LIKe; 1.
PROSITE; PSO0010; ASX_HYDROXYL;
PROSITE; PSO0022; EGF_1: 8.
PROSITE: PS00577; AVIDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61116 MW;
EMBL; L07045; AAA30045.1; -.
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US-10-008-355-1 (1-2139) x FBP3_STRPU (1-570) Gaps: DB:

Search completed: May 16, 2003, 13:07:56 Job time: 48.5 secs

us-10-008-355-1.rge

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 23, 2003, 01:38:11 ; Search time 3816 Seconds Run on:

(without alignments) 16313.129 Million cell updates/sec

US-10-008-355-1 2139 1 atgcaaatgaaattaaaaaag.....aagagctgaagttgatctaa 2139

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

Perfect score:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmb1:* Database :

gb_ro:* gb_sts:* gb_sy:* gb_un:* gb_ba:*
gb_htg:*
gb_on:*
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gb_pat:*
gb_pt:*

gb_vi:* em_ba:* em_fun:* em_hum:* em_mu:* em_in:* em_ov:* em_pat: em_or:* em_ph:

em_ro:* em_sts:* em_un:* em_pl:*

em_htg_other:* em_vi:*
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em_htgo_mus:*
em_htgo_other:* em_htgo_hum:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	а	AROUADOR XVIOLET		AF429315 Homo sabi	~~	Drosophi	_	Drosoph	Drosoph		Botryti	M15810 R.meliloti	Sinorhiz		Xenopus		L24395 Emericella	AL583920 Mycobacte	X79242 Paracoccus	AC099055 Homo sapi	AC105363 Oryza sat	AC118980 Oryza sat	AL646080 Ralstonia	AC017879 Drosophil	AC007414 Drosophil	AE003831 Drosophil	AC019786 Drosophil	Drosop	AL669952 Mouse DNA	Mus		Homo	AP002997 Mesornizo	AF4330L ACLINOSYN	AXIIU931 Sequence	AUZSOIUZ POUOSPOIA	AEUU4/50 Pseudomon		283, Pyrococ	106 Sequenc	78952 Z	ں م	327 Molluscum	1231 Homo sap	ношо в	3148 Homo sap	
CO LIVERING CO	Ω	AEOO4OO8	AE01172		AF4034	AY05179	AC01425	AC00823	AC00835	AE00368	~	RHMNTRB	SME5917	AF429315	AF05178	AC12185	EMEFLBA		PDSOX	AC09905	AC10536	AC11898	AL646080	AC01787	AC00741	AE00383	AC01978	AC007452	AL6699	AC10175	AC07434	AC01354	AP00299	AF40300	AXIIO931	PAN2301	AE004/5	AC10432	CNSPAXO		AF17895	CRENOLM	MOCDRN		AC01690	AC02314	•
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ALIGNMENTS

Xylella fastidiosa 9a5c, section 154 of 229 of the complete genome. AE004008 AE003849 AE004008.1 GI:9106961 Xylella fastidiosa 9a5c. Xylella fastidiosa 9a5c Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; RESULT 1 AE004008/c LOCUS DEFINITION ACCESSION VERSION ORGANISM KEYWORDS SOURCE

Xylella.
I (bases 1 to 10689)
Simpson.A.J., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
Simpson.A.J., Rathach,F.C., Arruda,P., Baia,G.S., Baptista,C.S.,
Alvarenga,R., Alves,L.M., Araya,J.E., Baia,G.S., Baptista,C.S.,
Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.,

REFERENCE AUTHORS

TITLE

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CTLAREWQKMMEEARATAPQGGLAASDPQRITDALQKTVSHKRRHAANETASIIQLRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MLNUTGAPGNGKTLYAVDWLIRQIEIDKSLVKSGAVPRSFYTD
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DTHRHGGYDLMFVTQWPTKIHHELRRLVGEHVHLNRAMGLQTAGLYRWSRAQDDPYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQREKAEEEVWKFPKDRYALYASSTLHTVSHKRRIPKKVWSALSVCVTCSVIGLVFWH
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                                               /translation="MMEEARATAPQGGLAASDPQRITDAPKKTGLRKRKYPTTGSASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to SPIP03625 (percent identity: 36 %/query alignment coverage: 85.1 %/subject alignment coverage: 86.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="XF1877"
/note="hypothetical protein; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="phage-related protein"
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complement(1839. .2918)
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                                                                                                                                                                                                                                                                                     The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis.

Nature 406 (6792), 151-157 (2000)
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MEDLINE
PUBMED
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by sequence
Glimmer/RBSfinder"
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ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAATGCGCGTATTTACGTGCTTGAGCAGATTACCGATGTCACCGCTCAAGCTAAAGCTG 10088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CICTGGCTGCTGCCGGTAAIGACCCCTTCAAGCGTACGACGCATTGGAGACATTCAGCA 10028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAGAAATCGCCAAATGCGAGGAAGAGCAGGTTATCGCTGCCAATTCTTCAGTTTCG 9968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 129.4; DB 1; Length 10689;
larity 44.9%; Pred. No. 3.1e-23;
Conservative 0; Mismatches 1051; Indels 38;
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                  complement(4481. .4702)
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  similarity; putative;
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ses 888; Conserv
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Matches
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ACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAA 1141 TCG---GTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATC 1258 1319 CGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCG 1378 CCGCCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCGCGCCTATTCAGGCCGATGCG 1608 ATGGCCAATGCCTATGCCATTGAGAGGGCAAGCGTTTTTCTTTGCCGGTTTGCGTGAG 1668 AAAATCCGTACTGGAGAACTACTTAAAAGCGCGTCCGATCTACTTGCAAGCCTTAGCTGAC 8832 9367 ITGATCTGACAGAACAATACAAAGCAAATCAGGATCGTGATTTTGTATTGGGTCAGTTCA 9308 9787 GCTTCTGAAAGAAAGATACCCTACCGTCCCAAACACTGGCTGÄAATTTAGCGATCAAC 9728 CTTTGGTGGCCGAATTTGAGAATACTGCTCACTGGACTTATCCGGTGATTGGCCAGCATT 9608 9847 GTCATACCGGTGACTTTTCTTTCTACCGTGCCTACGTCGGTAAAGACGGTAAACCAGCGA 902 GCGGTATCAAGCCATCTGGAAGGAAGCCATGAGCCAGATCAGGCTACCCGTATCA 9607 TCAAGAATCTCATTGCTTTGATTGAGGGGGCTAGCAAACAGAATCCAGACATTCAAGTGA AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACC 1022 GCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAG 9427 CTTGGTTGAAACAGCCAGACCATACGTGGACACGAAGCATTGG AGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCT ACGGAAGTGGTGTCATTGGTGTAGCGGTGAACCTATATCGCTTGGCAATCGAGCGCACAA 9247 AATCTGATGCCCAACGTGAAGGGGGATATCAGGAGGGGGGATCTGCCAACCATTGAAGGCA ACTTAAAGCAGATGGAGCGACGTTACTTACCGGAAATGGATCGCCAG----ATGCAGCAAT ACAAGCTCCCCGATATATTCAAGAATGTAATCGACAA------GAAATTCAAAGGC GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAG TTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGAT 9011 TCTGAGGAAAGGCTGAAGTGGTTTAATGCCGACCGTGCAGCCTTCGAAAGCAGTCAAGAT CCAGCGATCCGTTATGCTGTGGCCATCATGCCAGCATTACTGGAGGTTGAACGTCAGAAT 722 AATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAG 782 GCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACC CTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCT GGTTGGGAGATGGCATCCCAGCAACTCTCAAGCGCTTGGGTGACACCAAATTAAG-CAGT TCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTC TTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC 1142 9307 1259 9070 1549 8891 842 9130 1429 1489 1609 2996 962 1082 9187 8951 1379 602 662 qq g g δ qq ολ qq ŏ g ŏ QQ ōλ QQ οy qq QΥ Dp οy Dp $^{\circ}$ q ò g ò g δ Db ŏ a ò d à à

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Almeida
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                                                                                                                                                                                                                                                                                                                                                                      8595
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                                                                                                      1723 TACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACA 1782
                                                                                                                                                                                                            1783 GGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAAT 1842
                                                                                                                                                                                                                                                                                                                  1843 ATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGA-----GAACGGTCAG 1896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2077 CTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGCTGAAGTTG 2133
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                                                                                                                                                                                                                                                                                                                                                                                                                        8654 CTGATTAATGCGATAAAGGCAAAGAGCTACGCCAATTTAGCCGATCAGCGTATTGGCACT
                                                                                                                                 8831 TACAACAAGAGTCATGGCAAATTTGTTTACCCAGACGCCAACTCATCATTACGTATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1957 TTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGT
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Xanthomonas axonopodis pv. citri str. 306
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Nature 417 (6887), 459-463 (2002)
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AE011732 AE008923
AE011732.1 GI:211071
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Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighteri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., M., Lemos, B.G., M., Lemos, M.V.F., Locall, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Maidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Olivelra, M.C., Olivelra, V.R., Pereira Jr., H.A., Tanita, J.R., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Rossi, A., Sena, J.A.D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.

Litajima, J.P.

Direct Submission

L. Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade de Sou Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900, DVIGEDVLITGAGPIGITAAGICKHIGARNVVTDVNDFRLKLAADMGATRVVNVSKT SLKDVMADLHMEGFDVGLEMSGNSRAFNDMLDCMYHGGKIAMLGIMPRGAGCDMDKII FKGLTVQGIYGRKMYETWYKMTQLVLSGFPLHKVLTHQLPIDDFQKGFDLMEEGKAGK ARLVQTVGSDATRRTEVRADTGDRDGLSAYLSYANASTDKWKGYGDQTSEQANLKTVY WGDGNRLSLEPUDTSRRKEDYDMDLSLTSQRALGAWIDYLDDWATAVOWRARYONTG ATGGVANGYPQSLAGLPSDYSWLDASYYAGGGLRRDNLAGLGSGTFVFGGATLDASGYY HGNRGEGQWVTPYVRTSAQIPVSMRTTDYGLDRFGGTSALKWSWGNHDLEVGAWAENA ALATLLPVISQAATPADPAAVAPAEAALTADAAANATQLDAINVVSOGSTRQVQRISQ QDIEQLTPGSSAFKAVEKLPGVQFQSADPFGTYEWSTQVTLHGFDQSRLGYTLDGIPL GNMSYGVTNGLHITRAIISENLGSVEIAQGAGALGTASNTNLGGTWQFYSADPQTTPG AAFGFTPFATSQAAFDRSRSTLEPEQSQTVQVGYRVQDAQFQLSADAYFTKFSNRLLIT TSPCTAVQTVSTLSBVGGANISAGADLALMWRPPEGLSWLNSLSBWNSRYDDTINNG VVATSGRDVVGIPALMESSSASYQIGNLRLDLDGKYVDKRYTTFLNDSQVPSYWLFNA GARYDFGRVGGVADVALALNISNLTDKRYFASTGTNGYVASDPDGYNQTMVVGAPRQY /translation="mkaLvkREanKGIWLEQVPVPTPGPNEVLIKLEKTAICGTDLHI YLWDEWSQRTIEPGLTIGHEFVGRVAELGSAVTGYQIGQRVSAEGHIVCGHCRNCRGG RPHLCPNTVGIGVNVNGAFAEYMVMPASNLWPIPDQIPSELAAFFDPYGNAAHCALEF /product="Tonb-dependent receptor" /protein_id="AAM35906.1" /db_xref="GI:21107163" /translation="WFHEPLTPCVAKRRLCTVRPPSAVPEQDSPMTSARRFHVTPLAL RTTGGRNY FALGNEGYTSLYNVY EAQTPFRRDFLQRYTTQTRMLY VQDTVRLLDDRLT LNY GAKALSTTTRAQSLVPTTALAGGRIRAEDNFLPQLGINY KLDERQDLYASY SKNI /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark" /codon_start=1 /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark" /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark" /organism="Xanthomonas axonopodis pv. citri str. 306' /product="threonine 3-dehydrogenase" /protein_id="AAM35905.1" /db_xref="G1:21107162" /db_xref="taxon:190486" /note="pathovar: citri" complement(293. .1315) .4260) complement(1840. .4260) complement(293. .1315) Location/Qualifiers complement(1840. /gene="fecA" 4369. .6450 /gene="XAC1024" 4369. .6450 /transl_table=11 /transl_table=11 4369. .6450 /gene="XAC1024" /note="XAC1022" /note-"XAC1023" /codon_start=1 /strain="306" /gene="fecA" /gene="tdh" /gene="tdh' .10811 FMSLDVKF "VVLSWN"

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                                                                                                                                                                                                                                                                                                                                                                          VIVVGGTNGKGSTVAFIEAIGRAAGWKVGÄYTSPIILLRYNERVRIDGQEASDAQLVDA
FAAVEAARGDTALTYFEFGTLAALWLFQQSALELÄVLEIGLGGRLDAVNIVDSDVAVI
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1 (bases 1 to 125020)

14 (bases 1 to 125020)

16 (bases 1 to 125020)

17 (bases 1 to 125020)

18 (Bases 1 to 125020)

19 (Bases 1 to 125020)

10 (bases 1 to 125020)

11 (bases 1 to 125020)

12 (bases 1 to 125020)

13 (bases 1 to 125020)

14 (bases 1 to 125020)

15 (bases 1 to 125020)

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18 (bases 1 to 125020)
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
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located using Blastx/Glimmer/Genemark; dihydrofolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996 GGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2056 AGCGTGGACATCCGCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTC
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1. 125020
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/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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56.4%; Pred. No. 5e-05;
Live 0; Mismatches 89;
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/db_xref⇒"taxon:9606"
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/qene="folc"
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Matches 115; Conservative
                                                                                                                                                                                        synthase"
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                                                                                                                                                                                                                                                                GSTAGNAATTQAEHLVAAIAADVRANRLPQVSWVIPPTAYCEHPEAPPAYGESLVARL
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GLGIRVPMLVISPWTRGGWVNSQVFDHTSVLRLLERRFGVAEPNISPWRRAVSGDLTS
                                                                                                                                                                                                              AFTICDGYYCSLHGPTNPNRMYLFTGTSGPSVGNVGAQAVTNADDGNWTADMARDKPG
YAALQWTTYAQKLQAAGVDWRVYQEYDNFGCNSLAYFSHYRDLRTDDERYLRARACVP
                                                                                                                                                                                                                                                                                                                                                                          LOVHARVQEGAAVQLQFVNSGAAAARNVYNSAAGGGPWYYTVLPGTQLDDAPTGATH
EGAYALRVHGPNGFLREFAGQVPRASAPSAAPWVEARQEGDALVLETGNAGQRACTVQ
LRALDYADPSARTLSLAAGQRETIRLALAASDHWYDLVVEQPGSAFRRRLAGHLETGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation="MRPNLFAVSVLATLAVAASAQAGEGMWVPQQLPEIAGPPQQAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGAVVALGGCTASFVSPQGLVVTNHHCAYGAIQLNSTAQKNLIK
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                                                                                                                                                                                                                                                                                                                                              VFDFRKPDDSALSALPSVDDYRARTAAVRDKPLPSAPAAATMPRQEPGQRPARALPYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"
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/note="identified by sequence similarity; putative; ORF
located using_Blastx/Glimmer/Genemark"
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/gene="XAC1025"
6617. 676
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/transl_table=11
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7329. .7973
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5791, 7054
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/rpt_type=tandem

repeat_region

/translation="MRILLARHGETPWNAEGRYQGQIDIPLSPVGEGQARALGERLHS LQIDRAVASPLSRAQATAKAALGASRQALLQTDADLQEIAHGEWEGLLASEINDKDPA RLRAWREEPDTVLMPGGESLRQVLDRSWRGLMRAADGLGAHDTLLVVAHDAVNRVILC

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HVSDPTAHELLTMPAALADLPPPPPTDDEINRSFYATALPSVVPTSDTLWGTASYEI
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LTGREDERGWYRLLSTLTKKSTPSTWYTSDWTLDTTTGLTKPPVTGFNARATVKDSAI
VWWFPAPDIATSARRAIVSPMSCVFE"
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                  Grass carp reovirus, Striped bass reovirus and golden ide reovirus (genus Aquareovirus, family Reoviridae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1461)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K.
Yu, C., Lewis, S. E., Rubin, G. M. and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1858 CGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCG 1917
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This clone was sequenced as part of a high-throughput process
                                                                                                        2 (bases 1 to 820)
Attoui,H., de Micco,P. and de Lamballerie,X.
Direct Submission
Submitted (30-JUL-2001) Virologie, Faculte de Medecine de
Marseille, 27 Boulevard Jean Monlin, Marseille 13005, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 684 TTTAACGGTCGCACGGCGTTGAATCCAGTGACGGGGGGTTTGGTCAGACCGGTGGTGT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                    /product="non-structural protein NS3"
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/db_xref="G1:22128471"
of Golden
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                                                                                                                                                                                                                                                                    /organism="Golden shiner reovirus"
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                                                                 Virol. 83 (Pt 8), 1941-1951 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14;
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/note="Golden shiner reovirus
segment: 11"
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genome characterization
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54.0%; Pred. No. 4.0
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Lawrence Berkeley National
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                 /translation="MSSGGRFNFDDGGSYCGGWEDGRAHGHGVCTGPKGQGEYTGSWS
HEPVLGAVYTWPSGNTYQCTGTWAGGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQGCYGTFTYSDG" 4254 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRL 07-AUG-2002
                                                                                                                                                                                                     complex between plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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1 (bases 1 to 820)
Attout, H., Fang, Q., Jaafar, F.M., Cantaloube, J.F., Biagini, P., Micco, P. and De Lamballerie, A. Micco, P. and Orthoreovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50905 MMRDMWYDKMRMKVSSGTRGYHBHSAWMCKSMSRDSDSGYSGMYHMKSYWKSSASKHMYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51141 SRWWTSSMACMYWYKGSRRKTKSMATSGCMRWGAMRSKGGMRKYWSCRYKGMRWGRWSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 GCCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 AACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGCGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                        membrane and endoplasmic reticulum"
                                                                                                                                                                                                   /note="component of the junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                  .>36887)
                                                                                      .>36887)
                                                                                                                                /product="junctophilin 3"
complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.0%; Score 43.2; 1
9.8%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                   complement(<36507.
                  complement(<36507.
                                                                                                                                                                                                                                               /codon_start=1
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/rpt_unit=ctq
                                       /gene="JPH3"
                                                                                                             /gene="JPH3"
                                                                                                                                                                            /gene="JPH3"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADKOPLQEVGFINSAADHLAEMAKPÖNVLMLRVSVDGVAKAHGEKSVAVEEANKLLSA
AISRLLAASOKSSDSVLFVQTTEKDVAASRAKRDTIAASTTNPYNLAVYYGSDYPVIF
NIILWFWVVFGLSLLAICYAIAAMDPGRDSIIYRMTSTRIKKDN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVLYASMGNAVSGDTNWNGLTINDPFNLAKGVILVHVOGIGHVTTAGNVKTYELTGSG
TDASLNALAAELEAANEPVCDINFEQFDDGVQAWKSCFGDFEAPAAKPTKHLNPSLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLRVFVIFSLFIAAINASGEFTVLNRPKAISFKGNDALESHYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 GGCCGCTATCAGCCGCCTGCTTGCTGCTCCCAGAAGTCCAGCGACTCGGTTCTGTTTGT 762
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763 CCAGACCACGGAGAAGGACGTGGCAGCATCGCGTGCCAAGCGTGATACCATTGCCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="alignment with genomic scaffold AE003682"
/db_xref="FLYBASE:FBgn0037671"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAK93214.1"
/db_xref="GI:15291891"
                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila
                                                                                                                                                                                                                                                                                                                                                                                          /strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="85D8-85D9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Longest ORF"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="LD30634p"
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HTG; HTGS_PHASE2.
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EUKATYOTCA; METAZOA ATTHIOPODA; HEXAPODA; Insecta; Pterygota; BURATYOTCA; METAZOA ATTHIOPODA; HEXAPODA; Insecta; Endopterygota; Diptera; Brachycera; Muscomorpha; Behydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

E Loases 1 to 148847)

S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatidea, P.G., Brandon, R.C., Rogers, Y.A., An. H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hostin, D., Howland, T.J., Inseyman, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Morlntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
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Drosophila melanogaster, chromosome 3R, region 85D-85D, BAC clone
BACR22M04, complete sequence.
                                                                                                                                                                                                This sequence was identified as CDM:10211789 by the submitter. For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589
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                                                                                                                                    Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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/db_xref="taxon:7227"
21897 a 15665 c 15830 g 23356 t
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 76748)
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                                                                         Adams, M. and Venter, J.C.
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2 (bases 1 to 148847)
Celniker,S.E., Agbayan
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                                                                                                           Direct Submission
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                                                                                                                                                                                                 Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley abboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 17, 2001 this sequence version replaced 91:6984365. Sequence submitted by:
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Drosophila melanogaster.

Drosophila melanogaster

Eukaryota: Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases I to 162593)

1 (bases I to 162593)

1 (Clanker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Holt, R. A., Evans, C. A., Gocayne, J. D., Amanatides, P. G., Brandon, R. C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D. A.,
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BAC clone
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelifer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="3R"
/map="85D-85D"
/clone="BACR32M04 (D969)"
/clone_1b="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.

Location/Qualifiers

1. 162593
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Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Sep 6, 2001 this sequence version replaced gi:12957666.
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., MINTOSH, T.C., MOY, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfelifer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, K., Tector, C., Williams, S.M., Saveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 3R, region 85D-85D
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished

(Dases 1 to 162593)

(Calliker, S.E., Agbayani, A. Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Humasti, S.R., Karraw, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Syriskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and Rubin, G.M.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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complement(join(3004. 3235,3300. 3914,3972. 4605,
4986. 5199,5255. 6265,6330. 7367,7561. 7747,7809. >7907))
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/db_xref="FLYBASE:PBan0037663"
/db_xref="FLYBASE:PBan0037663"
/dpan0="Capada"
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GGAGSGSGDSVKTPGSAKKRKAGRPKKHQPSDSÈNEDDQDEDDDGNSSIEERRPVGRP
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RPRGRPKANAAPVEKHEDNDDDQDDBNSGEEEH5SPEKTVVAPKKRGRPSLAAGKVSK
EETTKPRSRPAKNIDDDADDADSADQGQHNSKKESNDEDRAVDGTPTKGDGLKWNSDG
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DLVEKHLAGIENERLRNLLASMIDIHSMNRKSAİDYLDQERGQLFPEYFYSFLQSYLQ
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LAKSAVYFLEETQRNAPNDMPTPRYEAELNALHIIVRQAVLSLLTDSQPVVKQTLMES
GICDLCAFFCKEKANDVILSHIMTFLNDEDKNLRGAFYDNIAGVAGYVGWQASDILVP
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GMIATTARNLSAIDVQCKIMPAIGAFLKAPLIQVEKPHILLDCVHPPVPRQIFDSVLR
FQDIHHFIRALEARSRVRSQTRQGALPQYEEMGÖTLRNLFRRLSSEGLTDLIEMQLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLILIITVVTSCIRGLKQSNTKIAALELLQKLSKYTTSETILDRILPYILHLAQKSPA
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LASLRPHGSLFASGSIDGTVRLWDCSKLNGNQGVNKSRQVYSANTPIYALAACDSGQS
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GGIVAMDTRMQHSAWRLQNELRHGVITTICADPTGSWLATGTSGGKHICWDLRFRLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEIKHPADSWIRKVACHPTEPSYLISASQSNNEVSVWNIETGGROTVLWASPVAALSS
                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MEEVAVKKRGRPSKASVGGKSSTAAVAAISPGIKKRGRPAKNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MGNQLVGIAPSQIYAVEHYFSGQFGSEIAFSSNMGSTRFFKVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNPFLISMKHKALQDLDDTASGNGRIVVSRKQVÄCHEYPLADKASKMPLDNRSSEGPT
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                                                                                         /db_xref="FLYBASE:FBan0009745"
/db_xref="FLYBASE:FBgn0000412"
complement(join(672. .1324,1643. .2057))
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/db_xref="FLYBASE:FB40009746"
/db_xref="FLYBASE:FBgn0037663"
                                                                                                                                                                                                                                                                                                                                                       /db_xref="FLYBASE:FBan0009745"
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/db_xref="FLYBASE:FBgn0037664"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<3004. .>7907)
                                                                                                                                                                                                                                                                                         /protein_id="AAF54341.1"
/db_xref="GI:7299143"
                                                                                                                                                                                                                           /note="D1 gene product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13366. .13591)
/gene="CG8420"
                                                                                                                                                                                                                                                              /codon_start=1
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/gene="CG8420"
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13366. .135
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                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                Ephydrodae; Drosophilidae; Drosophila.

Adams, M.D., Celliker, S.E., Holt, R.A. Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherrs, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfelifer, B.D., Man, K.H., Doyle, C., Bayter, E.G., Helt, G., Malson, C.R., Gabor, Man, K.H., Doyle, C., Bayter, E.G., Helt, G., Malson, C.R., Gabor, Mallos, G.L., Abrill, J.F., Agbaytani, A., An, H.J., Beach, R., Bernos, F.V., Bernan, B.D., Bandani, D., Ballew, R.M., Beson, K.Y., Benden, B.J., Bayrakraroglu, L., Beasley, E.M., Beson, K.Y., Benden, B.J., Bayrakraroglu, L., Beasley, E.M., Beson, K.Y., Benden, B.Y., Bulter, H., Cadicu, E., Center, A., Chandra, I., Bouck, J., Brockstein, P. Brotherter, P. Brotherter, P. Brother, E., Durke, S., Borkova, D., Bockham, R.P., Bouck, J., Brockstein, P. Brother, E., Dattis, K.C., Busam, D.A., Buller, H., Cadicu, E., Center, A., Chandra, I., Dadson, K.J., Doulo, E.C., Davenport, L.B., Dattis, K.C., Busam, D.A., Buller, H., Doyle, E., Davense, M., Dugan, Rocha, S., Dunkov, B.C., Cherriach, C.G., Ferriera, S., Fleischmann, W., Fosler, C., Gaptelian, A.E., Garg, N.S., Gelbart, M.M., Glasser, K., Glode, M.S., Gorge, J.T., Houthof, K.J., Wolphellian, A.E., Garg, N.S., Kentpen, C.H., Karpen, G.H., Kapter, C., Malshin, M., Marphy, L., Mellin, M., Katpen, C., Liu, X., Mattei, B., McIntosh, T. Li, Z., Lidan, Y., Liu, X., Mattei, B., McIntosh, T. Li, Z., Lidan, Y., Liu, X., Mattei, B., McIntosh, T. Li, J., Moshreil, A., McEson, D.R., Merkel, B., McInton, K., Nukon, K., Nusoko, M., Supoki, M., Palazolo, M., Palazolo, M., Palazolo, M., Palazolo, M., Shep, C., Siden Kiamos, I. Stapleton, M., Skupski, M.P., Nather, S., Simpson, M., Skupski, M.P., Nather, S., Shen, L., Scheeler, W., Ressen, M., Stun, R., Shen, R., Wester, J., Sc
                                                          INV 05-OCT-2000
Drosophila melanogaster genomic scaffold 142000013386035 section 7 of 105, complete sequence.
AR003882 AE002708
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
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complement(join(235. .1324,1643. .2221,2355. .2417))
/gene="D1"
                                                                                                                                                                                                                                                                                                                        Pterygota;
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On Oct 9, 2000 this sequence version replaced gi:7299142.
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygc
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chromosome="3R"
                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="FLYBASE:FBan0009745"
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1. .224400
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                                                                                                                                                                                      AE003682.2 GI:10726402
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Drosophila melanogaster
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JOURNAL
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JOURNAL
MEDLINE
PUBMED
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AUTHORS
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AUTHORS
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.10588,10978. .11126,12073. .12352,12809. .13132,

oin(9827.

CDS

24193 CATCATCCTGTGGTTCATGGTCGTCTTCGGACTGTCTCTGCTG 24235

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Botrytis cinerea strain T4 cDNA library under conditions of AL116666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr) The cDNA library to be analyzed within the framework of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT 26-APR-1993
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 1700)
22cto, W.W., Nixon, B.T., Ronson, C.W. and Ausubel, F.W.
Identification and characterization of the Rhizobium meliloti ntrogene: R. meliloti has separate regulatory pathways for activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1542 GAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCTCGCGCTATTCAGGC 1601
                                                                                                                                                                                                                                                                                                                                                                                        St Cyr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 GGCTGAACCAACTGCCGATGCAACAAAGACCGATGCAGCTGCTGCTGCTACTGCAAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                           Pezizomycotina; Leotiomycetes;
                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Solerotiniaceae; Botryotinia.
1 (bases 1 to 720)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-SEP-1999) Phytopathologie, INRA, 78026 Versailles, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Botryotinia fuckeliana"
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                                                                                                                                                                                                      cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
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/db_xref="taxon:40559"
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ilarity 57.8%;
Conservative (
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M15810.1
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TITLE
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CNS01DBA
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VLPPFLEHIHVLMDHFSNSELADALYEKSGVNKIMKGFKGSDGKLDYDKLFESLNNQS
FRRRWIKSATLYLADWASYLANPEVYLRYFQTAQIMFNGLLKSQGYPKQTHFDPSRPG
                                                                                                                                                                                                                                                                                                              ETISNLLDHVAKHHLNVKIDSRQYVKPAVGŸAKĒLLKLGQARGLLQFNĀTEISDKLTD
TLNLEVIEPVLKVHRAYRYISKSPQCDRYVLCQLNAAALDQOEKQROHDQYQQQLNRPTSASSLIAGVSPKIVKIGSMGAAIFISTEGTPFWTLFGVINAPYNCEAKY
PVDCNNFPEGBAKYTEXIHNRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF54344.1"
/db_xref="G1:7299146"
/db_xref="FLYBASE:FBan0016733"
/db_xref="FLYBASE:FBgn0037665"
/db_xref="FLYBASE:FBgn0037665"
/translation="MQLIYRELEEDILRRTNAVFPVQNCFVEVLPDQFIIPRKYVELG
                                                                                                                                                                                                    NQNGGNNGGGGAGLAGVASLIGTFMQASGKSGGAGGGGGGGGGAMQILSGLGSLLSKS
QGGQSGGFDPSIIGNVLEMFTQGDDEEATPQQKRSNGGGSESGIGLDTILQVASAFMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESIRSLPVYQDDVWMVSYPRTGSTWAQEMVWLLGHQLDYVAAEQDLRLRSPLIELSAL
FSIDHHETVAQKFGNTVDLVRNLPRPRFARSHLPWPLLPEQFETVKPRIVYTARNPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCVSYYHYFKLLHGMNGDFEQFVDLFLEGHTPMGSYMRHVLPFWKRSQDDNVLFIKYE
DMVKDLPSVVRRCARFLGVQSLLDVSTLQKLCDHLTFDKMRANKAVNLEKLLPESSSK
FIRNGKIGDWRNHMGNEMSERFDEWTERHMRGSGLNFDYV"
                                                                                                                                                                               /translation="MYVRRALLEACLECLOPLGPSMASEDESNPLLDMASMFFQEALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24073 CCAGACCACGGAGAAGGACGTGGCAGCATCGCGTGCCAAGCGTGATACCATTGCCGCTTC 24132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCG 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1590 CGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLYBASE:FBgn0037666"
join(<16163. .16213,16307. .16490,16637. .>16836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBan0016735"
/db_xref="FLYBASE:FBgn0037666"
join(16163. .16213,16307. .16490,16637. .16836)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FLYBASE:FBgn0037665"
join(14006. .14358,14503. .>15118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="FLYBASE:FBan0016733"
/db_xref="FLYBASE:FBan0037665"
join(14024. .14358,14503. .15118)
/gene="CG16733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 113;
                                                                                       /protein_id="AAF54343.1"
/db_xref="G1.7299143"
/db_xref="FLYBASE:FBan0008420"
/db_xref="FLYBASE:FBgn0037664"
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                                              /note="CG8420 gene product"
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/map="85D2-85D4"
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13366. .13446)
/gene="CG8420"
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                                                                  /codon_start=1
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Best Local Similarity
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/gene="acpD OR SMc01329"
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                                             AUTHORS
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                                                                     TITLE
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Rhizobiaceae: Sinorhizobium.
1 (bases 1 to 32910)
2 Capela.D., Barloy-Hulber,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J., Boistard,P., Becker,A., Boutry,M.; Cadieu,E., Dreano,S., Gloux,S., Godie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D., Pohl,T., Portetalle,D., Puehler,A., Purnelle,B., Ramsperger,U., Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F. Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021
L Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
D 11481430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQTRSTGREEQAEGGTLFLDEIGDMMDAQFRLLRVLQQGETTVGGFRPIRSDVRIV
AATKDLKOS INOGLFREDLY YRLWYPLRLPPLRDRAED IPDLVRHFVQQAEKEGLD
VARPDGAELELMKAHPWFORV RELENIV RRLTALYPODVITREI IENELRSEIPDSPI
EKAAARSGELSI SOWYEBNNRQY FASFGDALPPSGLYDRVLAEMEYPLILLAALTATRG
NQIRAADLGLNRNTLRKKI RELGVSVYRSLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="MGGAIILVADDDAAIRTVLNQALSRAGYDVRITSNAATLWRWIA
AGGGLUVYTDVVWPDENAFDLLPRIKKARPDLPVLVWSAQNTFWTAIKASEKGAYDYL
PKPFDLTELIGIIGRALAEPKRRPSKLEDDSQDGMPLVGRSAAWQEIYRVLARLMQTD
LTLMITGESGTGKELVARALHDYGKRRNGPFVAINMAAIPRDLIESELFGHEKGAFTG
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                                                                                                                                                                                                                                                                                                                      /translation="EFCVHDNGPGVPPDLLPHLFDPFITTKTNGSGLGLALVAKIIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1654 GCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATG 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1714 CGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTAT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741 ATGATCACCGGCGGGCACCGCCAAGGAACTCGTTGCCCGTGCACTGT 800
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AL591787 AL591688
AL591787.1 GI:15074266
of nitrogen fixation genes in free-living and symbiotic cells J. Bacteriol. 169 (4), 1423-1432 (1987) 87165745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9%; Score 41; DB 1; Length 1700; 55.2%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                              HGGIVECDSQHSRTTFRVLMPASKGLAADEETPMTKGTNG
                                                                                                                                                 /organism="Sinorhizobium meliloti"
/db_xref="taxon:382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                              /transl_table=11
/protein_id="AAA26345.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA26346.1"
/db_xref="G1:152393"
                                                                                                                                                                                                                                                                                                /db_xref="GI:152392"
                                                                                                          Location/Qualifiers
1. .1700
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/transl_table=11
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Sinorhizobium meliloti
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                                                                                                                                    source
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ACCESSION
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PUBMED
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SME591787
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KEYWORDS
SOURCE
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                                                                                           PUBMED
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                                                                   MEDLINE
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ERWYRRGDEEVGNRQFVVADPDGYLLRFYEPLGRRPRTS"
Gouzy,J.
Direct Submission
Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
                                                                                                                                                                                        Plantes Microorganismes, UMR215-CNRA, BP27, F-31326 Castanet, France, Laboratoire de Genetique et Developpement UMR6061-CNRS, Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes, Oniversitaet Bielefeld, Biologie IV (Genetik) Universitaet Bielefeld, Biologie IV (Genetik) Universitaet Bielefeld, Unit dermany, Unit de de Biochimie physiologique, Universitae Catholique de Louvain, Place Croix du Sud 2, Be 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, http://sequence.toulouse.inra.fr/meliloti.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPMLADILPAFHRRYPGVRLLITASNRRIDLIEERIDVALRARDQLDTDSQLIVRKFG
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GLLPATRALIDFLAENLIKALERCREVDPRPAASFEI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="codon recognized: ACA; predicted by tRNAscan-SE"
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complement(373. 798)
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/gene="SMc01330"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CONSERVED HYPOTHETICAL PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Product confidence : hypothetical
Gene name confidence : hypothetical
predicted by Homology"
                                                                                                                                                                  Laboratoire de Biologie Moleculaire des Relations
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Gene name confidence : hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAC45913.1"
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predicted by Homology
predicted by FrameD"
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/gene="SMc01330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(373. .798)
/gene="SMc04435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="1021"
/db_xref="taxon:382"
152. .227
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/product="tRNA-Thr"
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AADGPMPQTREHILLARQVGVPAIVVFLNKVDQVDDAELLELVELEVRELLSSYEFPG
DDIPIVKGSALAALEDSDKKIGEDAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSI
SGRGTVVTGRVERGIVKVGEEIEIVGIRPTTKTTCTGVEMFRKLLDQGQAGDNIGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAITKYFGEFKAYDQ
IDAAPEEKARGITISTAHVEYETPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGVDRNGVERGQILCKPGSVKPHRKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTD
VTGIVTLPEGTEMVMPGDNVTVDVELIVPIAMEEKLRFAIREGGRTVGAGIVASIVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 117556 ATGATCACCGGCGAGTCCGGCAAGGAACTCGTTGCCCGTGCACTGCACGACTAT 117615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G.; Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
                                                                  GGA; predicted by tRNAscan-SE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1654 GCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATG 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 1714 CGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTAT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                              /function="macromolecule metabolism; macromolecule synthesis, modification; proteins and peptides - translation and modification"
/note="Product confidence: probable Gene name confidence: probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Profable ELONGATION FACTOR TU PROTEIN"
/protein_id="CAC45918.1"
/db_xref="G1:15074272"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental/transl_table=11
                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:0925Y6"
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                                                                                                                                                                                                                                                                                                                                         predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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4602, .5777
                                                                                                                                                                                          /gene="tufB OR SMc01326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tRNA-GLY_TCC"
/product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 1774 CATACGACAGGCAAGGGCGTATTGG 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SMC01325"
6125. .6790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11694876
2 (bases 1 to 125020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 80;
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ACCESSION
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MEDLINE
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REFERENCE
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AF429315
trna
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SOURCE
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                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="Sptrembl:092016"
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LKAWIDRLAVAGKTFRYTEAGPEGLAKGKKLIVASTRGGHYSVAPASAMDHQETYLRS
                                                                                                                                                                                                                                                                                        /product="PROBABLE ACYL CARRIER PROTEIN PHOSPHODIESTERASE"
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/note="Product confidence : hypothetical
Gene name confidence : hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="PUTaTIVE TRNA/RRNA METHYLTRANSFERASE PROTEIN"
                                           /function="small molecule metabolism; fatty acid biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFGFFGITDIEFIRAEGLNLGPDQKQFAIAEAEKTIAEGNVLKLAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="HYPOTHETICAL TRANSMEMBRANE PROTEIN"
                                                                                      /note="Product confidence : probable
Gene name confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Product confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology
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                                                                                                                                                                                                                                          /evidence=not_experimental
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                                                                                                                                         predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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predicted by FrameD"
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1063. .2683
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                                                                                                                                                                                                                                                                                                          /protein_id="CAC45915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="tRNA-GLY_TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="tRNA-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2/92. 3076
/gene="SMC01328"
2792. 3076
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/gene="SMc01328"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission
Submitted (OS-CCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17437 WWGKSAMYRMRRWWKGRGAMMCKYSRMSRCMMMKKSYCASCRSCAMSGTYMKGASY 17496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17023 KCYMSSYWTMSASYWSRRSYWKRSMKCWSRMCSRSRSSKCKSRGCGGSMGKGKGGKSYGR 17082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17143 SYCYAKCKSMCYSCYYGMSMKGYYYACSYRGSMSSKYCMRGSTYSTSCGCCCTTTTTCCC 17202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17259 CTKYKSSMTMSMASYCWCMSMYYCSMRSMASRGMSWSSYMKMMKSSWRMSCYMKCCWCMK 17318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17379 WSRCWGSMWGSASRSSCYKCYK--SMRCSMMSSKCYRCAGCMMWKGGYMRYMRCWSMKRR 17436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17319 MCYCMMRSMRSRGMSYYMYASWKSSSRGCYCTRCYWCMSSKSCYKSYYMMMRSKRMKGMK 17378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCAT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 TCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGGGTAGCCAAAGCCGACAAAGGCATGTG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 TITCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="16q24.3; between D16S520 and WI-12410"
//note="lagolated from a patient with Huntington's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4254 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 40.4; DB 9; Length 1 llarity 9.7%; Pred. No. 33; Conservative 349; Mismatches 379; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane and endoplasmic reticulum"
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                                                                                                                                                                                                                                                                                                                                                                        complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                /rpt_unit=ctg
complement(<36507. ,>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                      /product="junctophilin"3"
complement(<36507, .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                                                                                 Disease-Like 2 (HDL2)"
complement(35581. .35746)
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                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="JPH3"
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Best Local Simmatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Losada,A., Hirano,M. and Hirano,T. Identification of Xenopus SMC protein complexes required for sister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISFVLGEKTSNLRVKTLRDLIHGAPVGKPAANRAFVSMVYSEDSGEEKVFSRVIVGGS
SEYKINNKVVQLSEYSDSLEKLGILIKARNFLVFQGAVESIAMKNPKERTALFEEISR
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AQIQLQLFKLYHNESEIEKLNKELSVKNKGIEKDKKHMDKVEEELKDKKKELGKMMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>OQAIEKEIKEKDAELNOKLPOYIKAKENPSHKIKKFRAAKKSLQNAQKQYKKRRADMD</u>
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EQKNLEETLTEEVEMAKRRIDEINSELNQVMEQI,GDARIDRQESSRQQRKAEIMESIK
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ARRIAFGGHQRHKTVALDGTLFQKSGVISGGASDLKAKARRWDEKAVDKIKEKKERLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EELKEQMKAKRKEAELROVOSOAHGLOMRLKYSOSDLEQTKTRHLAMNMOEKSKLESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRT 18-JUL-1998
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Losada,A., Hirano,M. and Hirano,T.
Losada,A., Hirano,M. and Spring Hirano,T.
Submitted (03-MAR-1998) Cold Spring Harbor Laboratory, 1 Bungtown
Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                             17497 MCMSSYWCTCWCTSYMSYYRCTCWCKGWSSYTKSKSWSSSMSSYKKGRRKSYSMCCTSRG 17556
                                                                                                17557 AMSCWRRCCYMRGASSMRAGSMSRRRAKGRSWGGRSKWWMTGGWWRSKYYYYCTGRRMM 17616
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17737 KRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCYSSUSCTSMYRCCWGGMKS 17796
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                                                                                                                                                                                                                                                                                            CCGCGTGTATGCCGGTGCCGACAACCGGCCGGAGAATACAGCAAGGACAATAAACCTA 746
                                                                                                                                                                                                                                                                                                                                                                                                         747 TAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACGACTATGCCAT 806
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Xenopus laevis 14S cohesin SMC1 subunit mRNA, complete cds.
AF051784
                                                                                                                                                                      627 GTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATT
                                                                                                                                                                                                                               17617 TYMCCCWRRRSYMYYRSMSAMGMRKSSWSGMRMMGSASSRRCKSASRSSWCSRRMKGMRG
                                                         567 CGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         807 GACCATCGGTTTCCCGGGCAGTACGGATCGCTA 839
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TITLE
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PUBMED
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SOURCE
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soon as it is available and the accession number will

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                                                                    LESYRDK FØET SDEFEAARKRAKAAKOAF EQTRKRERFDRFNACFESVAT NIDEIYKAL
SYROSAQAFELGDENPERPYLDGINTWOVAPGKRERPMINLSGGEKTVAALALLFAIHS
SKRSPFFVLDEIDAALDNTAIGKVANTIKEQSMSNFQAIVISLKEEFYTKAESLIGVY
PEQGDCVISKVLTFDLIKYPDANPND"
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 21-MAY-2002
                          IETKLEQKRSDRHNLLQACKMSDIKLPLSKGTMDDISQEEGSSQGEESASSSQRSSTV
YAKEALIEIDYSDLSEDLKDAVADDDIKQEMSALHQKINEQQSILQRISAPNMKAMEK
<u> QRHMKIIDETMAQLQDLKNQHLAKKSEVNDKNHLMEDIRKKLGSANKEVTHLQKEVTA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 202306)
I (bases 1 to 202306)
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 GAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCT 458
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC121850 202306 bp DNA linear HTG 21-N
Mus musculus chromosome UNK clone RP24-92E18, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                          916 GAAGCATATGGACAAGGTGGAGGAAGAGCTCAAGGACAAGAAGAAGAGTTGGGGAAGAT
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* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Insert size: 172000; agarose-fp
Insert size: 201306; sum-of-contigs
Insert size: 201306; sum-of-contigs
Quality coverage: 21.02 in 020 bases; sum-of-contigs
Quality coverage: 11.20 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                        Length 4314;
                                                                                                                                                                                                                                                                                                        50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASEL; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
Mus musculus
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Pred. No. 28;
0; Mismatches 5
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McPherson, J.D. and Waterston, R.H.
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ilarity 58.3%;
Conservative
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Best Local Similarity
Matches 70; Conserv
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AUTHORS
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KEYWORDS
SOURCE
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LOCUS
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COMMENT

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Db 147941 GTACCCTTCAACTCTGACAATAGTATGTATCTTCATATGGTGGTGGGGGTTGGCCATCTTA 148000
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contig of 5169 bp in length
app of unknown length
contig of 49909 bp in length
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45;
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44381 c 43982 g 57115 t
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1207. .2283
/note="assembly_name:Contig28"
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/note="assembly_name:Contig34"
5531. .6547
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21676, .43695
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/note="assembly_name:Contig39"
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/note="assembly_name:Contig40"
145564. .202306
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/note="assembly_name:Contig35"
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/note="assembly_name:Contig36
                        contig of 1106 b
gap of unknown l
contig of unknown l
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contig of 1279 b
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of 2145
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Llarity 52.4%; Pred. No. 45;
Conservative 0; Mismatches
                                                                                                                                     contig of 1017
gap of unknown
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/chromosome="UNK"
/clone="RP24-92E18"
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Search completed: May 23, 2003, 05:02:07 Job time : 5341 secs

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Travis J, Potempa JS, Banbula A, Bugno M;
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P. pantotrophus GB
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14730.961 Million cell updates/sec
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16-MAY-2002

Merozoite surface		C.	Human kidney disea	Human polynucleoti	Human kidney-speci	Human polynucleoti	C glutamicum codin	Mouse secreted exp	Mouse neuropeptide	NPY6-R gene. Mus	C glutamicum codin	Corn tassel-derive	Human immune/haema	Human immune/haema	Human immune/haema	DNA encoding a hum	Yeast AOD9604-asso	Arabidopsis cDNA e	DNA encoding novel	Fusarium venenatum	Streptococcus poly	Stealth virus nucl	Aspergillus oryzae	M. capsulatus gene		Drosophila melanog	. Drosophila melanog	Listeria innocua c	Sequence encoding	Drosophila melanog	Neisseria meningit	Polymerase gene.	. Thermococcus litor	T. litoralis DNA p
AAC68978	AAU01671	AAF86431	AAC66137	AAI58976	AAZ35391	AA160762	AAH67046	AAA43983	AAT36127	AAI72369	AAH68530	ABL71482	AAK81576	AAK81577	AAK81578	AAV68139	AAH24065	ABK65331	AAS85131	AAF08951	ABN68375	AAX84332	AAF13795	ABQ90235	ABL16623	ABL16622	ABL09568	1 ABQ67197	AAN70566	ABL06895	AAS97214	AAQ14461	AAQ43966	AAQ43515
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1.7		1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
37	ָר אַר מילי	30.0	36.4	36.4	36.4	36.4	36.2	36.2	36.2	36.2	36.2	36	35.6	35.6	35.6	35.2	35.2	35	35	34.8	34.8	34.8	34.6	4	4.	4.	4	34.4	4.	34	34	34	34	34
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Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence. Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis. Location/Qualifiers
1.2139
/*ta.a a //ta.a a //to.a (UYGE-) UNIV GEORGIA RES FOUND INC. 08-NOV-2000; 2000US-246827P. 08-NOV-2001; 2001WO-US46782 (first entry) Porphyromonas gingivalis. WO200238742-A2 05-SEP-2002

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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalise dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protect and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontilis). The present DNA sequence encodes the Porphyromonas of isolated dipeptidylpeptidase useful for identifying inhibitor dipeptidylpeptidase for protecting an animal from periodontal ase caused by Porphyromonas gingivalis or periodontitis). The present DNA sequence encodes the Porphyror gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention Claim 11; Fig 4; 65pp; English 2002-490075/52 AA015205 P-PSDB; disease Novel the

Sequence 2139 BP; 544 A; 543 C; 565 G; 487 T; 0 other;

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240 300 540 120 120 300 360 360 420 420 480 480 099 Gaps 9 9 TATTCCAACAACAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA 1 ATGCAAATGAAATTAAAAAGTATTCTTCTCGGAGCAGCCCTGCTGGTTGGGTGCTTCAGGG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT TATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCCAAAGCTCAGGAGGTATGC CAAGAACTGGCCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTC CAAGAACTGGCCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTTC TTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCG DB 24; Length 2139 ö Indels . 0 Mismatches 100.0%; Score 2139; 100.0%; Pred. No. 0; ; Best Local Similarity 100. Matches 2139; Conservative Query Match 121 121 181 181 241 241 301 301 361 361 421 421 481 481 541 541 601 601 a ò 8 QQ a a g QQ ολ g ò QQ ò g õ ô ò ò ò

1140 1260 CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080 CGCGGTCTCGCTCGTTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080 TATGCAGACTTCGTATTCGACAAGAGTGTGCTTCCTTATAGCGACAAGTTCCATGCCATG 1500 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCCAAGGGCGTATTGGAG 1800 960 GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC AAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAAC GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA AAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTC TTCGGTGGTACCGAGGTGGTTCGTTTTGCACGTTTGCCAACGCATTGGCTACAAATCCT GATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCG CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG TATGCAGACTTCGTATTCGACAAGAGTGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA CGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGA GGCTACAAGGCTGACGACTATGCCATGACCATTGGTTTCCCGGGCAGTACGGATCGCTAC CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC 1021 1081 1081 1141 1201 1261 1381 1441 1501 1681 1741 961 1021 1141 1201 1261 1321 1321 1381 1441 1501 1561 1561 1621 1621 1681 199 661 721 721 781 781 901 901 961 Db Op Dp Db Db Óγ ŏ Db ò οy Db οχ Q qq QQ Dp ò q ŏ g ò g ò g ò g δ g δ ŏ Ω ò δy pp δ ò

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1741 TATGAACCGCAGGACGGTGCCTGGTACAATCATACGACAGGCGAAGGCGTATTGGAG 1800
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                                                                                       1861 ACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAAC
                                                                                                                                                                                                        1981 GGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGAT
                                                                                                                                                                                                                                             CTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTTCTTCATGATTGACAAATGGGGGT
                                     1801 AAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 36749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                   1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                                                                                         1530 CAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589
                                                                                                                                                                                                                     711 GGCGGCTATCAGCCGCCTGCTTGCTGCCTCCCAGAGTCCAGGCGACTCGGTTCTTTTTTT 770
                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                                                                                                1590 CGCTATTCAGGCCGATGCGATGCCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signalling and cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 36746.
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                                                                                                                                                Indels
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sequences (ABL01840-ABL16175) and the encoded proteins
(ABB57737-ABB72072).
                                                                        Sequence 1147 BP; 257 A; 335 C; 303 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                      1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                       2256 CCAGACCACGGAGAAGGACGTGGCAGCATCGCGTGCCAAGCGTGATACCATTGCCGCTTC 2315
                                                                                                                                                            1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                             2196 GGCCGCTATCAGCCGCCTGCTTGCTGCCTCCCAGAAGTCCAGCGACTCGGTTCTGTTTGT 2255
                                                                                                                                                                                                                                                                                                                                           2316 CACCACCAATCCCTACAACCTGGCCGTCTACTACGGCAGCGACTACCCGGTGATCTTCAA 2375
                                                                                                                            Gaps
                                                                                                                                                                                                                                 1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG
                                                                                                                                                                                                                                                                                                          1590 CGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide
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                                                                                         Length 3632;
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                                                                                       Score 42.2; DB 23; Length
Pred. No. 0.2;
0; Mismatches 113; Indels
                                                  Sequence 3632 BP; 1062 A; 799 C; 773 G; 998 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                              1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
                                                                                                                                                                                                                                                                                                                                                                                                              CATCATCCTGTGGTTCATGGTCGTCTTCGGACTGTCTCTGCTG 2418
                at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL21554 standard; DNA; 2868
                                                                                     Query Match 2.0%;
Best Local Similarity 49.3%;
Matches 110; Conservative
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2000US-0614150.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                    1494 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGC 1553
                                                                                                                                                                 1554 AGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCGCGCTATTCAGGCCGATGCGATGGC 1613
                                                                                                                                                                                                                           CAATGCCTATGCCATTGAGAAGGGCCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTA 1673
                                                                                                                                                                                           AGCATCGCGTGCCAAGCGTGATACCATTGCCGCTTCCACCACCAATCCCTACAACCTGGC 129
                                                                                                                                                                                                                                                       CGTCTACTACGGCAGCGACTACCCGGTGATCTTCAACATCATCCTGTGGTTCATGGTCGT 189
                                                                         Gaps
                                                                                                                      developmental biology; cell signalling; insecticide;
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                                        Length 2868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 7432
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                                                                         Indels
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              C; 624 G; 850 T; 0 other;
                                          DB 23;
                                                                       66;
                                                                         Mismatches
                                          Score 40.6;
Pred, No. 0.
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                                                                                                                                                                                                                                                                                   CCCCGGACGTGCTCTGCCG 1692
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              Sequence 2868 BP; 737 A; 657
                                                                                                                                                                                                                                                                                                                                                                                          ABL18653 standard; DNA; 4013
                                                                                                                                                                                                                                                                                                       190 CTTCGGACTGTCTCTGCTG 208
                                          1.9%;
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2000US-0614150.
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                                        Query Match
Best Local Similarity
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                                                                      Matches 100;
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Query Match
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sulphur; thiosulphate; transgenic plant; transgenic animal; ds.
                                                                                                          1473
                                      1294 GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGAT 1353
                                                                       1354 ATTGTACGCCGCCTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGAC 1413
                                                                                                                                          1474 CCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAG 1533
                                                                                 282 ATGGGTCAGACGCTTGTGGCCTACGACAACCGGCGGACCATCCACGGCAGTAACATCCAT 341
                                                       222 GACAATAATACGGAGTGGCTCATTTGGATGGTCGGTAATATTCCGGGCTGCCGATGTCGCC 281
                                                                                                                   342 CGAATCGTCTTCTGGCCTTCAAGCAGTATCTGGAGCTTGGATTTCGACGAGACTTTCGTT 401
                       Gaps
                                                                                                        1414 AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT
                                                                                                                                                        402 CCCGAGGCGAGGAAAAGGATGACGAGGACTTCACCTCGTCGCTGGGTACGATGCAGAT
                       0
       Length 4013;
                                                                                                                                                                                                                                                                                       P. pantotrophus GB17 DNA encoding ORF2, ORF3 and soxXYZA.
                       Indels
                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos:643..645,aa:Leu)
    Score 38.8; DB 23;
Pred. No. 2.1;
0; Mismatches 132;
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/product= "soxx"
1941..2363
      1.8%;
     Query Match 1.8
Best Local Similarity 47.2
Matches 118; Conservative
                                                                                                                                                                           1534 GCTATCGAGA 1543
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                                                                                                                                                                                                         This invention describes novel genes (I) of the sox (sulphur oxidation) region designated ORF1, ORF2, ORF3 (Open Reading Frame), and soxXXZA from Paracoccus pantotrophus GB17. The proteins (II) encoded by (I) are used for oxidation of reduced sulphur compounds in cellular or cell.-free systems, particularly of thiosulphate to sulphate. (I) is also used for expression of the proteins and to prepare transpenic plants or animals. Or transformed microorganisms. This sequence encodes the ORF2, ORF3 and the soxXXZA proteins from the P. pantotropus sox region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; sox; ORF1; ORF2; ORF3; soxX; soxY; soxZ; soxA; thiosulphate; transgenic plant; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGCGGCCGTGCGGTCTTGGTCACGACCGGTCCCGTTGTCGTTTCGATGACC 2847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1847 TCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCG 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3026 TCGAGGCCGCGATCCACGAAGACCATGGCGGGGTTGTCGAAATCGTCCGCTCAAGATC 2967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGA 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
WPI; 2001-497622/55.
P-PSDB; AAB86529, AAB86530, AAB86531, AAB86532, AAB86534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGGCCGTCTGATCGGTCTTCGATGGCAACTGGGAAGCTATGACTGCATCG
                                                                   New genes involved in oxidation of reduced sulphur compounds, particularly conversion of thiosulphate to sulphate, and related proteins, from Paracoccus pantotrophus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes involved in oxidation of reduced sulphur compounds, particularly conversion of thiosulphate to sulphate, and related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3621 BP; 650 A; 1153 C; 1186 G; 632 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 38.6; DB 22; 48.8%; Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTCGAACCCGATCTGCAGCGCACAATCAGCG 2059
                                                                                                                                                               Claim 1; Page 10-14; 22pp; German
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Matches 104; Conservative
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Indels

Length 10757;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                           1343 CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGA 1402
               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ0511), expressed DNA sequences (ABLJ6175) and the encoded proteins (ABB7737-ABB72072).
                                                                                                                                                                                                                                                                                              1403 ATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                          6826 AAGTAAAAACAAAAATTTCAATCAAACTCCATGAATTATGCACACTTTCTGTTTGCCA
                                                                                                                                                                                                                                                                                                                                                                          GT---GACTTTATCATCGCCAGGGTGACGACGCCGATAACTTTTATGTTATTGAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                             Sequence 10757 BP; 3125 A; 2268 C; 2226 G; 3138 T; 0 other;
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                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                          1.8%; Score 37.8;
54.1%; Pred. No. 7;
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2000US-0614150.
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                                                                                                                                                                                                          Query Match 1.85
Best Local Similarity 54.1;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1463 AGAGT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6886 AAAGT 6890
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                                                          This invention describes novel genes (I) of the sox (sulphur oxidation) region designated ORF1, ORF3 (Open Reading Frame), and soxXXZA from Paracoccus pantotrophus GB17. The proteins (II) encoded by (I) are used for oxidation of reduced sulphur compounds in cellular or cell.-free systems, particularly of thiosulphate to sulphate. (I) is also used for expression of the proteins and to prepare transgenic plants or animals or transformed microorganisms. This sequence encodes the P. pantotropus sox region associated proteins described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or more cell-cell
                                                                                                                                                                                                                                                                                                          1847 TCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCG 1906
                                                                                                                                                                                                                                                                                                                               1907 CTTTCCTATCGAACAACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGA 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4133 AAGGCGGCGCGCTCTTGGTCACGATCTCGACCGGTCCGCTTCGGTTTCGATGACC 4074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
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and cell
                                                                                                                                                                                                                                                                                                                                                                                                        4193 CGCGTGCTGTCGTCGCGAAAGTGCCAGCCGGAATAGATCGTGTCGAACGTATCGGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                      1967 ACGCCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster genomic polynucleotide SEQ ID NO 15907
                                                                                                                                                                                                                            DB 22; Length 4848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 15907; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                                                           Sequence 4848 BP; 885 A; 1584 C; 1552 G; 827 T; 0 other;
                                                                                                                                                                                                                                          Score 38.6; DB 22;
Pred. No. 2.7;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2027 AGTICGAACCCGAICTGCAGCGCACAATCAGCG 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4073 AGCCCGTCCTCGACCGGGTCCGCGAAGGCCGCG 4041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EW;
 proteins, from Paracoccus pantotrophus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL21478 standard; DNA; 10757 BP
                                                                                                                                                                                                                                          1.8%;
                               Fig 1; 22pp; German
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2000US-0614150.
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                                                                                                                                                                                                                                                          Local Similarity
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11-JUL-2000;
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27-FEB-2001
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AAC68976
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                                                                                                                                                           GACAAGTACAAAGACTACCTCCCCTCGCTCGACCGTAAGGTGCTGCCGGCCATGCTCGAT 1353
                                                                                                                                                                               8624 GACAATAATACGGAGTGGCTCATTTGGATGGTCGGTAATATTCCGGGCTGCGATGTCGCC 8565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic
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                                                                                                                                       Gaps
cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                         (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uthaipibull
                                                                                                                                                                                                                                                      1354 ATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGAC
                                                                                                                                                                                                                       8564 ATGGGTCAGACGCTTGTGGCCTACGACAACCGGCGGACCATCCACGGCAGTAACATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                            1414 AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT
                                                                                                                                      0;
                                                                                                                   Length 9845;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Merozoite surface protein; protazoacide; vaccine; malaria; ss.
                                                                                             Sequence 9845 BP; 2751 A; 2130 C; 2204 G; 2760 T; 0 other;
                                                                                                                                     96; Indels
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                                                                                                              Score 37.4; DB 23;
Pred. No. 8.8;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                        Merozoite surface protein-133 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-0009072.
99US-0311817.
99CA-2271451.
                                                                                                                  1.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-GB01558
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                     95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                    1474 CCTTATAGCGA 1484
                                                                                                                                                                                                                                                                                                        8444 CCCGAGGGCGA 8434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birdsall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-015762/02.
                                                                                                                            Similarity
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25-MAY-1999;
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                                                                                                                  Query Match
Best Local (
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cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2. Compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-133
                                                                                                                                                                                                                                                                                                                                                                                                              1377 CGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 CGTTAACGTCAAGGACATTTTGAACTCCAGATTCAACAAGAGAGAAAACTTCAAGAAGGT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TCTGGAGTCTGATTCCATACAAGGATTTGACTTCTTCTAACTACGTTGTTAAGGA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGC
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                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merozoite surface protein; protazoacide; vaccine; malaria; ss.
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                          Sequence 786 BP; 245 A; 164 C; 159 G; 218 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Syed
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1497 CATGCTCAAGTCCATGGACAAGGAAAGTTTGCCAAG 1533
                                                                                                                                                                                                                                                                                 Score 37; DB 22;
Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merozoite surface protein-142 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface protein-1, useful as vaccines for malaria
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99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                    1.7%;
52.2%;
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.23
Matches 82; Conservative
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                                                                                                                                                                coding sequence.
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25-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                1377 CGACAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                    1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGC 1496
                                                                                                         135 CGTTAACGTCAAGGACATTTTGAACTCCAGATTCAACAAGAGAAAACTTCAAGAACGT 194
                                                                                                                                                                195 TCTGGAGTCTGACTTGATTCCATACAAGGATTTGACTTCTTCTAACTACGTTGTTAAGGA 254
                                                                                                                                                                                                                                                                                                                                                                                                      detection;
                                                                                                                                                                                                                                                                                                                                                                                                Species specific, genus specific, family specific; probe; detection identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boissinot M, Huletsky A, Menard C, Ouellette M;
                                                       ;
0
                            Length 1077;
                                                    75; Indels
Sequence 1077 BP; 338 A; 228 C; 225 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Fonsecaea pedrosoi nucleotide sequence SEQ ID NO:1664
                           Score 37; DB 22;
Pred. No. 3.6;
                                                                                                                                                                                         1497 CATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAG 1533
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Page 1264-1265; 1580pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC
                                                                                                                                                                                                                                                                                      AAH01671 standard; DNA; 810 BP
                           1.78;
52.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000; 2000WO-CA01150.
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19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-245006/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; primer; ds
                                     1 Similarity
82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fonsecaea pedrosoi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200123604-A2.
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                                                                                                                                                                                                                                                                                                                                             24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Picard FJ,
                                                                                                                                                                                                                                                                                                                    AAH01671;
                           Query Match
                                          Local
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                                                      Matches
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least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonada group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 TTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 TGCCGFGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGAT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 TGGCGATGTCACGCTCGGGGGTCCCAGGTGTCGACGTGCTCGAGGAGCTCGTCAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 CTTTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 CGACGAGCTCCAACATCTCCTTGTCCTCAATGGCATCGACCTTGTTGACGAAGACGACAA
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 810 BP; 167 A; 254 C; 228 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thierry JC, Prieur D, Dietrich J, I
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%; Score 36.8;
46.2%; Pred. No. 3.
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGCTTGACACCGACCTGGCGGG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 122;
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2000-665116/64.
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                                                                                   The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. the proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. The same patent family as WO200065062, which AAH75903-AAH75902 and AAG66436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nephrotropic; cytostatic; human; kidney disease associated; hypertension; Bartter's syndrome; Gitelman syndrome; nephrolithiasis; renal failure; renal amyloidosis; primary aldosteronism; Addison's disease; cancer; glomerulonephritis; dysplastic malformation; medullary cystic disease; medullary sponge kidney; tubular dysplasia; Alport's syndrome; ds.
                                                                                                                                                                                                                                                                                                                    168164 CGATGAGCTTGAGGATGAAGACTTAAGGAAATCCTGGAGGTGGCTGAAAAGGTTGCAAG 168105
                                                                                                                                                                                                                                                                                                                                                          GGAAAAAGGAGACGTCGAGCTCTTAAAGATGGTAACTTACTATTACGCCGAATTCTTTGG 168045
                                                                                                                                                                                                                                                                                                                                                                                                     1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGC 1496
                                                                                                                                                                                                                                                                                                                                                                                      1497 CATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGT 1556
                                                                                                                                                                                                                                                                                            1377 CGACAAGCTCCCCGATATTTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                                                                                                          Sequence 349980 BP; 95167 A; 78444 C; 78870 G; 97499 T; 0 other;
                                                                                                                                                                                                                                                 Length 349980;
                                nucleotide sequences isolated from Pyrococcus abyssi encode
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                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human kidney disease associated gene SEQ ID 7.
                                                                                                                                                                                                                                                            84;
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                               Score 36.8;
Pred. No. 84
                                                               Claim 1; Page 183-279; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC66137 standard; DNA; 1090 BP.
                                                                                                                                                                                                                                             1.78;
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                                          proteins useful in industry
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                                                                                                                                                                                                                                                                     95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 167984 CCAGCTCGCCGA 167973
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         WPI;
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                                                                                                                                                                                                                                                                                                                                                                 Db 168104
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Polynucleotides AAC66131-C66139 represent human kidney disease associated genes. Proteins AAV85678-Y85680 represent human kidney disease associated proteins. The polynucleotides have nephrotropic and cytostatic activity. The polynucleotides, encoded proteins and pharmaceutical compositions containing renal disorders such as Bartter's syndrome, treating and preventing renal disorders such as Bartter's syndrome, ditelman syndrome, autosomal dominant polycystic kidney disease and nephrolithiasis. The genes and proteins are also useful for identifying biomolecules that are associated with a specific disease, regulatory pathway, subcellular compartment, cell type, tissue type or species, which is useful in diagnosis, prognosis, treatment and evaluation of therapies for renal diseases for e.g. renal amyloidosis, hypertension, primary aldosteronism, Addison's disease, renal failure, clomerulonephritis, chronic glomerulonephritis, tubulointerstitial nephritis, cronic glomerulonephritis, tubulointerstitial nephritis, cronic disease (PRD), medullary cystic disease, medullary cystic disease (PRD), medullary cystic disease, non-renal
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                                                                                         Novel kidney disease associated gene useful for diagnosing treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1674 CCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCAT 1733
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myeloma and nephrotoxic disorders.
                                                                                                                                    preventing renal disorders, is uromodulin, NKCC2, NCCT, aldolase B, ROMK1, ATP1G1, PDZK1, NPT1, calbindin, kininogen or CIC-Kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.4; Di
Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0; Mismatches
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                                                                                                                                                                                                                                                                   Claim 2; Page 33-34; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%;
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P-PSDB; AAY85680
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26-JUL-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                                                                                                                                                                                                                                                      Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1292 BP; 254 A; 422 C; 368 G; 248 T; 0 other;
                                                                                                                                                                                                                                                                      Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                  Tang YT, Liu C, Asundi V, Chen R, Ma Y, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Zhao QA, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1179; 10078pp; English.
                                                                   2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                         2000US-0653450.
2000US-0662191.
2000US-0693036.
                                 26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                               29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM39820
                                                                                                                       19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                   21-JAN-2000;
25-APR-2000;
09-JUL-2000;
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1794 ATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCT 1853 ò q

1674 CCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCAT 1733

ò q ò g

1734 CAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACGGCAAGGGCGT 1793

1854 CTTCCGCACC 1863

519 CTTCCATGCC 528

Search completed: May 23, 2003, 04:52:58 Job time : 958 secs

May 23, 2003, 02:43:56 ; Search time 62 Seconds (without alignments) 10580.348 Million cell updates/sec US-10-008-355-1 2139 1 atgcaaatgaaattaaaaaag.....aagagctgaagttgatctaa 2139 GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Title: Perfect score: Run on:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 scoring table:

Sequence:

882724 Total number of hits satisfying chosen parameters: .441362 seqs, 153338381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2, Appli	3, Appl	2, Appl	17, Appl	-	551, App	3, Appl 3, Appl	1, Appl	4, Appl	8, Appl.	4, Appl	8, Appl	4, Appl						
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-08-459-444-2	US-09-053-549-3	US-09-547-422-2	US-09-007-005-17	US-09-244-796-17	US-08-998-416-551	US-07-951-715A-3	US-08-459-448A-3	US-08-459-595A-3	US-08-459-504B-3	US-08-459-444-3	US-09-547-422-3	US-08-289-653-1	US-07-951-715A-4	US-07-951-715A-8	US-08-459-448A-4	US-08-459-448A-8	US-08-459-595A-4	
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3468	3468	3468	289	289	823	1947	1947	1947	1947	1947	1947	2845	3468	3468	3468	3468	3468	
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	
32.2	32.2		32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	
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1081 TTCCATGCCATGCTCAAGACCATGGACAAGAAAGTTTGCCAAGGCTATCGAGAAAGAT ATGGCCAATGCCTATGCCATTGAGAAGGCCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAG 1847 TCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCG CTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGA AGTICGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTTCTTCATGA ATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGC TCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAG GGCGTATTGGAGAAGCAGGAT - - CCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCC ACGCCCGTCTCATCCGTCTTCCTTTCCATCGCAACTGCGAAGCTATGAGTGCTGACATCG ATCCCTGCCGACAAGCTCCCCGGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGC TTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGAT CCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCG TACCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGT THEREOF USES AND NUCLEOTIDES Sequence 382, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION: APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto STATE: CA 94304-1018 US-09-221-017B-382

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906 TGCTTACAAACGTGCTATAGGTGCCAACTGGGCGATC
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PP154 FILING DATE: 30-JAN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: 23-DEC
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 755 PAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-221-017B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AGTGTCCGATCAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 CCAAAGCACGGTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 CAAGGTAGAAGGACAGCTCAAGGGTATCACTGA-------CGAGATGGAGCGTCT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 CGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 CGTTTCCGATCGCGGACTGGTACTGACCAATCACCACTGCGGATACGATATGATCCAGGC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GAAGTATGCGCAGATGAAAGAGCGCGCGCTTAAGATGAAGGAATACGACCTTTATAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 207.4; DB 4;
Pred. No. 5e-56;
0; Mismatches 421;
                                                    SYSTEM: Windows
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                         27340-20021.00
                                                                                                                                                       PROCR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTONEY/AGENT INFORMATION:
NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                            JABER: US/09/221,0178
23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERY 650-42. TELERY 70614 INFORMATION FOR SEQ ID NO: 382 SEQUENCE CHARACTERISTICS: SEQUENCE : 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 53.1%;
Matches 498; Conservative
                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | NAME/KEY: misc_feature
| LOCATION: 1...1317
| US-09-221-017B-382
                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
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HYPOTHETICAL: NU
THEFT UNKNOWN
                                                   OPERATING SYSTEM:
                                                                                                                        FILING DATE: 2 CLASSIFICATION:
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                                                                     SOFTWARE
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666 GAAGCGTTTCTTCAATATCTCCCTTGGTGAGTACAAGAGAACGACTACGCCATGATAAT 725 632 546 TGCCGATACGGACAACTGGATCTGGCCTCGTCATACTGGCGACTTCTCCATCTTCCGTAT 605 812 726 GGGTTTCCCCGGTACTACGCACCGCTATTTCACGGCTTCCGAAGTAGACGAATGGAAAG 785 426 GGGGCTTTCCGTAGAGATCAAAGCCTTCTATGGGGGCAATCTCTACCTGATGTTTACCAA 485 813 CGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGA 872 933 CATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAA 992 366 GAAGTACCTGCAAAAGTTGGCTGACAAGAAGGCCGGCAAGAACTTTTCTGCCAAGAATCC 425 519 ACTCTGCATCGTAGAG-----CCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTA 573 CGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGG 486 AAAGACTIATATACGGATGTTCGACTGGTGGGACCACCCACCACCACCACTTGGCAATTCGG 693 GTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCC 753 CGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCAT 786 CATCGACAACGATATTCGCATCCGCATGCGTGATATTCGTCAGGGTGTCATGCTCAGGGA Sequence 12, Application US/09221017B
Patent No. 6444709.
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
ATITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS: 993 CTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTC 1029 OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: PP2911 APPLICATION NUMBER:

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ORGANISM: PORYPHYROMONAS GINGIVALIS
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REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                             FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PE2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                   PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                      FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                2384 base pairs
                                                                                                                                                                                                                                                    NAME: Monroy, Gladys H
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1...2384
                                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2384 base pai
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
  PRIOR APPLICATION DATA:
                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOMN
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Best Local Similarity
Matches 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1
US-09-221-017B-1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 CGAATGCGTGAGCTCGGCTTTA--CCTCCCGTGGATTCGCTCTACAGTTTCGACAAGCCG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCAAATGAAATTAAAAAGTATTCTTCTGGAGCAGCCCTGCTGGTTGGGTGCTTCAGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
ANDRESPONDENCE S: ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.7%; Score 164.4; DB 4; Length 561; Best Local Similarity 95.7%; Pred. No. 1.7e-42; Matches 180; Conservative 0; Mismatches 6; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                         NAME: MODIOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: PORYPHYROMONAS GINGIVALIS
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/221,017B
FILLING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1045, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
LECULE TYPE: DNA (genomic)
                                                                                                                                                                         TELEFAX: boc.
TELEX: 706141
INFORMATION FOR SEO ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
TYPE: "TENGTH: 661 base pairs
09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1...561
                                                                                                                                                             TELEPHONE: 650-010
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: UNKNOWN ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1664 GTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCT 1723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1844 TCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGA---GAACGGTCAGCTCC 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1901 ATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCG 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAAGAACGGCCGTCTGATCGGTCTTGCATTGGCAACTGGGAAGCTATGAGTGGTG 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 AACTTGGTCCCTATGACGATCCTATTCTAAGGGCACAACGCACCTACATTGCAGGTCTCT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AAGATCCTATGGTACTCTTCGCCTCTTCGGTTTTCGACGAATACCGCAAACTCTACAACG 90
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55.0%; Pred. No. 1e-38;
tive 0; Mismatches 262;
27340-20021.00
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-415-818-5
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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256 CGTGGACCTGCTGGATGGGCTGGTGGATGAGTCGGACCCGGACGTAGATTTCCCCAACTC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 CCTGGACCGTGTCTTCACCACCTACAAGCTCATGCACACGCACCAGACAGTGGACTTCGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                        : Sequence 7, Application US/09289349;
; Batent No. 6277574;
; GENERAL INDEMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY;
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT APPLICATION NUMBER: US/09/289,349
; WUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL PROGRAM
; SEQ ID NO 7
; LENGTH: 1090
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                                                      2081 TCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGCTGAA 2129
                                                                                   Score 36.4; DB 4; Length 10
Pred. No. 0.23;
0; Mismatches 96; Indels
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ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
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APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cascieri, Margaret A. APPLICANT: Linemeyer, David L. APPLICANT: MacNeil, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08415818 Patent No. 5621079 GENERAL INFORMATION:
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MacNeil, Douglas J.
Shiao, Lin-Lin
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US-09-289-349-7
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Best Local Similarity 49.5'
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1854 CTTCCGCACC 1863
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409 GACAAGGIAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468
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                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.2; DB Pred. No. 0.44; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/383,746
FILING DATE: 03-FEB-195
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITME, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390
                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cascieri, Margaret A.
Linemeyer, David L.
MacNeil, Douglas J.
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; Patent No. 5939263
; GENERAL INFORMATION:
ZIP: 070b5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
computer: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3462
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55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.0%
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822..1937
                                                                                OPERATING SYSTEM:
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409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468
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                                                           YYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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0; Mismatches
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                           APPLICATION NUMBER: PCT/US96/01444
                                                                                                                           APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-ARR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITON NUMBER: 34,087
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390;
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
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                         Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.0°
Matches 71; Conservative
                                                                                                    CURRENT APPLICATION DATA:
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 822..1937
PCT-US96-01444-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.7%; Score 36.2; DB 2; Length 2280; 55.0%; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Indels
                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cascieri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: Menceli, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Mary A. Appollina
P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                            APPLICATION
FILING DATE: 03-FEB-1995
PRICING DATE: 08-K18:
APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITIA, MATY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEPHONE: 908-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                             APPLICATION DATE:
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/383,746
TITLE DATE: 03-FEB-1995
                                                                                                                           APPLICATION NUMBER: US/08/894,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application PC/TUS9601444 GENERAL INFORMATION:
COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PAPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.0°
Matches 71; Conservative
                                                                                                      CURRENT APPLICATION DATA:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-894-236-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US96-01444-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53...
And 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 ATTACGACATTAAAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                   449 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 ATTCCAACAACGAATA 557
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASSACHUSETTS
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: PROSTUTO8
CLONE: 1654275
                                                                                                             COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Comb, I
     Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOSTON
                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                        FILING DATE:
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                                                       94304
                        CA
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US-07-686-340-1/c
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                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1091 GTAAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATA 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCA 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 7218;
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08825782
Patent No. 5834239
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: COFACTOR A-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1;
04; Mismatches
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc.
                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991 ATTONER/AGENT INFORMATION:
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36;
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.7%; Sc
Best Local Similarity 3.2%; Pre
Matches 12; Conservative 204;
                                                                                                                                                                                                               29,768
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                                                                                                                                                                                                                                                                       (703)836-9300
                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                      (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                 pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                      CLASSIFICATION:
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                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                    TELEFAX:
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89 GACAGATCAAGATCAAGACCGGCGTGGTGAAGCGGTTGGTCAAAGAAAAAGTGATGTATG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 AAGAACTGGCCAAAAAAGAAATGCAGAGAGAACCAACTCTGCAYCGTAGAGCCTTTCT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AAAAAGAGGCAAAACAACAAGAAGAAAGATTGAAAAATGAGAGGTGAAGACGGTGAAA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 GACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCC 481
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Pred. No. 0.32;
); Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Comb, Donald G.
APPLICANT: Comb, Donald G.
APPLICANT: Perler, Francine
APPLICANT: Rucera, Rebecca
APPLICANT: Jack, William E.
TITLE OF INVENTION: Purified Thermostable DNA Polymerase
TITLE OF INVENTION: Obtainable From Thermococcus Litoralis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: & CUSHMAN STREET: 130 WATER STREET
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                      PF-0263 US
           Sequence 1, Application US/07686340 Patent No. 5322785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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3686 GTCATCGTCCAGAGTTAGTGCTTCAACATTCGAGAATGCAGTATTCTTTTTCGCCAAT 3627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08117491

Patent No. 5500363

GENERAL INFORMATION:
APPLICANT: Comb, Donald G.
APPLICANT: Comb, Donald G.
APPLICANT: Rucera, Rebecca
APPLICANT: Nucera, Rebecca
APPLICANT: Nucera, Rebecca
APPLICANT: SECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERS FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: & CUSHMAN
                                                                                                                                                                                                                                                                                                                              1.6%; Score 34; DB 1; Length 5837; 57.5%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3626 GCTGTAGTCCACCTTAGAGAAAAGATCCTTTATTTTCACAAATCTA 3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,491
                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39296C3FWC2
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APPLICATION NUMBER: US 07/811,421
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
                   REFERENCE/DOCKET NUMBER: 42188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELEFA: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/117,491
07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Resnick, David S. REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
  REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 WATER STREET
                                                                                                                                                                                                                                      SS: double not relevant
                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: BOSTON
                                                                                                                                                                                                                TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-117-491-1/c
                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-004-139B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: XU, MING-QUN
APPLICANT: ADGES, ROBERT A.
APPLICANT: JACK, MILLIAM E.
TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION
WUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 34; DB 1; Length 5837; 57.5%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3626 GCTGTAGTCCACCTTAGAGAAAAGATCCTTTATTTTCACAAATCTA 3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/686,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      39296-CIP-II
                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FRILNG DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
ATTORNEY/AGBNT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REGISTRATION NUMBER: 39296-CIP-I
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 09-DEC-1992
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08004139B
Patent No. 5496714
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
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NAME: RESNICK, DAVID S.
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                                                                                        19910417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 61; Conserve
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STRANDEDNESS:
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APPLICANT: SOUTHWORTH, MARRICE W.
TITLE OF INVENTION: FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: NEW BNGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                         Score 34; DB 1; Length 5837;
Pred. No. 4.1;
0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          1465 AGTGTGCTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,364A
FILING DATE: 06-JUL-1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/811,421
FILING DATE: 18-DEC-1991
PRIOR APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
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FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: WILLIAMS, GREGORY D. REGISTRATION NUMBER: 30901 REFERENCE/DOCKET NUMBER: NEB-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-271-364A-1/c

Sequence 1, Application US/08271364A, Patient No. 5756334, GENERAL INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
                                                                                                                                                                                                                                                         Query Match 1.6%;
Best Local Similarity 57.5%;
Matches 61; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STATE: MASSACHUSETTS
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US-08-117-491-1
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                                                                                                                                                                                                                                                                                                                                   3686 GTCATCGTCCAGAGTTAGTGCTTCAACACCTTCGAGAATGCAGTATTCTTTTTCGCCAAT 3627
                                                                                                                                                                                                                                                                                    1405 GTAATCGACAAGAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAG 1464
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                                                                                                                        Length 5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1465 AGTGTGCTTCCTTATAGCGACAAGTTCCATGCCCATGCTCAAGTCCA 1510
                                                                                                                                                                                                      45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3626 GCTGTAGTCCACCTTAGAGAAAGATCCTTTATTTTCACAAATCTA 3581
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,492
                                                                                                                    DB 1;
                                                                                                                    Score 34; DB 1
Pred. No. 4.1;
0; Mismatches
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REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC\_DOS/MS\_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/496,247 FILING DATE: 28-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: XU, MING-QUN
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: ADAM, ERIC
APPLICANT: ADAM, ERIC
APPLICANT: SOUTHWATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us 08/580,555
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US-08-811-492-1/C
; Sequence 1, Application US/08811492
. Patent No. 583424
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                                                                                                                    Query Match 1.6%;
Best Local Similarity 57.5%;
Matches 61; Conservative (
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CLASSIFICATION: 435
    not relevant
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 29-DEC-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MODITALE OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: PROJECT OF INVENTION: P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
; TOPOLOGY:
US-08-271-364A-1
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Search completed: May 23, 2003, 04:44:48 Job time : 122 secs

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

May 23, 2003, 03:33:01; Search time 529 Seconds (without alignments) 5339.261 Million cell updates/sec

US-10-008-355-1 2139 1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa Perfect score: Sequence:

2139

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

1657494 Total number of hits satisfying chosen parameters:

828747 seqs, 660231138 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published_Applications_NA:* ••

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	008-355-1 Sequence 1, Appli	US-10-123-155-20 Sequence 20, Appl	81	,	US-09-294-093B-856 Sequence 856,	-878-574-5240 Sequence 5240, Ap	S	184-634-346 Sequence 346, App		•	US-10-184-644-116 Sequence 116,	•-	.	S	-		184-634-312 Sequence 312, App		JS-10-123-155-344 Sequence 344.
	B ID	9 US-10-0	9 US-10-1	0 US-09-7	-60-SD 01	10 US-09-	10 US-09-	9 US-10-1	9 US-10-1	9 US-10-2	9 US-10-2	9 US-10-1	9 US-10-1	10 US-09-	9 US-10-1	8-60-SD 6	9 US-10-1	9 US-10-1	10 US-09-	9 US-10-1
	Query Match Length DB	2139	867	345	2281	292	369	671	671	1896	2060	489	489	268	20000	50937	802	802	256	607
æ	Query Match	100.0	1.9	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
	Score	2139	40.8	36.2	36.2	36	36	35.2	35.2	35	35	34.4	34.4	34	34	33.6	33.4	33.4	33.2	33.2
	Result No.	-	7	m	4	S	9	c 2	ω υ	6	10	11	12	13	c 14	15	c 16	c 17	18	19

Sequence	Sequence 434,	Sequence 273,	Sequence 332,		Sequence 568,		3 Sequence	_	Sequence 4, Appli			9	Sequence 9, Appl	1,			Sequence 278		'n	4,	Sequence 1, Appl.	4	æ	10,	1	
US-10-184-644-434	US-10-184-634-434	US-09-754-853A-27	US-10-184-644-332	US-10-184-634-332					US-09-754-853A-4	US-10-184-644-346	US-10-184-634-346			US-10-108-580-1	US-09-988-462-2	89	US-10-123-155-278	US-10-090-455-3	US-09-988-462-3		US-10-090-455-1	US-09-988-462-4	US-09-988-462-8	US-09-988-462-10	US-09-988-462-12	
σ	6	6	σ	σ	10	6	10	10	6	6	σ	10	12	6	6	σ	6	0	σ	6	σ	σ	σ	σ	6	
666	666	171	520	520	777	846	987	1011	513509	671	671	860	2010	2169	3468	418	491	1941	1947	3455	3455	3468	3468	3546	3546	
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	,
33	33	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.2	32.2	32.2	32.2	32.2	32.2	32	32	32	32	32	32	32	32	32	. 32	
20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

APPLICANT: Potency, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US,/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFWARE: Patentin version 3.0 ; Sequence 1, Application US/10008355; Patent No. US20020164759A1
EABNEAL INFORMATION:
APPLICANT: Travis, James US-10-008-355-1

Gaps 1 ATGCAAATGAAAATTAAAAAGTATTCTTCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG 60 ; 0 Length 2139; Indels DB 9; 0; 100.0%; Score 2139; 100.0%; Pred. No. 0; tive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 2139; Conservative ò

; TYPE: DNA ; ORGANISM: Porphyromonas gingivalis US-10-008-355-1

2139

LENGTH:

0;

GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT 120 61 61 Db δλ a

CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG 180 121 121 δλ QQ

181 181 Dp ŏ

421 GG 421 GG 421 GG 481 CA 481 CA 481 CA 601 TT 721 GA 721 GA		0y 1501 CTCAAGTCCATGGACAAGGAAAAGTTGCC Db 1501 CTCAAGTCCATGGACAAGGAAAATTTGCC Oy 1561 CTTTCCAAGAGGCTAATAGCTGCTCGCG Oy 1621 TATGCCATTGAGAAGGCAAGGAAAGTTTTCC Oy 1621 TATGCCATTGAGAAGGCAAGCACTTTTCCAAGAGGCAAGGCAAGGCAAGGCTTTTCCAAGAGGCAAGGCAAGGCAAGTTTTCCAGGAGGCAAGGCAAGGCAAGTTTTCCAGGAGGCAAGGCAAGTTTTTCCAGGAGGCAAGGCAAGTTTTCCAGGAGGCAAGGCAAGTTTTTCCAGGAGGCAAGGCAAGTTTTGCCAGGAGGCAAGGCAAGTTTTGCCAGAGGCAAGGCAAGTTTTGCCAGGAGGCAGGC
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2040 1680 1800 ATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG 1500 SAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTCCGC 1860 rccctatgccgagaacgcrcagcrccatatcgcrtrccrarcgaac 1920 3GGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATC 1980 PAGCGTGGACATCCGCTACGTTCTCTTCATGACAAATGGGT 2100 AAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG 1560 AATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC 1620 **ATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG** SGGCAAGCGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA CGGTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAG TGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGAT CATCCAAGAGCTGAAGTTGATCTAA 2139 CATCCAAGAGCTGAAGTTGATCTAA 2139

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 CGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCA 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1231 CAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTT 1290
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                                                                      APPLICANT: Wood, William
APPLICANT: Zhang, Zennin
TITLE OF INVENTION: SECRETED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURRENT PAPLICATION NUMBER: 105/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 ERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQ 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 VPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 HRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 931 GCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 MEFTINMLORKRLOTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 KLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAP 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692 KDKVWLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTS 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          691 GTGTATGCCGGTGCCGACAACCGGCCGGACGAATACAGCAAGGACAATAAAACCCTATAAG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751 CCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 SSILTGKYVHNHNTYTNNENCSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSY 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GRFQRDRRNIRPNIILVLTDDQDVELGSMQVMNKTRRIMEQGGAHFINAFVTTPMCCPSR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811 ATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 MPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.9%; Score 40.8; DB 9; Length 8 Best Local Similarity 7.6%; Pred. No. 0.01; Matches 55; Conservative 237; Mismatches 427; Indels
                                                                                                                                                                                               Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
Stewart, Timothy A.
                                                 Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-155-20
                                                                                                                                                                                                                                                                                                   SEQ ID NO 20
                                               APPLICANT:
APPLICANT:
APPLICANT:
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521 TCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTAT 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 TCACTGGTCTTGGTCTTGGATCCTCTGAATCCCCTAGGAACCTTCGGA 345
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APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NPY6-R
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NPY6-R
TITLE OF INVENTION: BURDEPTIDE RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R-639
CURRENT APPLICATION NUMBER: US/09/900,497
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
SOFTWARE FILING DATE: 2000-07-27
SOFTWARE FELSE FOR SOFT WINDOWS VERSION 4.0
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55.0%; Pred. No. 0.65;
tive 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.2; DB
Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                            APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATETSHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FLILNG DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum
Sequence 2081, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09900497 Patent No. US20020082232A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.7%;
Best Local Similarity 57.5%;
Matches 65; Conservative
                                                                          APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                      ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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TYPE: DNA
ORGANISM: Mus musculus
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RESULT 3 US-09-738-626-2081

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1573 GTAATAGCTGCTGCTGCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAG 1632
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                                                                                                                                                                                                                                                        1513 GACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C27
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SD.M..M..BS..MMM.BMYHKS.C.SYMYAY.BMB.MT..M...YBYM.M.C.MYT..A 421
                                                                                                                                                                                                                                                                                                                                                                                                 202 GAAACTGATGAAGCTCCTGCTGCTGCTGCTGCTGCAACTCCTAGCACCAATGAC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 TTM.KBHMNTMRYY.MM.ATBBHANM....SAB..AC...TN.GYMBH.SHBM.T.M.. 481
                                                                                                                                                                                                                                                                                                           142 GAGGAAGAAGAAATTGAGGTTCCAGTTTACAAAGAACCTGCAGGAGAAAATTCCAAGATG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 TY.Y..YHSC.YH.B.C.YBSHD.H.SSCGY.C..SHYC..D.MH.TS.CM.SAT.CNB.
                                                                                                                                             Score 36; DB 10; Length 369;
Pred. No. 0.25;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 138; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm NUMBER OF SEO ID NOS: 612
                                                ORGANISM: Glycine max
CTHER INFORMATION: Clone ID: LIB3028-035-Q1-B1-H8
US-09-878-574-5240
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Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10184644
                                                                                                                                                   1.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No. US20030044930A1
GENERAL INFORMATION:
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                                                                                                                                        Query Match .
Best Local Similarity 55.6%
Watches 69; Conservative
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Godowski, Paul J
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Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo Sapien
US-10-184-644-346
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  LENGTH: 369
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Number: US/09/878,574
CURRENT APPLICATION NUMBER: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SOO ID NOS: 15775
SEQ ID NO 5240
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNGLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CORRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: APPLI 21, 1998
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502 GACAAGGAGCATCAGAAGCTTAAGGACATCATTTTGTACATAGTGAGTTTGAGGAAAGCT 561
                                                                                                Gaps
                                                  469 CAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAGGAACCAACTCTGCATC
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700343414H1
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51.9%; Pred. No. 0.22;
iive 0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: a, t, c, g, or other US-09-294-093B-856
                                                                                                                                                                                                                                                                                                                                 Sequence 856, Application US/09294093B Patent No. US20010051335A1 GENERAL INFORMATION:
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Best Local Similarity 51.9
Matches 81; Conservative
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SOFTWARE: PERL P
                                                                                                                                                                                                      622 TAATATTCT 630
                                                                                                                                                     GTAGAGCCT 537
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LOCATION: 111
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LENGTH: 292
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NAME/KEY: CDS
LOCATION: (1)
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LENGTH: 1896
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US-10-213-990-52
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                                                               1877 GCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACACGACATCACGGGCG 1936
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CURRENT APPLICATION NUMBER: US/10/184,634
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420 SSS...MMTSMMT.Y...T...SHSSS...CYCYCMYCYMMB...HH.Y...HCSSCCCCY.T. 361
                                                                                             360 CYHTY.YYY.M.M.Y.YYYY....YYYYT...YYYT.HYYMW.S.YHB.HSHSSS 301
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Best Local Similarity 7.1%; Pred. No. 0.67;
Matches 29; Conservative 138; Mismatches 244; Indels
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SEQ ID NO 346
                                                                                                                                                                                                                                                                                                           Application US/10184634
p. US20030068684A1
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
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ORGANISM: Homo Sapien
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Publication No US20
GENERAL INFORMATION:
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US-10-184-634-346/C
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APPLICANT:
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APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
                                                                                                           APPLICANT: Storms, ROGERY REG
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: 2002-08-05
NUMBER OF ED ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.5;
); Mismatches 105;
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0; Mismatches 105;
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Pred. No.
Sequence 53, Application US/10213990 Publication No. US20030082595A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/10213990 Publication No. US20030082595A1 GENERAL INFORMATION:
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Best Local Similarity 48.3
Matches 98; Conservative
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Best Local Similarity 48.3
Matches 98; Conservative
                                                                     APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
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US-10-213-990-53
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CORGANISM: Aspergillus
US-10-213-990-52
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486 ACTGGCCAAAAAAAAATGCAGA
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Gurney, Austin L.
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Smith, Victoria
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US-10-184-634-116
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                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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                                    1091 CGATTCGTTCCGCTCGGTCTACGCGATCAACTCCGGCATCCCACAGGGCGCTGCCGTTTC
                                                                         705 CGACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGC
                                                                                                                                                        765 TGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 116, Application US/10184644 publication No. US20030044930A1 GENERAL INFORMATION:
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Wood, William I.
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; ORGANISM: Homo Sapien
US-10-184-644-116
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US-10-184-644-116
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361 FYLMVSSVVGFYSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGLTRFDL 420
426 GCTCAAGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGA 485
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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Best Local Similarity 8.3%; Pred. No. 1;
Matches 37; Conservative 116; Mismatches 291;
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SEQ ID NO 22
LENGTH: 50000
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APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNOLLEDTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/293,876
CURRENT FILING DATE: 2001-08-06
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PREL PROGRAM
SSEQ ID NO 5908
LENGTH: 268
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APPLICANT: HOLMES, Gregory
APPLICANT: HOLMES, Gregory
APPLICANT: YOLLE, Gabriel
APPLICANT: YAMADA, Toshiya
APPLICANT: WILKINSON, Lorine
APPLICANT: WILKINSON, Lorine
APPLICANT: WILKINSON, Lorine
TITLE OF INVENTION: NO. US20030082714Alel Nucleic Acid and Polypeptide
FILE REFERENCE: P2378
CURRENT APPLICATION NUMBER: US/10/152,724A
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PRIOR APPLICATION NUMBER: Australian App No. US20030082714A1PQ 4348
PRIOR FILING DATE: 1999-11-26
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OTHER INFORMATION: Incyte ID No. US20020013958A1 700457955H1
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48.4%; Pred. No. 0.98;
tive 0; Mismatches 97; Indels
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; LOCATION: 13, 50, 69, 179
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5908
                                                                                                                 Sequence 5908, Application US/09923876 Patent No. US20020013958A1 GAPERAL INFORMATION: APPLICANT: Lalgudi, Raghunath V.
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421 LGDFGRFNWLGNFYIVFLYNAAFA 444
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Best Local Similarity
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US-10-152-724A-22/C
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US-09-808-880-1
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APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/4808,880
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/1928
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
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                                                                                             Length 50000,
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47.2%; Pred. No. 31;
tive 0; Mismatches 114;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09808880 Publication No. US20030027287A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                             1.68;
56.18;
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Best Local Similarity 47.23
Matches 102; Conservative
                                                                                                                                          64; Conservative
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 1
LENGTH: 50937
TYPE: DNA ORGANISM: Homo sapiens
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	2117	C 14 15	17 18 19 20	c 21 22 23	C 24		C 29 C 30	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	35 36	37 38	39	41 42 43	44 45		RESULT 1 BH388186/c	LOCUS	ACCESSION VERSION	KEIWORUS SOURCE OPCANIEM	CECANO	REFERENCE AUTHORS TITLE JOURNAL	COMMENT		
5.1.4_p5_4578 Compugen Ltd.		arch time 2048 Seconds (without alignments) 16915.110 Million cell updates/sec	aagagetgaagttgatetaa 2139	·		32308132														by chance to have a the result being printed, e distribution.		Description	BH388186 AG-ND-124 BH392840 AG-ND-162 BH386991 AG-ND-148 BH375201 AG-ND-173 BH400391 AG-ND-173 BH375688 AG-ND-120
GenCore version 5.1.4 Copyright (c) 1993 - 2003 Compu	nucleic search, using sw model	May 23, 2003, 02:45:01 ; Search tin (without 16915.1)	US-10-008-355-1 2139 l atgcaaatgaaattaaaaagaa	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	16154066 seqs, 8097743376 residues	of hits satisfying chosen parameters:	seq length: 0 seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	*			o: em_estpl:* 6: em_estpl:* 7: em_estro:*	em_htc: gb_est1 gb_est	11: 9D_nc:: 12: gb_est4:* 14: gb_est4:*		17: gb_gss:* 18: em_gss_hum:* 19: em_gss_inv:*		22: em_955_1un: * 23: em_955_mam * 24. em_ges_mus.*	25: em_gss_roter:* 26: em_gss_pro:* 27: em_gss_rod:*	No. is the number of results predicted by chance to have greater than or equal to the score of the result being posterived by analysis of the total score distribution.	SUMMARIES	Query Match Length DB ID	5.1 537 17 BH388186 5.1 591 17 BH392840 5.1 500 17 BH386991 4.9 418 17 BH375201 3.4 426 17 BH400391 3.1 697 17 BH375688

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Location/Qualifiers
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Class: BAC ends.
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AG-ND-162P14.TF ND-TAM Anopheles gambiae genomic clone AG-ND-162P14
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BH392840
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to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryc
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                          /clone="AG-ND-124P3"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/ 112 c 94 g 178 t
                                                                                                                                                                      /organism="Anopheles gambiae"/strain="PEST"
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1 (bases 1 to 500)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
Email: bjloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 CAATTTCACTAAAAGGAAATAAGCCTGGTGATTTTGCAATGATTGTAGGATATCCTGGTA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 ACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 CCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="AG-ND-162P14"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/ note="Vector: pECBAC1; Site_1: HindIII"
/ 122 c 105 g 194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.1%; Score 110; DB 17; Best Local Similarity 55.9%; Pred. No. 1.6e-20; Matches 209; Conservative 0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="PEST"
/db_xref="taxon:7165"
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Unpublished (2001)
Contact: Brendan J Loftus
Coptentent of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PEST"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="AG-ND-173C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                        Shetty, J., Malek, J.,
Direct Submission of
                         (bases 1 to 418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .418
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BH400391
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      Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                     REFERENCE
AUTHORS
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                                                                                                       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH375201 418 bp DNA linear GSS 10-DEC-2001 AG-ND-173C3.TR ND-TAM Anopheles gambiae genomic clone AG-ND-173C3,
                                                                                                                                                                                                   This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 TCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 TGCTGAAGGATTTCTTCAAAGGAAATGAGTTTTACTACTTTGTATTCCAGGATTTCAAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 ACGITCGIATGGIATITGCICCICCAGCICTGIAGGIAAGIICGGAGGCGAIACGGACA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 ACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCG 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707 ACAACCGGCCGGAATACAGCAAGACAATAAACCCTATAAGCCCGTTTACTTCGCTG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 ATGGCAATCCTGCTGAATATTCAGCTAACAACGTTCCTTTAAAGGCCTAAGCATCATTAC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSs: AG-ND-148L11.TF
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 CCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108.2; DB 17; Length
Pred. No. 4.7e-20;
0; Mismatches 143; Indels
                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="Av .... /clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
inf c 90 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   827 GTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 CAACAAACAGATACCTTACTTTTGGGAATGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                            Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 5.1%;
Local Similarity 57.6%;
les 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                       partial digest.
Seq primer: M13 Rev
Class: BAC ends.
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KEYWORDS
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BH375201
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AG-ND-147H4.TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4,
                                                                                                                                                                                                                                                                                                                          This clone is from an A gambiae BAC library (ND-TAM) provided by Fh. Collins and sequenced by The Institute for Genomic Research (TIGA). The BAC library was generated from A. gambiae PESTS trrain DNA A. Library was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microcranisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: MI3 Rev
       and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710 ACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 770 TATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 TAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 TATCTGTAAAAGACCTTAAAGAAGGTGATTTCACATTCGTTTTCGGATTCCCGGGAAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 CGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 CAACTGAATACCTTCCTTCAATTGCTGTAGAAAAGATCATCAACGÁTACAGATCCTGCTA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koo,H., Collins,F., Gardner,M. and Loftus
BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     590 IICGIAIGGIAITIGCICCICCCAGCICIGIAGGIAAGIICGGAGGCGAIACGGACAACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                650 GGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 ATAAACCTGCAGAATATTCTAAAGATAACATTCCATACACTCCGAAATATTCACTTCCGG
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/note="Vector: pECBAC1; Site_1: HindIII"
1 81 c 70 g 122 t
                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0208
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 103.8; DB 54.6%; Pred. No. 8e-19;
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ORGANISM

VERSION KEYWORDS SOURCE

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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Score 66.4; DB 17;
Pred. No. 9.1e-08;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 GTGAAGTATCTGCGCAAGATCGTGAAGGTAAC 407
                                                                                              Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="AG-ND-120J9"
/clone_lib="ND-TAM"
/note="Vector: pECBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                    Other_GSSs: AG-ND-120J9.TF
Contact: Brendan J Loftus
                             African malaria mosguito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partial digest.
Seg primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.3
Matches 197; Conservative
                                                     Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 697
                                                                                                                                             (bases 1 to
                                                                                                                       Anopheles.
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                                                ORGANISM
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                                                                                                                                                                                                                                                                           Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from microorganisms that inhabit
the gut. The DNA is derived from microorganisms that inhabit
blorary was constructed at Texas A&M University BAC Center
University, College Station, Texas A?N University BAC Center
Seq primer: M13 For
Class: BAC ends.
                                                                                                                                                                                      Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH375688 697 bp DNA linear GSS 10-DEC-2001
AG-ND-120J9.TR ND-TAM Anopheles gambiae genomic clone AG-ND-120J9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1756 GGTGCCTGGTACAACTATCATACGACAGGCCAAGGGCGTATTGGAGAAGCAGGATCCTAAG 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1816 AGCGATGAGTTTGCCGTACAGGAGATATCCTCGACCTCTTCCGCACAAAACTATGGT 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1876 ---CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACG 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1933 GGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTC 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 GGTATCAAGCAGAATTACTATACCACAATGGAAGGTATGATGATTAAGAAGTACAAGAAAGGT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 GACGAAGAATTCGATCTTCCACAAGGACTTCTTGATCTTTATAAAAAGAAAATTATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72.4; DB 17; Length 426;
Pred. No. 1.2e-09;
0; Mismatches 106; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7165"
/clone="AG-ND-14744"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
79 c 76 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                          Other_GSSs: AG-ND-147H4.TR
                                              African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence.
BH375688
BH375688.1 GI:17321830
вн400391.1 GI:17346607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.4%;
Best Local Similarity 57.8%;
Matches 149; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1993 GATGGCAACTGGGAAGCT 2010
                                                                                                                                                                (bases 1 to 426)
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FEATURES

BASE COUNT

ORIGIN

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вн375688/с DEFINITION

LOCUS

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RESULT

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ACCESSION VERSION

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Department of EukaryOtic Genomics
Department of EukaryOtic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0348
Fax: 301 838 3343
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC.
Library was constructed at Texas ARM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                   Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 GGAGGAATGTGGATTCCTACAGAGTTAAATGAAAAGGA------AATGAAGGAATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 GGCATGAAGATTTCTGCGAAAGATATTTTCAATACTCAAAAACCTAGTATTAAAGATGCT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 ACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTAT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 CTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 AAAAACATCCTATTAGCACTAGCTTTACTCCCCGCAGTGACGGCTTTTGCTCAACAGGCG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 GTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTT
                                     Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 697;
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122 g 228 t
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us-10-008-355-1.rst

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307 CACGACTATCTGCGCGATGGTTT 329
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                                                                                                                                                                                                                         BH164253.1 GI:15737691
                                                                                                                                                                                   genomic, DNA sequence.
BH164253
                                         268 CAAAATCATTTAAAAAATGGTTT
                                                                                                                                                                                                                                                                 Entamoeba histolytica.
                                                                                                                                                                                                                                                                                     Entamoeba histolytica
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                                                                                                                                                              ENTTG63TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                              GSS
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                                                                                                                                                            DEFINITION
                                                                                                                       BH164253/c
                                                                                                                                                                                                                                                                                   ORGANISM
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: DBluescript SK -: Site_1: EcoRI; Site_2: Xhoi; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Strategene and packaged using Glapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                     AW774807 398 bp mRNA linear EST 07-SEP-2000 EST333958 KV3 Medicago truncatula cDNA clone pkV3-24C3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots,
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae, Trifolieae;
                                                                                                                                                                                                                                                                                                                                                             ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                             1 (bases 1 to 398)
VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 CGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 CTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 TIGGITCITACCAAICACCACTGIGGITAIAGGGGGATIGCAGAACTITCAACTGCAGAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
TTE: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AAAGATGCGATTGTACAATTCAATGGGGGTTGTACTGCAGAAATGGTTTCAAACAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AGAGCCGATGAAGGAATGTGCTTCCTGATGTTTATCGAAAGATTAAATCACAGGGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 GCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6%; Score 55; DB 10; Length 39
50.6%; Pred. No. 0.00013;
Live 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:380"
/clone="pK3-2403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR sequence name: MTEBG14TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kvandenb@cbs.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas A&M EST name: T258226e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="KV3'
                                                                                                                     AW774807.1 GI:7718724
                                                                                                                                                                               Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.6
nes 133; Conservative
                                                                                                                                                              barrel medic.
                                                                                                                                                                                                                                                              Medicago.
                                                                                 sequence
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                                                                                                    AW77480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                               ORGANISM
                                                        DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                ACCESSION
                                                                                                                  VERSION
KEYWORDS
SOURCE
RESULT 7
AW774807
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/strain="HMI:IMSS"
/db.xref="taxon:5759"
/db.xref="taxon:5759"
/cloxe="taxon:5759"
/cl
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GSS 24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: blloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
MAN library
Seq primer: M13-Forward
Class: shotgun
1005 bp DNA linear GSS 24-SEP-200
Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library (2001) unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 CGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 TACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
71: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 TCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64

    1005
/organism="Entamoeba histolytica"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%; Score 49.2; DB 56.0%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 1005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 15
High quality sequence stop: 487.
Location/Qualifiers
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BH400866/c DEFINITION

RESULT 9

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

ACCESSION VERSION

KEYWORDS

SOURCE

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BH391233 721 bp DNA linear GSS 11-DEC-2001
AG-ND-141L2.TF ND-TAM Anopheles gambiae genomic clone AG-ND-141L2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Corgan: head; Vector: poT2; Site_1: EcoR1; Site_2:
Xho1; Sized fractionated cDNAs were directly ligated into
poT2. Plasmid cDNA library." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 721)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
     Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1590 CGCTATTCAGGCCGATGCGATGCCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 CACCACCAATCCCTACAACCTGGCCGTCTACTACGGCAGCGACTACCCGGTGATCTTCAA 433
                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
Plate: 252 row: D column: 6
High quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH25242"
/clone="ib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCATCCTGTGGTTCATGGTCGTCTTCGGACTGTCTCTGCTG 476
                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Other_GSSs: AG-ND-141L2.TR
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                                                                                                                           Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 110; Conservative
                                                                                                                                                                                                 One Cyclotron Rd,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae
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                                                                                                                                                     BDGP
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DEFINITION
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                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434
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COMMENT
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VERSION
REFERENCE
                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
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                                                                                                                           COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Breadan J Loftus
Contact: Breadan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Fax: 301 838 3543
Email: bloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas ARM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1405287 692 bp mRNA linear EST 19-APR-2001 GH25242.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone.GH25242 5prime, mRNA sequence.
                                                 GSS 11-DEC-2001
                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 555)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSS: AG-ND-125M4.TF
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                                       BH400866 555 bp DNA linear GSS 11-DEC-200
AG-ND-125M4.TR ND-TAM Anopheles gambiae genomic clone AG-ND-125M4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 AGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGA 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 ATGAAAATATGCGTACTGATAATGCAACCCGTATTAAATATGCATCTAAATATGCATCCG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.8; DB 17; Length 555; Pred. No. 0.6; 0; Mismatches 32; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l; Site_1: HindIII"
204 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 GTGCTAACTATTGGAAGAATTCGATCGGTATGAA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xrref="taxon:7165"
/clone="AG-ND-125M4"
/clone=11b="ND-TAM"
/note="Vector: pEcBAC1; S.
a 105 c 94 g 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                               African malaria mosquito.
                                                                                                                                             BH400866.1 GI:17347082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="PEST"
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66.0%;
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Seq primer: M13 Rev
Class: BAC ends.
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                                                                                                                                                                                                                            Anopheles gambiae
                                                                                                DNA sequence.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     Anopheles.
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source

FEATURES

BASE COUNT ORIGIN

Matches

Dp ò

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SOURCE ORGANISM

KEYWORDS

VERSION

DEFINITION

RESULT 10

AI405287

ACCESSION

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Query Match
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AL728310
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822 bp DNA linear GSS 10-DEC-2001
AG-ND-162M17.TF ND-TAM Anopheles gambiae genomic clone AG-ND-162M17
, DNA sequence.
BH371846.1 GI:17317971
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Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from .microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W University BAC Center
Daniversity, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1044 GATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 CAAAGCTGTTTATGGAAATGTATTAGCAAATACTGATGCATACTACAAGCAAATTTCTAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924 GAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGGAAGTATGCTCA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae
Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota;
Neoptera: Endopterygota: Diptera: Nematocera: Culicoidea;
Anopheles:
1 (bases 1 to 822)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus
Direct Submission of BAC-end sequences from Anopheles gambiae
Other_GSSS: AG-ND-162M17.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GAAGAAGCATATGGATAAAGACGATGCTACAAGATTAGCTTACGCGTCTAACTATGCAAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
712: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                          l; Site_1: HindIII"
183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.2; DB 17;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                               /organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                               /clone="AG-ND-141L2"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1;
122 c 147 g 18
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1164 GGCCAACCGTGAGATGACTTAT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 CAGAAATATCGAGAAAAATTAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                      /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.9%;
Best Local Similarity 47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 124; Conservative
                                                                                                                                                                                                                                                Class: BAC ends.
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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coimbra, W. Well, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BNOAA098ZA08" /clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2007 AGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACAT 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACCTTTAAGCGGTGACATTGTTTTGAACCTAAATTACAAGGAACGATTAACGTAGACGT 60
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7165"
/clone="AG-ND-162M17"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
| 142 c 155 g 290 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
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/dev_stage="embryonic"
/note="subtracted to 100 is7 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                   /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.4; DB Pred. No. 7.6; 0; Mismatches
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL728310
AL728310.1 GI:20192914
                                                                                                                                                                                                                                                                                                                                                                                             /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
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Unpublished (2002)
                                                                                                                                                                                                                         partial digest.
Seg primer: M13 For
Class: BAC ends.
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nes 58; Conserv
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Best Local Similarity
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                               RESULT 15
AW375157
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1517 AGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAA 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1457 TCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACA 1516
                                                                                                                                                                    972 CAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 TAATAATGAGAGCGCAGCTAAAATGATAAAGGAGTCGATGGATAAGAAGTTTGGGAGCTC 295
                                                                                                                                                                                                                                       1032 TCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCC 1090
                                                                                                                                    176 TGAAGAGATGCGGGTGGAGACCATGGAGCTCTGTGTTACAGCGTGTGAAAAGTTTGCCAC 235
                                   852 GGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAA 911
                                                                 116 GGAAGAGGCAGATTATAAGAGACTACATAACTTTCCTCTTATAAGGCATACTGATATGCC 175
                                                                                                  912 GCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAG 971
   Gaps
                                                                                                                                                                                                                                                          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 296 TIGGGTICGAAATCACATGAGAGTCAAGAACC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" 117 c 159 g 202 t
                                                                                                                                                                                                                                                                                                                                                         BH448937 687 bp DNA linear GSS 12-1
BOGZL67TR BOGZ Brassica oleracea genomic clone BOGZL67, DNA
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
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Mismatches 125; Indels
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Pred. No. 12;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
DNA is from a doubled haploid provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 687
/organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 ATGCAACTGTTAGGCATCTATAGGATTAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3712"
/clone="BOGZL67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BOGZ"
 0
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Similarity 53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
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Brassica oleracea
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Fax: 301-838-0208
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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BH448937/C
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   Matches
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/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1: A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mrNA and cDNA amplification were performed under low standard productions. The continuous conditions at 183 c 58 g 44 t
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                                       04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-QV2&t2=QV2-CT0121-280999-001-e01&t3=1999-09-28&t4=1)
Seq primer: puc 18 forward
QV2-CTG121-280999-001-e01 CTG121 Homo sapiens CDNA, mRNA sequence. AM375157.1 GI:6879811 EST 04-FEB-20C EST.
                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 CAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGG 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACTICICCACGAAGCICITGICGGIGGCITIGGGGAACCAGCACICCICGICCAGCCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACA 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                   HCGP http://www.ludwig.org.br/ORRSTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 38.4; DB
51.1%; Pred. No. 5.7;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 18
High quality sequence stop: 88.
Location/Qualifiers
                                                                                                                                                                                                                  Chordata; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 23, 2003, 05:18:34
Job time : 2069 secs
                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                            (bases 1 to 184)
HCGP http://m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Sun May 25 15:40:28 2003

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - nucleic search, using frame_plus_p2n model

May 23, 2003, 08:43:01; Search time 3929.8 Seconds (without alignments) 5272.840 Million cell updates/sec

Run on:

3719 1 MOMKLKSILLGAALLGASG......LFMIDKWGQCPRLIQELKLI 712 0.5 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext US-10-008-355-2 **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum [Maximum [

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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GenEmbl:* Database :

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gb_un:*
gb_vi:*
em_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			ø			SUMMARIES	
Result	ult No.	Score	ouery Match	Length	DB		Description
1	1 1 1 1	1 1 1 1 1 1 1			i		
υ	П			10689	Н	0	-
O	7	86.		253217	~	59	290
	m	7	•	10811	Н	73	Xanthom
	4	147.5		50372	~	$\overline{}$	1150
	5	46.	•	10889	~	AE006549	646
	9	44.		1556	~	AE000733	333
υ	7	37.		162754	œ	OSJN00169	2969 Oryza
	œ	33.		4004	Н	MSP207AAM	M.sp 207
	σ	133	•	10292	~	AE008428	AE008428 Streptoco
O	10	3	-	11362	7	$\overline{}$	AL449945 Streptoco
	11			14169	Н	S	AE009858 Pyrobacul
	12	3		2652	9	10	A81135 Sequence 1
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	14	3	•	2652	9	74	E26074 Novel vals.
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υ	16	3		10029	М	AE010493	-
	17	2		4141	Н	CLOCOLA	
υ	18	2	•	6004	9	BD003707	BD003707 Polynucle
	19	2	•	11280	Н	AE007366	٠,
O	20	12		2670	m	CBRG45011	
υ	21	128.5	3.5	291150	Н	AP003135	AP003135 Staphyloc
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	25	- 1		90348	<u></u>	AF497482	
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	58	Ď.	٠	52900		AE014138	
	50			9389		AE008276	
O	30	٠.	٠	11199	Н	AE009339	
	31	12		36380	e	AF106581	
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ပ	32	2		1018	г	AE001761	
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	38	22.		4731	9	13695	S
	39	22.		7009	14	F2960	
	40	22.		7858	_	53	U35629 Lactococcus
Ö	41	22.		1082	J	\sim	37
υ	42	22.	3.3	3905		L59616	σ
	43	22		9985	٠	151	514
	44	122.5	m c	349980	6	AX413017	<u>_</u>
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ALIGNMENTS

KEYWORDS

SOURCE

TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYSPAHLSEAASSVAGASGQASLRAAPASLSSSRSLVSGMRTYAVLETESAPTLSGCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to SPIP03625 (percent identity: 36 %/query alignment coverage: 85.1 %/subject alignment coverage:
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1351. 1662
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Xylella fastidiosa 9a5c, section 154 of 229 of the complete genome. AE004008 AE003849
AE004008.1 GI:9106961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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/clone="9a5c"
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Xylella fastidiosa 9a5c
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                        AE004008/C
                                                                                                          DEFINITION
                                                                                                                                                          ACCESSION
VERSION
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MEDLINE
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JOURNAL
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CDS

FEATURES

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/translation="MCSRSFFLYFISALGLTLVISFPFCLFAGNVPPTVEVVPTSVRY
SSVISDGVSTSATFEARSTALVNGVRYYTVPVDISASTLGSLAKVAVRRGMAFYNVYS
MLSGLINGAGWVIDELTHEVMSGPALKEIPVGTVAWWWQRPGDGHVFYSVTPQGLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INAYQSSLSPPQPLVTSSGPSSVSSERWLYHLEGGGEYIGHLSKTDQSVPDYSSGLPP
SYLLDVDLGQLVRSDPSTYNNYLTDSQTGAVLLTPETVSAKTKLRREJEDELKARHAP
BQQPSSGGASPPSSGTAMPSCEGWASVUCDFIDWVKSDEFLKPFLVPDVYVDKL
PQAKTWSSGLGEGGACPSPTIPIEFSGYKTSVEISYQPFCDFAALMRPVVIVIATILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified by sequence shallarity; putative; ORF located using Glimmer/RBSfinder" /codon_start=1 /transl_table=11 /product="hypothetical protein" /product="hypothetical protein" /protein_id="ApR84685.1" /protein_id="ApR84685.1"
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                                                                                                                                                                                                                                                                                                   /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder" /codon_start=1
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similarity; putative; ORF located using Glimmer/RBSfinder"
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86.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder" /codon_start=1
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Matches:
Conservative:
                                                                                         /product="phage-related protein"
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Indels:
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complement(3195. .4412)
/gene="XF1877"
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                                                                        /transl_table=11
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Best Local Similarity:
Query Match:
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10388 CCTCTAAAGCAGGCTGGCCTACAACTGTCACCAGAACAATTGTCAAATTTGACAGGTGAC 10329
                                                                                                              10328 CCCATGGGGGCAGTGTCTCTCTCTC----GGCAATTGCACGGGGTCTGGTTTCACCA 10275
                                                                                                                                                                      10154 GCGGGTCCGAATGCGCGTATTTACGTGCTTGAGCAGATTACCGATGTCACCGCTCAAGGT 10095
                                                                                                                                                                                                                                                                                                                                                                                                                   10094 AAAGCTGCTGTGCTGCTGCTGCTGATGACCCCTTCAAGCGTACGACGCATTGGAGACA 10035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10034 TTCAGCAAACAAGAAATCGCCAAATGCGAGGAA---GAGCAGGGTTATCGCTGCCAATTC 9978
                                                                                                                                                                                                                             101 ValAspHisAspTyrLeuArgAspGlyPheValSerArgThrMetGlyGluGluLeuPro 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311
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ArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysPro
                                                                         SerIleAlaAsnAlaValValIlePheGlyGlyGlyGlyCysThrGlyIleThrValSerAsp
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AC016590 253217 bp DNA linear HTG 20-APR-2001 N Homo sapiens chromosome 19 clone CTD-3220F14, WORKING DRAFT SEQUENCE, 39 unordered places.	AC016590 AC016590.6 GI:1369959C HTG; HTGS_PHASE1; HTGS_ HOMO SADIEDS	Homo Eukar Mamma	1 (bases 1 DOE Joint G Sequencing Unpublished		Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711568. Genome Center Center: Joint Genome Institute	<pre>Center Code: JG1 Web Site: http://www.jgi.doe.gov</pre>	Center Project Name: 940643, BC905667 Center clone name: CITB-EL_3220F14	Summary Suctionary 207648 bases at least Q40 Consensus quality: 225569 bases at least Q30 Consensus quality: 232428 bases at least Q30 Estimated insert size: 250510; aqarose-fp estimation	Estimated insert size: 249417; sum-of-contigs estimation Quality coverage: 9.03 in Q20 bases; agarose-fp estimation Quality coverage: 9.07 in Q20 bases; sum-of-contigs estimation. * NOTE: This is a 'working draft' sequence. It currently	<pre>* consists of 39 contigs. The true order of the pleces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.</pre>	* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 1019: contig of 1019 bp in length	1119: gap of unknown 2152: contig of 1033 2252: gap of unknown 3701: contig of 1449	3801: gap of unknown 1 5053: contig of 1252 b 5153: gap of unknown 1 6184: contig of 1031 b	6284: gap of unknown 7809: contig of 1525 7909: gap of unknown 8986: contig of 1077	9086: gap of unknown 10090: contig of 1004 10190: gap of unknown 11225: contig of 1035	11325: gap of unknown 12365: contig of 1040 12465: gap of unknown 14535: contig of 2070	* 14536 14635; gap of unknown length * 14636 16489; contig of 1854 bp in length * 16590 16589; gap of unknown length * 16590 19109; contig of 2520 bp in length * 19110 19209; gap of unknown length * 19210 21841; contig of 2632 bp in length
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LysAlaasnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVal ::::: 	408 ArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHis 423 	424	432 AspLysTyrLysAspTyrLeuProSerLeuAspArgLysVal	446	460	476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495	LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys	ASPECALAVALGIULEUSSETLYSSETVAIILEALAALAALAALAALAALAALAARS (HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	. 536 AlaMetalaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArg 555 1	556 GlumetTyrProGlyargalaLeuProSeraspalaAsnPheThrmetArgMet 573 ::: ::::: :::	574 SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr 593 :::::	594 ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGlu 613	614 ASDILELEUASPLEUPHEARGTHrLYSASDTYRGLYARGTYRALAGLUASDGLY 631 .::::::::::::::::::::::::::::::::::::	632 GlnLeuHisileAlaPheLeuSerAsnAsnAspileThrGlyGlyAsnSerGlySerPro 651 :::	652 ValPheAspLysAsnGlyArgLeulleGlyLeuAlaPheAspGlyAsnTrpGluAlaMet 671 ::: ::: :::	672 SerGlyAspileGluPheGluProAspLeuGlnArgThrileSerValAspileArgTyr 691 	692 ValLeubhemetileAspLysTrpGlyGlnCysProArgLeulleGlnGluLeuLysLeu 711

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gap of unknown length
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(bases 1 to 10811)

(a Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R. Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
Jr.,N.E., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
Curbanbergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutlinho,L.L.,
Cursino-Santos,J.R., El-Dorry,H., Faria,J.B.F., Ferreira,A.J.S.,
Ferreira,R.C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Meidanis,J.,
Madeira,A.M.B.N., Martinez Rossi,N.M., Martins,E.C., Meidanis,J.,
Mandeira,A.M.B.N., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,
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4580 GCGAGTTCAATGCACCAGCGAAACAACTGGCCGCTGATCAATGGCCTAAGGACTTCGGCA
SerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAla---ValGluLeu
                                      4819 -AACGTAATGCGGAAGAACTGAACAGCCGGTCAAGATCCACGCAAAGCTATGCCAAC
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Xanthomonas axonopodis pv. citri str.
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Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mehedirecvakrrlctvrppsavpeodspmtsarrhytplal
Alatilpvisoaatpadpaavaparaaltadaanantoldainvvsogstrovoriso
DieOltpossafkaverlepvoyofsadpfetytespestoverstrovoriso
GNMSYGVTNGLHITRAIISBNLGSVEIAOGAGALGTASNTNLGGTMOFYSADPOTTPO
ARLVOTVGSDATRRTFVRADTGDRDGLSAYLSYANASTDKWKGYGDOTSEQANLKTVY
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RPHLCPNTVGIGVNVNGAFAEYMVMPASNLWPIPDQIPSELAAFFDPYGNAAHCALEF
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FKGLTVQG1YGRKMYETWYKMTQLVLSGFPLHKVLTHQLP1DDFQKGFDLMEEGKAGK
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SP 05508-900,
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located using Blastx/Glimmer/Genemark"
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located using Blastx/Glimmer/Genemark"
/codon_start=1
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                                                                                                                                                                                                                         Comparison of the genomes of two Xanthomonas pathogens with differing host specificities Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-NOV-2001) Departmento de Bioquimica,
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
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/protein_id-"AAM35905.1"
/db_xref-"GI:21107162"
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/protein_id="AAM35906.1"
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GSTAGNAATTQAEHLVAAIAADVRANRLPQVSWVIPPTAYCEHPEAPPAYGESLVARL
IDALTANPEVWAKTALIINYDENDGFFDHVPAPLPALDARMGRSNVDTHGEVYDGVPI
GLGIRVPMLVISPWTRGGWVNSQVFDHTSVLRLLERRFGVAEPNISPWRRAVSGDLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQVHARVQEGAAVQLQFVNSGAAAAAFNVYNSAAGGGPWYYTVLPGTQLDDAPTGATH
EGAYALRVHGPNGFLREFAGQVPRASAPSAAPWVEARQEGDALVLETGNAGQRACTVQ
LRALDYADPSARTLSLAAGQRETIRLALAASDHWYDLVVEQPGSAFRRLAGHLETGR
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MTEVAPAPQLLKELGVR"
ATSGVANGYPQSLAGLPSDYSWLDASYYAGGGLRRDNLAGLSGTFVFGGATLDASGYY
HGNRGEGQWVTPYVRTSAQIPVSMRTTDYGLDRFGGTSALKWSWGNHDLEVGAWAENA
                                                             RTTQGRNYFALGNEGYTSLYNVYEAQTPFRRDFLQRYTTQTRMLYVQDTVRLLDDRLT
LNYGAKALSTTTRAQSLVPTTALAQGRIRAEDNFLPQLGINYKLDERQDLYASYSKNI
                                                                                                                        AAFGETPFATSQAAFDRSRSTLEPEQSQTVQVGYRVQDAQFQLSADAYFTKFSNRLLT
PSCTRAVITASLSBVGANSHSAGADLAMWRPFGLSALNSLSSWNRSBYTQDDI_LNNG
VVATSGKDVVGIPALMESSSASYQIGNLRLDDLDGKYVDKRYTTFLNDSQYPSYWLFNA
GARYDEGRVGGVADVALALNISNLTDKRYFASTGTNGYVASDPDGYNQTMVVGAPRQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEHVVILMQENRSFDHYFGALRGVRGFGDPRALQLRDGHAVWSQPTPDGRRVLPFAFD
SQNTCAPLIKSLDHSWRAGHGQDPARWAEYDAWVPYKGELTMGYFQRHDIPYYHALAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFTICDGYYCSLHGPTNPNRMYLFTGTSGPSVGNVGAQAVTNADDGNWTADMARDKPG
YAALQWTTYAQRLQAAGVDWRVYQEYDNFGCNSLAYFSHYRDLRTDDERYLRARACVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFDFRKPDDSALSALPSVDDYRARTAAVRDKPLPSAPAAATMPRQEPGQRPARALPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MRPNLFAVSVLATLAVAASAQAGEGMWVPQQLPEIAGPPQQAGL
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DGFNAVRPADELSAGPSARIYVLDAITDVTAPAKAAMATPVRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTSSSSRRDFLKRVAALTAAGALPSSIGRALALPANARTGTLRD
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located using Blastx/Glimmer/Genemark"
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/db_xrefe"GI:21107165"
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/protein_id="AAM35910.1"
/db_kref="G1:21107167"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="non-hemolytic phospholipase
/protein_id="AAM35907.1"
/db_xref="GI:21107164"
                                                                                                                                                                                                                                                                4369. .6450
/gene="XAC1024"
4369. .6450
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/gene="XAC1025"
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6791. 7054
/gene="XAC1026"
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/transl_table=11
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/genė="XAC1027"
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/gene="XAC1027"
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/gene="XAC1025"
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6791. .7054
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LMKKLTPHVKTVGILYASNEDNSLSQVKEFRRLAFKKGYQVISYAVPSTNEVPATMSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLGKVDAVFIPQDNTIASAFSSVMTTSKAAKIPVÝTSVDRMVEKGGLAAISONQYDLG
VQTANQVLKLIKGKRVVDVPVKVVDIGQPLINKNÝAAELGIAINREDFPSASFIEN"
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QFVTHEALDDIKRGIEDQLKKQMPQKQNVVIKVMÅAEGDQSKIQTWSRQLVQSGSDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLLTGKIFLQLLLLRINTKTCDIKGQEKITKNTLTEMNLDAKSD
                                                                                                                                                                                                                                                                            Direct Submission
Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, Mr 59840, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb|AAK99779.1| (AE008470)
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                                                                     serotype M3 strain of group A Streptococcus: , the high-virulence phenotype, and clone
    Manmarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
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hypothetical protein [Streptococcus pyogenes M1 GAS]"
/codon_start=1
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Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M.
                                                                                                                                        U.S.A. 99 (15), 10078-10083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptococcus pyogenes phage 315.1"
/db_xref="taxon:198538"
208. 1206

    .34426
    /organism="Streptococcus pyogenes MGAS315"
/strain="MGAS315"

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1157. .1375
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208. 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="group: A" 34427. .>50372
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/transl_table=11
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                                                                                                                                          Sci.
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                                                                                               Phage-encoded toxins,
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                                                                       Genome sequence of a
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                                                                                                                                          Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /focus
                                                                                                                                                                                                                                                             Musser, J.M.
                                                    Musser, J.M.
                                                                                                                       emergence
                                                                                                                                             Proc.
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JOURNAL
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                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNATDSLSAWLAYIEQQHPSAIAMGLERVREVAVRLQIAAPAKH
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FAAVEAARGDTALTYFEFGTLAALWLFQQSALELAVLEIGLGGRLDAVNIVDSDVAVI
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                                                                                                                                                                                                                                                    /db_xref="GI:21107168"
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                                                                                                                                                                                                                                                                                               LQIDRAVASPLSRAQATAKAALGASRQALLQTDADLQETAHGEWEGLLASEINDKDPA
RLRAWREEPDTVLMPGGESLRQVLDRSWRGLMRAADGLGAHDTLLVVVAHDAVNRVILC
KILGLPLSRLMSFRQAPTTLNLLEGDDVEHLEVVRLNDCAHHTPFFGEAKHRAL"
                                                                                                           /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark; dihydrofolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 GlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle
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Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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32
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                                                                                                                                                                                                         /product="phosphoglycerate mutase"
/protein_id="AAM35911.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Streptococcus pyogenes MGAS315,
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                                             /note="XAC1028"
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AE014150.1 GI:21904382
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/gene="folc"
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7329. .7973
/gene="pgmA"
                                                                     7329. .7973
/gene="pgmA"
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175.00
75.00%
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Best Local Similarity:
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6360. .8267
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/note="best blastp hit: gb|AAK33919.1| (AE006547) putative
ABC transporter (ATP-binding protein) [Streptococcus
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GYNQHVLSEPINLDVHKLDAIAIVGPNGIGKSTLIKSVIGQIPFIKGEVKYGANVEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYDĞTÇSHLTSSNTVLEELMQDFSTTPEVDIRNRLGAFLFSGDDVKKSVAMLSGGEKA
ŘLLLAKLSMENNNFLVLDEPTNHLDIDSKEVLENALIDFDGTLLFVSHDRYFINRLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVLEITENGSTLYLGDYDYYLEKKAELEELARLAAGETVEETKEASATDYQLQKANQK
ERRRLTRRYEEIEARLETIEERIGAIQEDMHASNDTAQLIAWQKEWDQLDQEQEALME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVTVSKEQHLDMFLKMERIREFDSRINKLVRRGFVQGMTHFSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative acetoin dehydrogenase (TPP-dependent) alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CTCTTTGATGATAGGTGATGAAACGCTTAAACGTCGCCGTTATACTGGTTGG 30335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30336 GGACGTTTGTCTCGAAAATTGATTAATGGTATTAGGGATAAGCAATCTGGCAAAACAATA 30395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AsnGlnGluAsnLeuAspArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyIleThrValSerAspGlnGlyLeu-----IlePheThrAsnHisHisCysGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GlnSerGlnSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 TyrSerPheAspLysProSerIleAlaAsnAlaValIlePheGlyGlyGlyGlyCysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GATAGGGAGATGATTGAGGAAAGACTTAAAAACATATGCTCAC------
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Matches:
Conservative:
Mismatches:
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32.478
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Q
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ABC transporter (ATP-binding protein) [Streptococcus
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LGELAYWQGVFGOFDDPDLDKHYLKNNWASSDGKTKFYAMCGYEDFLFARN
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YDLYDNLDYYLENGKYQGIFLSHGHDALGGLFYLLAEVSAPPVEGSELTIELAKLF
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KDMAKSFGINTDWMEVMGLVVSNSLIALSGALVSQQDGYADVSKGIGVIVIGLASIIV
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AENLLIARQRGEKRSLASRKITEHLASFEDLVKRTGNGLEKHLETPAGLLSGGQRQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADGRVIVAAVASNLVRIQOVFDSATAHGRRVVLTGTDAENĪVRTALRLEKLMITDERL
LIKPKDMSKFEDHELIILEAGRMGEPINSLQKMAAGRHRYVQIKEGDLVYIVTTPSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEAMVARVENLIYKAGGSVKLITQNLRVSGHANGRDLQLLMNLLKPQYLFPVQGEYRD
LAAHAKLAEEVGIFPENIHILKRGDIMVLNDEGFLHEGGVPASDVMIDGNAIGDVGNI
VLRDRKVLSEDGIFIVAITVSKKEKRIISKAKVNTRGFVYVKKSHDILRESAELVNTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLLMATLKKPALLLLDEHTAALDPKTSHSLMQLTDEFVTKDGLTALMITHHMEDALTY
GNRLIVWKDGNIIKDLNQMEKEQLTITDYYQLFD"
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// Agene="SpyM2_0657" blastp hit: gb|AAK74765.1| (AE007370)

metallo-beta-lactamase superfamily protein [Streptococcus

metallo-beta-lactamase superfamily protein [Streptococcus

phoemoniae TIGR4], andgb|AAK99342.1| (AE008432) Conserved

hypothetical protein [Streptococcus pneumoniae R6]"
                                                                                                                                                                                                                                                                                                                                                                                   /product="putative ABC transporter (ATP-binding protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyogenes M1 GAS]"
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5988. 6314
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	1 Juli 1 1 1 1 1 1 1 1 1	1 HisthrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGlu	
114 30453 126 30513 131 30573 30633	30693 168 30753 187 30789 202 30848	222 30849 242 30864 30864 30894 30894 30927 30987	322 31047 342 31077 31137 368 31197 368 31197 368
0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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Qy	369 SerAlaValTyrClyAspValLeuSerSerLeuGluLysA	383
Dp	31377 GAGTTTGTCTATGGTGATTATAAAGTTTATGATGTTCGTAAAATGATGCTAA	31436
δy dq	384 LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGly:::	402
3 8	703	į
g 9	3149	
ΟŊ	1	441
QQ	::: ::: ::: ::: ::: ::: ::: ::: ::: ::	31603
ΟŊ	441 uAspArgLysValLeuProAlaMetLeuAspIleValArgArgArg	456
QQ	31604	31663
δy	457AlakspLysLeuProAspIl	465
qq	31664	31715
Qy	465 ePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPheVa	485
QO	31716	31757
QY	485 1	505
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Qy	505	513
QQ	31814 GAAATCGAAGATTAAAATCCCTTAAAGAGTTACTAGGGATCACAATAATGGAAAGAAG	31873
Qy	514GluLySASpProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAl	531
QQ	31874 CTCTTT	31924
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qq	32102	32152
Qy	598	612
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Qy	612	612
qq	32213 CAATTTAGATAAAGTTCTTAGTGCATATAACAAACATAGAGACAAACCAATAGGTGAACA	32272
Qy	613GluAsnIleLeu	625
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Οy	626	636

pp ð

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YHQITSDGQLNAQAMIEWRAIKQTESETD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /hote="Best Blastp hit = sp|PS4589|YHCE_BACSU HYPOTHETICAL 29.5 KD PROTEIN IN GLPD-CSPB INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Best Blastp hit = pir!|H70023 N-acetyl-glucosamine catabolism homolog yutF - Bacillus subtilis spil263726|emb|CAB15219.1| (Z99120) similar to N-acetyl-glucosamine catabolism [Bacillus subtilis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Best Blastp hit = pir||H81982 hypothetical protein MAM6031 |Imported| - Neisseria meningitidis (group A strain 22491) >qi||7379363||emb||CAB83920.1| (AL162753) hypothetical protein NMA0631 |Neisseria meningitidis]"
                                                                                                                                                                                                                                                                                                      /note="Best Blastp hit = gb[AAB71730.1| (U65643) acyl-ACP
thioesterase [Myristica fragrans]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                >91|7475050|pir||A69822 hypothetical protein yhcE -
Bacillus subtilis >91|219980|cmb[cA65688.1| (X96983)
hypothetical protein [Bacillus subtilis]
>91|2633228|emb|CAB12733.1| (Z99108) yhcE [Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
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2695 3459
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3459. .4091
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4571 8677
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2126. .2605
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                                                                                                                                                                       Street 10889 bp DNA linear BCT 01-JUN-2001 Street Scroon pyogenes MI GAS strain SF370, section 78 of 167 of AE006549 AE004092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mtkQQIEKLADLLPPFAATLYLDMIPEFGGGYASYVYQTPKQDI
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MQEKLPSLSIMVSGESSKLFYQEQGFVLLAKGCKPGNENDSDVCQLVKYFSKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 10889)
Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S., Surorov,A.M., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
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Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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SL Young Blvd,
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32333 ATATTTTGATACAACAATTGATCGTAAACGATATACGTCTACAAAAGAAGTTTTAGATGC 32392
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                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Streptococcus/strain="SF370"
                                                                                  32393 CACTCTTATCCATCAATCCATCACTGGT 32420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /serotype="M1"
/db_xref="taxon:160490"
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Location/Qualifiers
                                                   636 aPheLeuSerAsnAsnAspIleThrGly
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Streptococcus pyogenes M1
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98. 720
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AUTHORS
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KEYWORDS
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TTTTTSTATTON="MAGNATYVVNTHSKLSYKNNHLIFKDAYKTELIHLSEIDILLLE
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VKVVDELVKVWGRHKPENIVIEMARRNQTTOKGQKNSREMKRIEEGIKELGSQILKE
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YVGPLARGNSRPAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNEDKNLDPEKYL)
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LPEDREMIEERLKTYAHLFDDKVWKQLKRRRYTGWGRLSRKLINGIRDKOSGKTILDF
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NLLAQIGDQYADLFLAAKNLSDAILLSDILRYNTEITKAPLSASMIKRYDEHHQDLTL
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MPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVV
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KHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTINLGA
PAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Best Blastp hit = pir||E81299 hypothetical protein
Cj1522c [imported] - Campylobacter jejuni (strain NCTC
11168) >q1|6968946|emb|CAB73942.1| (AL139078) hypothetical
protein Cj152c [Campylobacter jejuni]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIG
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hypothetical protein NMA0629 [Neisseria meningitidis]"
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/9874. ...
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/gene="SPy1047"
8677. .9546
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         10889
172
103
223
363
44
                            Conservative:
Mismatches:
Indels:
         Length:
Matches:
                                                          Gaps:
                                                                          US-10-008-355-2 (1-712) x AE006549 (1-10889)
               146.50
31.98%.
20.00%
                                              .948
         2.26
                           Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Query Match: DB:

Pred. No.:

Score:

Oy Db.	35 AsnG] ::	AsnGinGluAsnLeuaspArgMetArgGluLeuGlyPheThrLeuproLeuAspSerLeu :: :: :::: AATGAAGAAATGAAGATATCTTAGAGGATATTGTTTTAACATTGACTTATTTGAA	54 6451
٥y	r.S	Θ	74
qq	6452	GATAGGGAGATGATTGAGGAAAGACTTAAAACATATGCTCAC	6493
δλ	75 GlyI		92
gg	4	CTCTTTGATGATAAGGTGATGAACAGCTTAAACGTCGCCGTTATACTGGTTGG	6547
δλ	93 GLYA]	GlyAlaileGlnSerGlnSerThrVal	101
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δy	. 114	ThrMetGlyGluGluLeuProIleProGlyLeuSer	125
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Οy	143		150
QQ	6845 ATCG	TTATTGAAATGGCACGTGAAAATCAGACAACTCAAAAGGGCCAGAAAAATTCGCGA	6904
Qy	151 GluA	GluArgLeuArgLysAlaGlnGluValCysGlnGluLeuAlaLys~LysGlu	167
Dp	6905 GAGC		6964
Οy	168 AsnA	alGl	186
Dβ	6965 CATCO	GAAAATACTCAATTG	.7000
οy	187 PheLe	PheLeuIleValTyr	201
QQ	7001 CTCT	ATCTCTATTATCTCCAAAATGGAAGAGACAT	1060
οy	202 AlaPı	roProSerSerValGlyLysPheGlyGly	221
qq	1060		7060
δy	222 HisT	hrGlyAspPheSerValPheArgValTyrAlaGlyA	241
QC	7061		7075
ογ	242 TyrSe	sProTyrLysProValTyrPheAlaAla	261
QQ	7076 TATG	ATGTCGATCACATTGTTCCACAAAGT	7105
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δy	282 Thrs	hrSerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArg	301
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δy	322 TyrA	Tyrala SerLysTyralaGlnSerala AsnTyrTrpLysAsnSerIleGlyMetAsnArg	341

Db 8227 ATTACAAAAGG Oy 573 tSerTytGl Db 8287 TAGTCATTATGA Oy 588 pTyrAsnTyHi Db 8344 TGTGGAGCAGCA	608	613	Db 8455 CAAACATAGAGA Qy 621 rLysAsnTyrGl	8515	OY 020 GTYFALGELUAS 111 Db 8575 ATATACGTCTAC	2	ACCESSION AEU00733 ACCESSION AEU00733.1 KEYWORDS SOURCE Aquifex ae	ONGANISM AQUITES AG BACTETIA: REFERENCE 1 (bases: AUTHORS DECKETIG		JUNEAU 941		JOURNAL SUBMITTED COMMENT CA 92121 COMMENT PULAELIVE Hypothetic	FEATURES I SOUICE 1	gene	SQD CDD		
7259 342 7289 .359	7349 ATCACTAAGCATGTGGCACAAATTTTGGATAGTCGCATGAATACTAAATACGATGAAAAT 7408 368 368	7409 GATAAACTTATTCGAGAGGTTAAAGTGATTACCTTAAAATCTAAATTAGTTTCTGACTTC 7468 368 368	7469 CGAAAAGATTTCCAATTCTATAAAGTACGTGAGATTAACAATTACCATCATGCCCATGAT	368	369 SeralavaltyrGlyAspvalLeuSerSerLeuGluLysAlaTyr 383 	384 LysGluGlyAlaLysAlaAsnargGluMetThrTyrLeuSerGluThrLeuPheGly 402 ::	403 GlyThrGluValValargPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAs 421 	421 palaHisaladiyileLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLe 441 :::	441 uAspargLysValLeuProAlaMetLeuAspileValargArgArg 456 	457	465 ePheLysAsnValileAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPheVa 485 	485 IPheAspLysSerValValProTyrSerAspLysPheHisAla	500MetLeuLysSer	508 sPheAla	516 pProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAl 536 ::::: 8149 CTTAATCATTAAACTACCTAAA	536 aMetalaAsnalaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGl 556 	556 uMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMe 573 :::
9 6 6 6 04 04	da Vo	da Qy	qo :	da da	Qy Db	Qy	QV Pb	Oy Pp	. Q.	Oy Dp	Qy Db	Oy Db	Oy Db	Qy Db	Q7 Dp	9. do	Οy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCT 25-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adolicus:
Aquificae; Aquificae; Aquificales; Aquificaceae; Aquifex.; Aquificae; Aquificaeeae; Aquifex.; 1 Aquificaeeae; Aquifex.; 2 Lo 15569)
G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L., E., Overbeek, R., Shord, M.A., Keller, M., Aujay, M., Feldman, R.A., Short, J.M., Olsen, G.J. and Swanson, R.V. lete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                indicates no similarity to known proteins cal indicates similarity to a protein of unknown function. Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s 1 to 15569)
G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
, Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
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                                                    GAAATGAGCTGGCTCTGCCAAGCAAATATGTGAATTTTTTATATTTAGC 8286
                                                                                                                                                                                                                                                                                                                                                                                                                          2AT------AAGCATTATTAGATGAGATTATTGAGCAAATCAGTGA 8394
                                                                                                                                                                                                                                                                                                                                     GEGTEATTTTAGCAGATGCCAATTTAGATAAAGTTCTTAGTGCATATAA 8454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15569 bp DNA linear BCT 25 acolicus section 65 of 109 of the complete genome. AE000657
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gene

CDS

gene

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US-10-	US-10-008-355-2 (1-7	(1-712) x AE000733 (1-			DP	4618 GG
ò	. LenLenglvi	_			ΟŊ	289 gI
			AIRSELAIY VAIRIA ::: GAGCACGTAAGACAGGCTGGTTCTCTC	3879	qq	4678 GC
		LysAlaAspLysGlyMetTroLeu		38	Qy	303 eL
	3880 GTCGCGGACAAG	AAGTATTGAGGTTTGACT		3939	qq	4733
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0y	73			75	ΟŊ	344 aA
Db 4	4060 TACGGGGAA	AGGGTGAGGGTAATATCCT		4119	qq	4909 AA.
٥y	76 IleThrVals	SerAspGlnGlyLeuIleP	IleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyrGlyAlaIle 9	95	δy	364 9L
Db 4	 4120 ACGCACGTT1	ACGCACGTTTCCGCAACTGGAGACATA		4161	QQ	4969 AG
δ	96 GlnSerGlnS	GlnSerGlnSerThrVal		101	QY	384 sG
		::: AGCTCCGTGGGTGCGGGCG		4221	Dp	5026 AA
οy	102	AspHisA	-AspHisAspTvrLeuArqAspGlvPheValSerArgThr 1	114	ΟŊ	404 rG
4	222 TCCGTAGAAA	::: ACCGCCTTCAAAGAACACC		4281	Dp	2066
Qy	115 MetGlyGluG	GluLeuProileProGlyL	<pre>MetGlyGluGluLeuProileProGlyLeuSerValLysTyrLeuArgLysIleValLys 1.</pre>	134	δλ	424 aG
Db 4	282 GTGGGCGAGG	 GAG		4305	do .	
οy	135 ValThrAspI	LysValGluGlyGlnLeuL		154	δλ	
Db 4	306 AAAATTGAAG	:::::::: GAACTTAAGGAAGAAATCA		4365	qq	
οy	155 LysAlaGlnG	LysAlaGlnGluValC	AlaAsp	170	ΟŊ	464 pI.
4		AACT		4419	QQ	5215 CA
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	::: 4420 GAT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		4434	qq	5272 TT
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0y	211 GlyGlyAspT	ThrAspAsnTrpMetTrpP	GlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArg 2:	230	Οy	524 rV

an	DD .44/9 91	6/44
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8 8	277	ANIAMOGOMOGIC 4
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COMMENT On Jul 19, 2002 this sequence version replaced gi:17998481. Web site: http://www.ncgr.ac.cn	(http://genemark.biology.gatech.edu/GeneMark/), tRNAscan.SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan.SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan.SE (Fhe complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR. Location/Qualifiers Location/Qualifiers	/sub_species="japonica" //db_xref="laxon:4530" /chromosome="4". /clone="053N880043L24" /clone="053N880043L24" /clone="1b="CUGI-O53N88" ORIGIN ORIGIN	Scores: 256 imilarity: 36.64% l Similarity: 20.56% ch: 8	US-10-008-355-2 (1-712) x OSJNOU169 (1-162754) QY	Qy 87 ASNHiSHiSCYSGlyTYrGlyAlaIleGlnSerGlnSerThrValAspHisAspTyrLeu 106	Oy 127 LysTyrLeuArgLysIleValLysValThrAspLysValGluGlyGln 142 ::	Oy 163 LeualaLysLysGluasnalaAspGluasnGlnLeuCysIleValGluProPheTyrSer 182 :::::: :::	195 LysaspValargMetValPhealaProProSerSerValGlyLysPheGlyGly ::	Qy 213 AspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyr 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::||||||||
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                                                                                                                                                                                                                                                                                        ProGln---AspGlyAlaTrpTyrAsnTyrHisThrTh 594
                                                                                                                                                                                                                                                                                                                                                                                                    GlnAspProLysSerAspGluPheAlaValGlnGluAs 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHi 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsplleThrGlyGlyAsnSerGlySerProValPheAs 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Actinobacteria; Actinobacteridae; rococcineae; Micrococcaceae; Micrococcus.
                                                                                                                                                                          ThrMetArgMetSerTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ushi,K.
snce of an alpha-amylase gene from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GGGAAATGG 51753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAlaPheAspGlyAsnTrp 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Micrococcus sp
. 71, 35-42 (1990)
alifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se gene.
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BASE COUNT	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	-10-008-	141 (161 (181 1	201		1602	238	258	273		1812	295	315	331	
BASE	Aligni Pred. Score Percel Best Query DB:	ns-	Qy Db	Oy Db	Oy Dp	δ γ	9	Dp	Qy Db	Οy	oy B	οy	QQ	QY	Qy Db	ço q	δλ

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Qy	611	ValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGlu 629
QQ	2916	3GGCAACGATGTTCGAG
Qy	630	
qq Q	2970	ccattagctgacgagagaaaatatcgctftcttgtcargatattaccgcggg 3026
QY	647	AsnSerGlySerProValPheAspLysAsnGlyArgLeulleGlyLeuAlaPheAspGly 666 :::::::

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LMILLESFTODDWIQIAEESDAYGYAIIRPSEKWVPEROSFIEEKIAEEPVOLDTAEG
VOQVUTDTPERCHTITTPREKEAVLONDROQOAFGONYLLSWOANLLIAHLPMETTFV
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EMWFKSESRGKFVHIITVAAVHDEDGEFOGVLEYVODIQPYREIDTDYFRGLE
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nwtekelldikgigpatikklkengikfk"
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LERLGVHYEISERTQIPILDACPLVLDCRVDRIVEEDGICHIFAKILERLVAPELLDE
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/transl_table=11
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3099. .3548
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                                                   /gene="spr0486"
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Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S., Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S., Gilmour,R., Glass,J.S., Khoja,H., Kraft,A., Ladace,R., Lee,L.N., Lefkowitz,E.J., Lu,J., Matsushima,P., McAhren,S., McHenney,M., McLeaster,K., Mundy,C., Nicas,T.I., Norris,F.H., O'Gara,M., Peery,R., Robertson,G.T., Rockey,P., Sun,P.-M., Winkler,M.E., Yang,Y., Young-Bellido,M., Zhao,G., 200,K.C., Baltz,R.H., Jaskunas,S.R., Rosteck,P.R. Jr., Skatrud,P.L.
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Hoskins, J.A., Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, S., DeHoff, B.S., Estrem, S., Fritz, L., Fu, D.-J., Fuller, W., Geringer, C. Gilmour, R., Glass, J.S., Hann, A., Khoja, H., Kraft, A., Ladgoe, R., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., McHenney, M., McLeaster, K., Mundy, C., Nicas, T. I., Nortis, F. H., O'Gara, M., Peery, R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M. E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R. H., Jaskunas, S. R., Rosteck, P. R. Jr., Skatrud, P. L.
                                                                                 111 :::||||| :::|||||| 3087 ATTIGGATCAAGGTTCGGACAAGGTGTACACGTACGAACCGGTAGATTTGCCAGCA 3146
3027 GACGCGGCCAAAGACGGCGGAGATAAAGGCTTTACGATTTCTTCACCACCACAAGCAAATGAA 3086
                                                                                                                                                                                              AE008428 10292 bp DNA linear BCT 13-SE:
Streptococcus pneumoniae R6 section 44 of 184 of the complete
                                                   667 AsnTrpGluAlaMetSerGlyAsp-----IleGluPheGluPro---AspLeuGlnArg
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Genome of the bacterium Streptococcus pneumoniae strain R6
J. Bacteriol. 183 (19), 5709-5717 (2001)
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Streptococcus pneumoniae R6
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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353, 500
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AE008428 AE007317
AE008428.1 GI:15458055
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JOURNAL
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5143 GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTAAGCCTTATTCAATCGTTATTCCACCA 5202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 LysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLys
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KQSRGELTYEQVYEDATAYHHTIDASTEEADLVSLRIVELLSRRGFSFSPATLLAIHK
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CHSLRNYSOHTDLPINEVKAVSPDDETVIIDFYIDLDYLLNSNFKWKKLKGELIKLNO
ETSKIDAIALVKEYFNALTELYGNYNKLFLKLNHNTLVDIKSKLESLKLKHSRYYISK
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ALWPFSTMGWPEVDSEDFKRYFPTSTLVTGYDIIFFWVSRMIFQSLEFTGRQPFQNVL
IHGLIRDEQGRKMSKSLGNGIDPMDVIEKYGADALRWFLSNGSAPGQDVRFSYEKMDA
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TENFDKFEFGVAGHILYNFIWEEFANWYVELTKEVLYSDNEDDKVITRSVLLYTLDKI
LRLLHSIMPFVTEEIFGQYAEGSIVTAAYPTVNPAFEDLAAHTGVESLKDLIRAVRNA
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EIVKMLLASEGKKTGITIVEKPIVRTKFKRLQETGMEAENYFILHFDKEEKFQGGQLT
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LDDIPKLVLIDNPLKHFEFKKNIIKNEIIEYRSVEDLY"
                                                                                                                                                                                                                                                                                                                  /translation="MSDVKEEVSSLSEKQLRQIDVEYAELNDSDIIERLAYLEINNNE
KRIVISDIEPTKEIMSVSDQIFEIQKNFQKIKNMFELFISDVSDFLSIKNKLESKELE
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KIEKRVHSVGHSERTGVVVEPRLSTQWFVKMDQLAKNAIANQDTEDKVEFYPPRFNDT
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VITGAEIFLPLVDLLNVEEELARLEKELAKWQKELDMVGKKLSNERFVANAKPEVVQK
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ISRYDLGRESFLTKVWEWKDEYATTIKEQWGKMGLSVDYSRERFTLDEGLSKAVRKVF
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TRPETMFGDVAIAVNPEDPRYKDLIGKNVILPIANKLIPIVGDEHADPEFGTGVVKIT
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5068. .7719
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/protein id="AAK99297 1"
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/protein_id="AAK99296.1"
/db_xref="GI:15458063"
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/db_xref="GI:15458062"
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/codon_start=1
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/gene="spr0493"
7774. .854
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5068. .7719
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5721

456 ArgileProAlaAspLysLeuProAspIlePheLysAsnValileAspLysLysPheLys 475

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10292

Length:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 rLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu-- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 -ThrSerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValAr 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aThrArglleLysTyrAla---SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSe 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uArgAlaPheAlaAspTrpIleArgLys-----AsnGlyLysSerAlaValTy 372
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Matches:
Conservative:
Mismatches:
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Location/Qualifiers
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Thermoproteaceae; Pyrobaculum. REFERENCE 1 (bases 1 to 14169) AITHURDE Fitz-Gibbon C 13400r H Film H 1 Chattor W O Cimon M 1 and	Miller, J. H. Genome sequence of the hyperthermophilic cremarchaeon Pyrobaculu	aerophilum Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002) 11792869 2 (bases 1 to 14169)	7.S.T., Ladner,H., Kim,UJ., Stetter,K.O., Simo J.J.H. nission [12-DEC-2001] Microbiology and Molecular Genetic		/organism="Pyrobaculum aerophilum" /strain="IM2" //db_xref="taxon:13773" gene 144. 1019	/gene="PAE2116" CDS 144. 1019 /gene="PAE2116" /note="Protein fate; Protein modification and repair"	/codon_start=1 /transl_table=11 /product="methionine aminopeptidase" /protein_id="AAL63956.1"	/db_xref="G1:18160616" /translation="MLRILRQVGDVVNKALKYALDLTQPDMPVLELCERVEAFIRAND /kranslation="MLRILRARGDSLKIPKTGLVKIDVGAQRDGYIVDAAVTVTLGPV FNNLQRAAKSALESAAINAAKPGIKAWQIGEVVER?IKSFGLSPIYNLTGHKVERYLLH	AGHVIPNYSDKTASQALAPGDVYAIEPFATNGEGŸVVDGGEITIYRLARMRHKNYQHL IDIISARAGPLPPTPRWFPQLTDDAIREALKAGVĽQGYEVLVERSKGFVAQFEDTVYV GENEVIPLVYTLELL" gene 1060 2709	/11 /	/note="Protein fate; Protein folding and stabilization" /codon.start=1	/tanscable=la /product="thermosome (chaperonin) alpha subunit" /protein_id="AAL63957.1"	/db_xref="G1:18160617" /translatin="mSQNULTQIGGVPVLVLKEGYQRAFGKEALRLNIMJARAIAEVM RTTLGPKGMDKMLIDSLGDITITNDGATILDEMDYQHPIAKLLVEISKSQEEEAGDGT TTAVVLAGALLEEREKLLEKNIHPTVIVSGFKKALDVAABHLRKVAIPVNRYDVDYLR	KIAMTSMGGKISETVKEYFADLAVKAVLQVAEERNGKWYVDLDNIQIVKKHGGSLLDT QLVYGIVVDKEVVHAAMPKRVVNAKTALLDAPLEYERPEIDAEIR NUPPOMRAEUEB EERILGGYVDKLKSLGYVVLFTTKGIDDIAQYXLAKAGILAVRVKKSDIEKLVRATG ARLVTSIEDLTERDALGFAGLVEBRRVGDEKMVFYGQCKNPKAVSILUKGGFERLVDBA	ERNLDDALSVSDVVBDPY ILPAGGAAG TEAARAVRAFAFKVGGREQY AVEAFARALE VIPKALAEBRAGLDPIDILTELTHKHEQTDGWKYGLDVYGGKVDMVSLGLVEPLTVKI NALKVAVEAASMYLIRTDEIITAASKLEKEEEKKEEKKEEFD" complement (27063257)	/gene="PAE2118" CDS complement(2706. 3257) /gene="PAE2118" /note="Hypothetical"	/codon_start=1 /transl_trable=11 /transl_trable=11 /product="hypothetical protein" /protein_id="AaL63958.1" /db_xref="G1:1816618" /translation="MLABYVAGNVALIQERAYHRLVVILSATSMSSVMMSGLALFFEP AFKYLSALALGVLSRRVLRNAEEKIRKFMANVEREANARRYFATLKEYYNPIDYL TKLYABPTIEDPIIAARKKIRASTYLFSQSITALRAKNRLVITITALTISIPHLVLN	KDIIAIGVILLIVILLFRKRSWV" gene complement(32474278)
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Mismatches:
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Query Match:
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697		
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URCE ORGANISM	unidentified M unidentified unclassified	
REFERENCE AUTHORS TITLE JOURNAL	1 (bases 1 to 2652) Brown, J.R. and Wang, M. Valyl tRNA synthetase (EC 6.1.1.9) from Streptococcus pneumon patent: EP 0909818-A 1 21-APR-1999;	oniae
	SMITHKLINE BEECHAM CORP (US)	

FEATURE SOI	RES Source	e O	111	ocat	Location/Qualifier 1. 2652 Aorganism-"unident	alifiers	fied"	•			
BASE COUNT ORIGIN	COUNT	£4	733 a	g B	Krer∎" C 512 c	_xrer="taxon:3264" 612 c 621 g	e#				
Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	ment No.:: nt Si Local Matc	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	:: .ty: .arity:		5.67 130.00 32.81\$ 20.70\$ 3.50\$	120210	Length: Matches: Conservati Mismatches Indels: Gaps:	 	2652 106 62 166 178 25		
US-10	-008	-355-2	(1-712	2) x	x A81135	(1-2652	2)				
Oy Dp	192 76	Aspvall GATGTT	Phe	CCT	rcaggcg,	TCAAAAG	Lysast GCTAAGCCI	ovalAr TATTC	Aspvalphe	o 203 A 135	
oy.	204 136	_	Serval	.G1y1	ProSerSerValGlyLysPheGlyG ::: CAAACGTTACAGGTAAACTT	lyGlyAsp	ThrAspAsn	пТгрме	ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr 	r 223 T 162	
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oy op	244		AsnLys	Prof.	fyrLysP. ::: TTGCAAG	roValTyr ::: ATATTATC	Phealaala	aValSe \AAACG	LysaspasnLysProTyrLysProValTyrPhealaalaValSerMetGlnGlyTyrLys 	s 263 T 228	
Qy	264 229		рАзрТуг	rAla	detThri	leGlyPhe :: rrrGGCr9	ProGlySer CCTGGGATG	cThras sgacca	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr	r 282 270	
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oy Op	319 379		LysTyr AAGGAA	Ala.	SerLy 1 rGGGGCAA	ysTyrAla \GATGGGG	GlnserAla CTCTCTGTA	aAsnTy ::: \GACTA	ArglleLysTyrAlaSerLysTyrAlaGInSerAlaAsnTyrTrpLysAsnSerIle 	e 337	
Oy Dp	338 439		:AsnArç ::: :GACGAA	161y1 GGT	LeuAlaA. ::: TGTCA-	rgLeuAsp	valileGl _y	ArgLy	GlyMetasnargGlyLeualaargLeuaspValIleGlyargLysargalagluGluarg 	.g 357 .G 474	
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Qy Db	374 535		GCAGCT	,cec	ValLa	Leuserser CTTTCTGAI	::: ::: :arrGaGGrO	sAlaTy :: SATTCA	Asp	s 388	
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oy Ob	397 655		Serglu ccTGAG	Thri	ceuPheG ::: \TGTTTG	SerGluThrLeuPheGlyGlyThr ACTCGTCTGAGACCATGTTTGGGGACGTT	GluValVal	lArgPh	SerGluThrLeupheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn :: CCTGAGACCATGTTTGGGGACGTT	n 414 - 684	
oy Dp	415		AlaLeuAlaThrAsnProAsp. ::: :: GCGGTTGCGGTCAACCCAGAA	Asni 	AsnProAspA ::: AACCCAGAA-	laHisAla	GlylleLeu	ıLysse	AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLySSerLeuAspAspLysTyr 	r 434 C 717	

2y 435 LysAspTyrLeuProSerLeuAspArgLysValLeuProAla 448	2y 449 MetLeuAsp	456 ArglleProAlaAspLysLeuProAspIlePheLysAsnVallleAspLysLysPheLys 47	DD 835 CACGATCCAAATGACTTCTTGGTTGGCCAACGTCATAACTTGCCACAAGTCAAGGTCATG 894	476	895	2y 496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIJeGluLys 515 ::	516	Db 991 GGTGCCCTCGTCAAAATCGAAAAACGTGTCCACAGTGTTGGTCACTACAGGGTACAGGT 1050	2y 532IleGlnAla 534	Ob 1051 GTTGTGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110	535 AspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeu 554	1111 AACGCCATTGCCAACCAAGACAGAGACAAG	2y 555 ArgGluMetTyrProGlyArgAlaLeuProSer565 	266	1204 GACTGGGTTATCTCTCGTCAGCTCTGGTGGGGTCAC	586 GlyAlaTrpTyrAsnTyrHi	1246	<pre>2y 606 SerAspGluPheAlaValGluAsnIleLeuAsp 617</pre>	T 13 782 TTION SION ON	SOURCE UNKNOWN. ORGANISM UDKNOWN. URCLASSIFIEG. AUTHORS I (bases 1 to 2652) AUTHORS Brown,J.R., Jaworski,D.D., Lawlor,E.J. and Wang,M. TITLE Valy1 trna polynucleotides from Streptococcus pneumoniae JOURNAL Patent: US 5849555-A 1 15-DEC-1998; FEATURES. Location/Qualifiers	/or /or /or /or	Alignment Scores: 5.67 Length: 2652
Oy 4.	Oy 4		Db 8	0у 4	Db 8	Oy 4 Db 9	. yo	6 qa	0у 5	Db 10	•	DD 1.1	S H	0γ 5	Db 12	Qy 5	~	Oy 6 Db 13	RESULT AR06578 LOCUS DEFINIT ACCESSION VERSION KEYMORD	SOURCE ORGAN REFEREN AUTHO TITLE JOURN FEATURE	BASE CO	Alignme Pred. N

Glyaspthrlyslystyri aacgacgaaccatgi	LysPheHisAlaMetLeul ::: CGTTTTGAAGCTCGT	AspProAlaValGluLeu8 ::::: GGTGCCCTCGTCAAAATCC	GTTGTGGTTGAACCTCGC	Aspalametalaasnala: ::: :: aacgccaffgccaaccaac	ArgGluMetTyrProGly/ GTCGAATTCTACCCACCT	AspAlaAsnPheThrMet, ACTGGGTTATCTCTCGT	GlyAlaTrpTyrAsnTyrI CCTGCCTGGTACAAT	SerAspGluPheAlaVald ::: GGTGACGGATGGACTCAGG	E26074 Novel vals.	E26074 E26074.1 GI:130: JP 1999113577-A/. unidentified.	unidentified unclassified. 1 (bases 1 to 20 James, R.B., Deboo	Novel vals Patent: JP 19991. SMITHKLINE BEECH OS Unidentifie	PN JP 19991135 PD 27-APR-1999 PF 17-OCT-1997 PR	PI JAMES R BURA MING WANG PC C12N15/09, AS PC C07K14/335,	PC C07K16/12,C G01N33/569, PC C12N15/00,A0 CC Strandedness		Location 1265; /organis	733 a 612
476 895	496 946	516 991		Qy 535 As :: Db 1111 AA	1144	566	Qy 586 Gl	90	RESULT 14 E26074 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS						FEATURES source	BASE COUNT
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50% G AR065782 (1-26	CAGGCGATCAAAAG	ysPheGlyGlyAsp ACTT	heArgValTyrAla	YrLysProValTyr ::: :GCAAGATATTATC	etThrileGlyPhe ::: ACCCTTTGGCTT	spArgIleGluAsn :: ::: AGCGCTTGCGTGGT	ysGlnGlyIleTrp 	SerLysTyrAla 3GGCCAGATGGG	euAlaArgLeuAsp ::: GTCA	leargLys ::: acaagaaaggcTg	ValLeuSerSer CAGCCCTTTCTGAT	hrTyrLeu ::: ATTACATGCTGGAA	euPheGlyGlyThr :: rGTTTGGGGACGTT	roAspAlaHisAla ::: CAGAA	TyrLeu AAATGTCATCCTT	CAGATCCTGAGTTT	ysLeuProAspile	10110011001101
3. (1-712) x	ovalPhe GTTTTCAAGCCTT	SerSerValGlyLysPhe ::: \AACGTTACAGGTAAACTT	/AspPheSerValP 	LysaspasnLysProT TGGGATACAACTT	aAspAspTyrAlaM	SerTrpGlyValGluAspArg CAGGCTAAGGTAGAGGAGCGC	GAGTCTTCTTGACGAAGTCTGGAATGGAAAGAC	JIleLysTyrAla- ATCAAGGAACAAT	GlyMetAsnArgGlyLeuAlaAr ::::: ACTCTTGACGAAGGTTTGTCA	AlaPheAlaAspTrplleArgLys GTCTTTACAAGAAA	p l ccagcagcTcgca	AlaAsnArgGluMetThrTyrLeu 	397SerGluThrLeuPheGlyGlyThr 	aLeuAlaThrAsnP ::: GTTGCGGTCAACC	LysaspTyrLeupros 	MetLeuAsp ::: GTTGGAGATGAGCACG		
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	Oy 4	476 G	lyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495
		10	
	Qy 4	496 L	LyspheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515
	6 qa	: 946 C	:::
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	ORGANISM	MSIN	unidentilied .unidentilied
	REFEREN	Š E	unclassified. 1 (bases 1 to 2652)
	AUTHORS	SRS E	James, R.B., Deborah, D.J., Elizabeth, J.L. and Ming, W. Novel vals
	JOURNAL	MAL	Patent: JP 1999113577-A 1 27-APR-1999; SMITHKLINE BEECHAM CORP
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_	BASE COUNT	UNT	733 a 612 c 621 g 686 t

ORIGIN						i	i
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Percer	t Similarity:		Conservative: Wismatches:	62 166		qq	835 C
Query DB:		3.508 6	Indels: Gaps:	178 25		Qy	476 G
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;		,	-			QY	496 Ly
<u>a</u>		TTCAGGCGATCAAAA	Lysaspvalal GGCTAAGCCTTATT	ASPANDALFIIE	135	qa	: 946 CC
è		v. Lyspheglyglyae	Thrase as transfer		223	ΟY	516 A
S 8		TAAACTT	and timeudeu mid		162	qa	991 G
ολ	224 GlyAspPheSerVa	lPheArgValTyrAl	aGlyAlaAspAsnA	GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer	243	δλ	
qq	163 GGT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOSCACOL	171	a a	
٥y	244 LysAspAsnLysPr	OTyrLysProValTy	rPheAlaAlaValS	LysAspAsnLysProTyrLysProvalTyrPheAlaAlaValSerMetGlnGlyTyrLys	263	70 - 1	535 As
q	172 TGGGATACAAC	TTTGCAAGATATTAT	CATCCGTCAAAAAC	TGGGATACAACTTTGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTTTTGAT	228	3 3	
Qy	264 AlaAspAspTyrAl	aMetThrileGlyPh	eProGlySerThrA:	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr	282	Š t	
qa	229	ACCCTTTGGCT	TCCTGGGATGGACC		270	a :	
٥y	283 SerTrpGlyValGl	uAspArgIleGluAs	nGluAsnAsnProA:		302	ਨੇ ਫ਼ਿ	1204 AS
Dp	271 CAGGCTAAGGTAGA	GGAGCGCTTGCGTGC	TGAGGCATTTCCC	CAGGCTAAGGTAGAGGAGCGCTTGCGTGGTGAGGGCATTTCCCGCTATGACCTTGGTCGT	330	3 3	
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٥٧ ط	319 ArgileLysTyrAl 379 ACTATCAAGGAACA	aSerLysTyrA] ATGGGGAAGATGGG	aGlnSerAlaAsnTyr: ::: GTCTCTGTAGACTA	rpLysAsnSerIle :::	337	r dd	
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oy Dp	338 GlyMetAsnArgGlyLeuAlaArg ::::: :: 439 ACTCTTGACGAAGGTTTGTCA	yLeuAlaArgLeuAs ::: TTTGTCA	pvalileGlyArgLy	ysArgAlaGluGluArg ::: AAAGCTGTTCGTAAG	357 474	AE0135 LOCUS DEFINI	AE013500 LOCUS DEFINITION
රු පු	358 AlaPheAlaAspTrplleArgLys 	pIleArgLys ::: TTACAAGAAAGGCTG	AsnGlyLy ::	AlapheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGly	373 534	ACC! VERS	ACCESSION VERSION KEYWORDS
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Οÿ	C)	tThrTyrLeu			396	KEF I	REFERENCE AUTHORS
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Oy Dp	397SerGluTh 655 ACTCGTCCTGAGAC	rLeuPheGlyGlyTh ::: CATGTTTGGGGACGT	rGluValValArgPl T	SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn :: ACTCGTCCTGAGACCATGTTTGGGGACGTT	414	[I]	TITLE
Oý Db	415 AlaLeuAlaThrAs ::: 685 GCGTTGCGGTCAA	nProAspAlaHisAl ::: CCCAGAA	aGlyIleLeuLysS	AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr ::: :::	434	REFI	JOURNAL REFERENCE AUTHORS
oy	435 Lysasp	TyrLe	uProSerLeuAspA		448		
qa &	718 AAGACTTGATTGG	TAAAAATGTCATCCT	TCCAATCGCTA		774	E P	TITLE JOURNAL
ģ	449 MetheuAsp	1 1 1 1 1 1 4 6 6 6 6 6 6 6 6 7	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TleValArgArg	455		

Db 775 Qy 456 Db 835 Qy 476 Db 895 Qy 496 Db 895 Qy 496 Db 991 Qy 532 Db 1051 Qy 555 Db 1204 Qy 566 Db 1204 Qy 566	::: GTTGGAGATGAGCACCCAGATCCTGGTTTGGTACTGGTGTGTGGAAATCACACCTGCC 834	ArgileproalaAspLysLeuProAspIlePheLysAsnValileAspLysLysPheLys 475 	GlyaspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495 	LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515	ASPProAlaValGluLeuSerLySSerValIleAlaAlaAlaArgAla531 :::::: :: GGTGCCTCGTCAAAATCGAAAAACGTGTCCACAGTCTTGGTCACTCAGAGCGTACAGGT 1050		GTTGTGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110	AspalametalaasnalaTyralaileGluLysGlyLysargLeuPhePheAlaGlyLeu 554 	ArgGluMetTyrProGlyArgAlaLeuProSer	AspalaasnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585 ::: :::: ::: GACTGGGTTATCTCTCGTCAGCTCTGGTGGGGTCACCAAATC 1245	GlyalaTrpTyrasnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605 	SeraspGluPhealaValGlnGluAsnIleLeuAsp 617 ::	AE013500 9827 bp DNA linear BCT 17-MAY-2002 Complete genome. AE013500 AE008384 AE013500.1 G1:20907162	Methanosarcina mazei Goel. I Methanosarcina mazei Goel Archaea: Euryarchaecut; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.	l (bases 1 to 9827) Deppenmeier, U., Johann, A., Hartsch, T., Merkl, R., Schmitz, R.A., Martinez-Arias, R., Henne, A., Wiezer, A., Baeumer, S., Jacobi, C., Brueggemann, H., Lienard, T., Christmann, A., Boemecke, M., Steckel, S., Bhattacharyya, A., Lykidis, A., Overbeek, R., Klenk, HP.,	unsalus, K.F., FILLZ, HJ. and he genome of Methanosarcina ma ransfer between Bacteria and A Mol Microbiol Biotechnol	~ · c	., Overbeek, R., Klenk, HP., and Gottschalk, G. ttingen Genomics Laboratory, Institut
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	qq	Oy Dp	Qy Db	Qy	ογ Op	Óγ	QQ	Oy Db	oy Op	Qy Dp	Qy	Qy Dp	REST AEOJ LOCT DEFJ ACCE VERS	SOUI	REFI AC	LT F	" : 1월 1	11

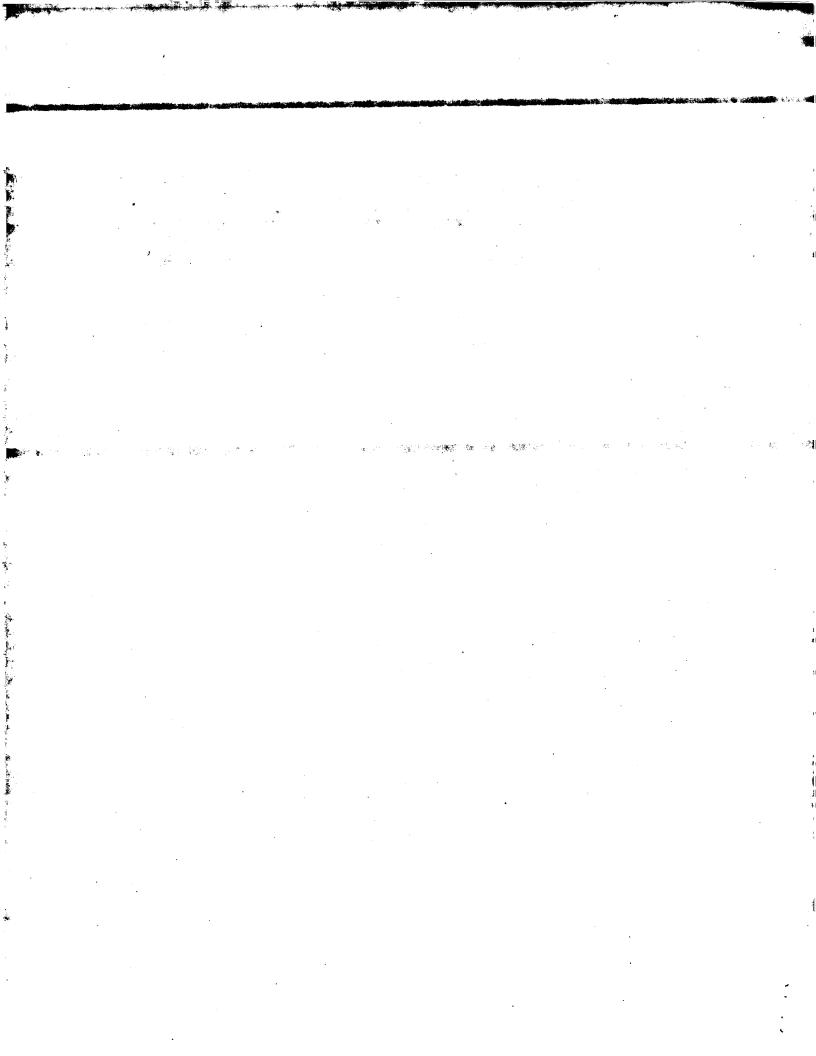
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Mismatches:
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32.49%
17.39%
3.50%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred No :
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                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
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2412. .3509
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KEALGLLESEI ENEPENI PVSENI EVSENI SVPKNI LESMA I ADMYKDSGL I FSDTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEELLETLTVLGTLFKENREFEKAIRMYERVLEVQKQLLEIMPPASCHDHDHNLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHNLNHSHNLNHTHDLNHDHDLNHDLDHDEMDHDHALEHCHDLDIETTYFELGVLHS
EIGDEEKASVYHRQALERFEQIIAEQSGNPEILILTSGKAFFSGMSLLEKLESENKDS
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                                                                                                                                                         gene
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٥y	93	GlyAlaIleGlnSerGlnSer 99	
qq	3306	GACGAGCCGGGCTGTGCCGTACTGAAAGCTGTTAAGGATGGGATTATTCCTGAGGAACGG 3365	
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Op	3366		
οy	120	ProlleProGlyLeuSerValLysTyrLeuArgLysIleValLysValThr 136	
QQ	3426	GGGTTGAAGAGGCTTGAAAAGGTTCAAGAAAATAGCAGTGGACATTAAAAAATAT 3485	
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QQ	3486	• ⋖	
οý	148		
qa	3546	GGTTTTATCAATCGTTTTCGACCTGGGAAGACTG3581	
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δλ	208	GlyLysPheGly	
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οy	228	ValPheArgvalTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLys 247	
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QQ	3771	GAAAAGATCGAAAAGGAAGTGAATAACCCTGAGATTTCATAT 3812	
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οy	327	nSerAlaAsnTyrTrpLysAsnSerI	
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QQ	3948	TTTA	

Qy	382 AlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLv 4002 CCCGTTAAAGCAAGAGAGTATATCTCTC	euSerGluThrLeuPhe 401 ::: :: CGATGAAAGGGATTTTT 4046
٥y	402 GlyGlyThrGluvalValArgPheAlaGlnPh	42
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Óγ	422AlaHisAlaGlyIleLeuLy	sSerLeuAspAsp 432
QQ	4104 TACCTGGAAGATTTCCTGAAAACGATCGAACACATAGGGCTCTGTTT	AGCCGGAGAA 4163
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δ.	547	TyrProGlyArg 561
qq	4683 GACTACTATACGAAGGCGÁGGAAACTTTCCGGGGACTGATTAATAAA	- 4
Oy	562 AlaLeuProSerAspAlaAsnPheThrMetArgMetSer	TyrGly 576
pp	Db 4740 CTGCTTGAAGCCGATAAAAACCTTGCCAGCTCTTTAGATGAACTGGCAGAG	GCTGTTTTCA 4799
Οy	577 SerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHi	r.G
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266	94	. 250			
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Dp	Qy	qq	Qy	qa	

Search completed: May 23, 2003, 11:33:15 Job time: 4235.8 secs



SUMMARIES

us-10-008-355-2.p2n.rng

GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd. Copyright

nucleic search, using frame_plus_p2n model protein May 23, 2003, 07:32:23 ; Search time 316.182 Seconds Run on:

(without alignments) 5071.208 Million cell updates/sec

US-10-008-355-2 3719 1 MQMKLKSILLGAALLLGASG......LFMIDKWGQCPRLIQELKLI 712 Title: Perfect :

score:

Sequence:

0.5 7.0 7.0 , Fgapext , Delext Xgapext Ygapext . . Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, **BLOSUM62** Scoring table:

2185239 seqs, 1125999159 residues Searched:

4370478 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Command line parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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. [7] 	371	100.0	•		 AAL43	Porphyromonas ging
	146.	r	4104		ABN68149	S
e	3 134.5	3.6	2853	20	AAX91754	s d
7	134.		2859		AAX91621	ß
	13	٠.	2652		AAS55647	treptococcus
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c 1	12		6004		16	Streptococcus pneu
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17	122.		4716		ABQ69595	
ï	122.		4731		ABQ67873	
1	122.		495269		ABQ67195	Listeria innocua c
1.	121.		2649	~	ABN66404	Streptococcus poly
ĩ	121.		2155561		ABN71527	Streptococcus poly
1,	12		2646		ABN66405	
2	119.		3271		AA164839	'n
5	117.		1664976		AAV21209	Methanococcus jann
c 5:		3.1	œ	17	AAT42063	Haemophilus influe
.23	116.		15424		AAC81763	Porcine Lelystad v
	116.	.3.1	15424		AAC81764	Porcine Lelystad v
2	11	3.1	3598		AAC77776	Human cancer assoc
2	115.	3.1	6822		ABN71008	Streptococcus poly
5.	115.	3.1	6834		ABN68971	Streptococcus poly
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miα	113.		2826		AAS52/31	
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C 4	11		3285		AAH54398	S. epidermidis gen
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C 4.	11		4411529		96	Mycobacterium tube
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4	_	٠.	266	19	AAV52267	ococcus b
4	110.	3.0		21	0	North American por

ALIGNMENTS

AAL43635 standard; DNA; 2139 AAL43635;

RESULT 1 AAL43635

BP

(first entry) 05-SEP-2002

Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence.

Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis.

Porphyromonas gingivalis.

Location/Qualifiers 1..2139

Key

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           GlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPhe
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(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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                     LeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGlu
                                               LeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAla
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                                                                                                                                                                                                                                                                                                       Streptococcus polynucleotide SEQ ID NO 4211.
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2000GB-0028727.
2001GB-0005640.
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07-MAR-2001;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bilogical sample. (I) is used to detect Streptococcus in a bilogical sample. (I) is used to detect Streptococcus in a become or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity contractography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1978 GGACGTTTGTCTCGAAAATTGATTAATGGTATTAGGGGATAAGCAATCTGGCAAAACAATA 2037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 TyrSerPheAspLysProSerIleAlaAsnAlaValIlePheGlyGlyGlyCysThr
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                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infe or disease caused by Streptococcus bacteria, such as meningitis, for detecting a compound that binds to the protein -
   ن
   Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 G; 1206 T; · 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grandi G,
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Matches:
Conservative:
Mismatches:
   Margarit Ros YI,
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                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 3578; 4525pp; English
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146.50
31.98%
20.00%
3.94%
Masignani V,
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ò	13 LysIleValLysValThrAspLysValGluGlyGln	qd 	3079 CAAGAAATAGGCAAAGCAACG
qq	2215 CAGACTGTAAAAGTTGTTGATGAATTGGTCAAAGTAATGGGGCGGCGTAAGCCAGAAAAT 2274	Δ	
oy.		qq	AAAACAGAAATTACA
QQ	2275 ATCGTTATTGAAATGGCACGTGAAAATCACACACTCAAAAGGGCCAGAAAAATTCGCGA 2334	^O	421 pAlaHisAlaGlvIleLeuL
Oy Dp	151 GluhrgLeuhrgLyshlaGlnGluValCysGlnGluLeuhlaLysLysGlu 167 	G QQ	
ογ		oy d	441 uAspargLysValLeuPro-
qq	2395 CATCCTGTTGAAATACTCAATTG	3 8	
ογ	187 PheLeulleValTyrAspValPheLysAspValArgMetValPhe 201	ž 6	3306 AGGCGGATTCTCCAAGGAGT
QQ	2431 CTCTATCTCTATTATCTCCAAAATGGAAGACATGTATGTGGACCAAGAATTAGATATT 2490	3 6	
οy	AlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArg	7 AC	
g	2490 2490		
ò.	HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGlu	ad	111111 3400 -TTTGATAGTCCAACGGTAG
Ω Ω		Qy	500MetLeuLysSer-
ò 6	242 TyrserLysAspAsnLysProTyrLysProVaLTyrPheAlaValSerMetClnGly 261 1 1	qa ·	
3 ,	203	٥٧	508 sPheAla
ον.	262 TyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu 281	qa —	 3519 CTTTGAAAAAAATCCGATTG
g	2536 TTCCTTAAAGACGATTCAATAGACAATAAGGTC 2568	· O	516 pProAlaValGluLeuSerL
oy D	282 ThrSerTrpGlyValGluAspArglleGluAsnGluAsnAsnProArglleGluValArg 301 2569 TTAAGGCGTTCTGAFAAAATGGGGTAAATGGGATAGGGTTAAGGAGAGAGA	ପ୍ର	
ò		Oy	536 aMetAlaAsnAlaTyrAlaI.
qq	2629 AAAAAGATGAAAAACTATGGAGACAACTTCTAAACGCCAAGTTAATCACTCAACGTAAG 2688	qa	
ô	322 TyralaSerLysTyrAlaGlnSerAlaAsnTvrTrbLysAsnSerIleGlyMetAsnArg 341	Qy	556 uMetTyrProGlyArg
op Op	TTTGATAATTTAACGAAAGCTGAACGTGGA	qa	
ò	342 GlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAla 358	δλ	573 tSerTyrGlySerIleLy
QQ	::	α α	
ογ	359 PheAlaAspTrpIle 368	Oy	
Op	::: 2779 ATCACTAAGCATGTGGGCACAAATTTTGGATAGTCGCATGAATACTAAATACGATGAAAAT 2838	aa .	
ογ	368 368	δ	
qq	2839 GATAAACTTATTCGAGAGGTTAAAGTGATTACCTTAAAATCTAAAATTAGTTTCTGACTTC 2898	<u>අ</u>	3825 ATTTTCTAAGCGTGTTATT
ò	368 368	δ	613
qq	2899 CGAAAAGATTTCCAATTCTATAAAGTACGTGAGATTAACAATTACCATCATGATGAT 2958	g D	3885 CAAACATAGAGACAAACCAA
ογ	368 368	δλ	
qq	2959 GCGTATCTAAATGCCGTCGTTGGAACTGCTTTGATTAAGAAATATCCAAAACTTGAATCG 3018	අ <u>ධ</u>	3945 GACGAATCTTGGAGCTCCCG
δ	369 SerAlavalTyrGlyAspValLeuSerSerLeuGluLysAlaTyr 383	Oy.	
Q	3019 GAGTTIGICTAIGGIGATTATAAAGTTTAIGAIGTICGTAAAATGAITGCIAAGTCIGAG 3078	දුර ්	4005 ATATACGTCTACAAAAGAAG
ογ	384 LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGly 402	RES	RESULT 3 AAX91754

TTAAAGAGTTACTAGGGATCACAATTATGGAAAGAAGTTC 3518 --AlaLeuProSerAsp---AlaAsnPheThrMetArgMe 573 ||||||||||||||||||| |TGGCTCTGCCAAGCAAATATGTGAATTTTTTATATTTAGC 3716 --AlaMetLeuAspIleValArgArgArg------ 456 :::::::|||||||:::::
TGCCCCAAGTCAATATTGTCAAGAAACAGAAGTACAGAC 3305 CAATTTACCAAAAAGAAATTCGGACAAGCTT----- 3357 ::|||| STAAAAAAGACTGGGATCCAAAAAAATATGGTGGT---- 3399 111 ::::::11111
ACTITITAGAAGCTAAAGGATATAAGGAAGTTAAAAAAGA 3578 ::|||| |||:::::: | IAGAAAACGGTCGTAAACGGATGCTGGCTAGTGCCGGAGA 3656 -----Gluasnileleuaspieupheargth 621 ||||||||||:: |||||| TACGTGAACAGCAGAAATATTATTCATTTATTACGTT 3944 ysLysPheLysGlyAspThrLysLysTyrAlaAspPheVa 485 roTyrSerAspLysPheHisAla-----499 leGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGl 556 PAGCAGATGCCAATTTAGATAAAGTTCTTAGTGCATATAA 3884 CTGCTTTTAAATATTTTGATACAACAATTGATCGTAAACG 4004 ysSerLeuAspAspLysTyrLysAspTyrLeuProSerLe 441 ----Ilepro-----AlaAspLysLeuProAspIl 465 ...-LysAlaIleGluLysAs 516 ysSerValileAlaAlaAlaArgAlaIleGlnAlaAspAl 536 ysGlyTyrGluProGlnAspGly------AlaTr 588 ------MetAspLysGluLy 508 LyLysGlyValLeuGluLysGlnAspProLysSerAspGl 608 S Page

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260 nGlyTyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTy
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                                     825 CACGTACGGAGGACAAT
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                                                                          rLeuThrSerTrpGly--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArg-ProAl 240
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                                                                                                                                                  periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 other;
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105
66
202
124
23
                                                                                                               Porphorymonas gingivalis protein PG67 encoding DNA
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 A; 685 C; 691 G; 741 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-008-355-2 (1-712) x AAX91754 (1-2853)
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Webb EA;
 BP
                                                                                                                                                 gingivalis; PG;
 2853
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97AU-0001182.
98AU-0001546.
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98AU-0003338.
98AU-0003654.
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                                                                          (first entry)
                                                                                                                                                                                                         Porphorymonas gingivalis
AAX91754 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barr IG,
Rothel LJ,
                                                                                                                                                                    antigenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY34536
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                                                                                                                                                  Porphorymonas
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                                                                          25-AUG-1999
                                                                                                                                                                                                                                                                                                                     10-DEC-1998;
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09-APR-1998;
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31-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gingivitis
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                                 AAX91754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ross BC,
                                                                                                                                                                      vaccine;
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DB:
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ATGGTACGAGAAGTTGAGTGTGGGGCTATTCCGGTCAGCTTCGCAATAGTATCTTGACAAA 1448
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                                                                                           -ValGluAspArgIleGluAsnGluAsnAsnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 aAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 aGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAs
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-CGCTATGGATTT-
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Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY343812. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivalis is involved in periodontal disease
------TITICCTICGGAGGCAATCICATTATGATCCGTCATCG 1772
                                                                                                                                                                                                                                          1833 TTGGGAGCTTCTTGAGCATACGGATCAGAACGCCAAGCTGCATACGCTGCTCTACTCTCC 1892
                                                                                                                     1773 CTTCACGCCCACTGTCAGTTTCTCCTATATGCCGGACTTCACGAAACGCCGATATGGCTT 1832
                                                                                                                                                                                                                                                                                                                                                                      1941
                                                            ----PheArgThrLysAsnTyrGlyAr
                                                                                                                                                                                 gTyrala-------GluAsnGlyGlnLeuHisIleAlaPheLeuSerAs
                                                                                                                                                                                                                                                                                                       640 n-----AsnAspIleThrGly------GlyAsinSerGlySerProValPheAs
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                                                                                                                                                                                                                                                                                                                                          1893 TTATTTCGAGCAGATATTCGGTGCTCCCTCCATGGGCAATGCAGGATCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                         654 pLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphorymonas gingivalis protein PG67 ORF encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic Porphorymonas gingivalis peptides
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Webb EA;
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98AU-0001546.
98AU-0002264.
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98AU-0003338.
98AU-0003654.
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Rothel LJ,
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TTGGAAACCT
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10-DEC-1997;
31-DEC-1997;
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1053 CTACAGCAAGACCACCAGTCTGAATATCCGATGGACACACAGTCAGGATCCGAAGGCCAA 1112
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                                                                                                                                                                                                                                           334 sAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAl 354
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                                                                                                                                                                                                                      221 ArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArg-ProAl
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 692 G; 742 T; 0 other;
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Conservative:
Mismatches:
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Sequence 2859 BP; 738 A; 687
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                                                              1515 CGTACCGATCAGTTTGACTGTCCCTTTGTTGGATTATCAATCTGACTATGGGGGGTTAA 1574
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                    1455 AGAGAAAGATTTGCTCCAGAGCAATCTCGTGCGCGATTGGAAGAATGGTATGCGTCATTC
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tAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLysSe
                                                                                                                                                                       rGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLy
                                                                                                                                                                                                                                                            -----PheArgThrLysAsnTyrGlyAr
                                         rValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGl
                                                                                   544 uLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyr------ProGlyAr
                                                                                                                              gAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTy
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                                                                                                                                                                                                                  sGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu-
                                                                                                                                                 1635 ATTCCTGCCTTCGGACACGACCTATAAATTCCGCAGACTGTAC-----
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Xu HH;
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200005-207727P-
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200005-253625P-
200005-257931P-
200105-269308P-
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Yamamoto'RT,
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26-MAY-2000;
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27-NOV-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential cannot be accepted by the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella proteminae, Pseudomonas aeruginosa and Enterococcus facells. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WipO at the wipo.int/pub/published_pct_sequences.
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New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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CCAAACGTTACAGGTAAACTT-----CACCTT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnAsnProArgIleGluValArgGly 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04 ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 LysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLys 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 TGGGATACA---ACTITGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTTTTGAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu---Thr 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is invention describes the isolation of a novel Streptococcus neumoniae valS protein. The new polypeptide and antagonist are seful for the treatment of an individual with abnormal valS cotein levels, by administering valS to individuals requiring als polypeptide, and administering the antagonist to individuals equiring inhibition of valS polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               w vals polypeptide and polynucleotide - useful for treatment of inditions associated with abnormal vals protein levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence 2652 BP; 733 A; 612 C; 621 G; 686 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                 pneumoniae valS coding region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aim 4; Page 24; 27pp; Japanese
  BP
                                                                                                                                                                            1S; treatment; antagonist; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MIK ) SMITHKLINE BEECHAM CORP.
X57027 standard; DNA; 2652
                                                                                                                                                                                                                                                                                                                                                   97JP-0321886.
                                                                                                                                                                                                                                                                                                                                                                                              97JP-0321886.
                                                                                   (first entry)
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130:00
32.81%
20.70%
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                                                                                                                                                                                                                       pneumoniae.
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ocal Similarity:
Match:
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                                                                                                                                                                                                                                                             11113577-A.
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                                                                                   -JUL-1999
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                                           X57027;
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171

9 RESULT 1246 CCTGCCTGGTACAAT-----GCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCCAGAA 1299

606 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 617

586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605

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This DNA encodes a S. pneumoniae vals polypeptide (EC 6.1.1.9), a member of the valyl tRNA synthetase family. The polypeptide can be expressed recombinantly by transforming host cells with vectors comprsing the vals gene. Vals polypeptides and polynuclectides are useful for diagnosing diseases due to an infection of an organism and also the stage and type of the infection. The polypeptides are also used for screening for their modulators which can be used in the treatment of diseases. Diseases diagnosed, prevented or treated include otitis media, conjunctivitis, pneumonia, bacteremia, sinusitis, pleural empyema, endocarditis and especially menimptis. Vals polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LysAspValArgMetValPheAlaPro 203
                                                                                                                                                                                                                                                                                                                                                             Valyl tRNA synthetase; valS; otitis media; conjunctivitis; pneumonia; bacteremia; sinusitis; pleural empyema; endocarditis; meningitis; bacterial adhesion; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                           S. pneumoniae valyl tRNA synthetase (ValS) polypeptide encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus pneumoniae valyl tRNA synthetase (vals) gene and protein, useful for screening for antibacterial compounds, for prevention and treatment of Streptococci infections e.g. meningitis and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2652 BP; 733 A; 612 C; 621 G; 686 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
1300 GGTGACGGATGGACTCAGGACGAGAGACGTCTTGGAT 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawlor EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 6-9; 35pp; English.
                                                                                                                                        AAX32814 standard; DNA; 2652 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-0308257.
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                                                                                                                                                                                                                                                   25-JUN-1999 (first entry)
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130.00
32.81%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown JR, Jaworski DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 AspValPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-231674/20.
P-PSDB; AAY06828.
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lest Local Similarity:
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11111		qa	946 CGTT
GATGTTTCAAGC		Οy	516 AspP
Proserservaldiylyskhed :: CCAAACGTTACAGGTAAACTT-	ProcestservaloutytysknedlyciyaspinraspasnirpMetirpProarginr 223 ::: 	Op	991 GGTG
GlyAspPheSerV 	GlyaspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 243 11 12 12 12 12 12 12	Qy Db	532 1051 GTTG
LysAspAsnLysF		QY	535 AspA. ::: 1111 AACGG
264 AlaAspAspTyrA	AlaAspAspTyrAlaMetThr1leGlyPheProGlySerThrAspArgTyrLeuThr 282	QY	555 ArgG. 1144 GTCG/
		Qy	566 AspA
283 SerTrpGlyVal 271 CAGGCTAAGGTA	283 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly 302 :: :: :: :: - - - - - - - -	qa	1204 GACTO
GAGTCTTTCTTG	303IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr 318 	Oy QQ	586 GlyA. 1 1246 CCTG
319 ArgileLysTyr 379 ACTATCAAGGAA	319 ArgileLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerile 337 	Qy	606 SerAs 1300 GGTG
338 GlyMetAsnargGlyLeuAlaar :::::: 439 ACTCTTGACGAAGGTTTGTCA	338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 357 ::::: :::	RES AAA ID XX	RESULT 8 AAA14369 ID AAA14369 XX
358 AlaPhealaAsi 111 11 475 GTCTTTGTGGA	AlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGly 373	XX AXX	AAA14369; 15-AUG-200
Asp GACCCAGCAGC	374 AspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLys 388	DE XX KW KW	DNA encod: Valyl tRN/ drug scree
AlaAsnArgGlu GCCTTCTACCA	389 AlaAsnArgGluMetThrTyrLeu	XX XX XX XX	antibody; Streptocod
SerGlu ACTCGTCCTGA(397SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414	FH FT FT	Key CDS
AlaLeuAlaThi ::: GCGGTTGCGGT	415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLySSerLeuAspAspLysTyr 434 	FT XX PN XX	US6051413
Lysasp AAGGACTTGAT	435 LysAspTyrLeuProSerLeuAspargLysValLeuProAla 448	PD XX XX	18-APR-200
449 MetLeuAsp ::: 775 GTTGGAGATGA	449 MetLeuasp	PR PR XX	18-APR-199 17-OCT-199 18-APR-199
ArgIleProAl CACGATCCAAA	456 ArglieProalaAspLysLeuProAspliePheLysAsnVallieAspLysLysPheLys 475 	PA XX PI	(SMIK) SN Brown JR,
GlyAspThrLy AACGACGACGG	476 GIYASPThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495	R X X T	WPI; 2000- P-PSDB; Al
LysPheHisAla	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515 :::	T T X	treating c

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/*tag=" a Streptococcus pneumoniae valyl tRNA synthetase (vals)"
                                                                                                                                                                                                                      3TGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110
                                                                                                                                                                                                                                                                                                      SCCCTCGTCAAAATCGAAAACGTGTCCACAGTGTTGGTCACTCAGAGCGTACAGGT 1050
                                                                                                                   AlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeu 554
                                                                                                                                                                                                                                                                             565
                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
----AAGGCAGTCGTTGCTAAGTTGGAAGAATC 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ding Streptococcus pneumoniae valyl tRNA synthetase (valS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1S polypeptides of valy1 tRNA synthetase family useful for otitis media, conjunctivitis, pneumonia and bacteremia s a specified amino acid sequence
                                                                                                                                                                                                                                                                             AlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA synthetase; valS; inhibitor; stringent response; eening; antibacterial; antibiotic; genetic immunisation; ; bacterial infection; meningitis; ds.
                                  ProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGluPheAlaValGlnGluAsnIleLeuAsp 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang M, Jaworski DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           occus pneumoniae strain 0100993.
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1..1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 2652 BP.
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97US-0953492.
97US-0844064.
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TTTGAAGCTCGT----
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9AY90514.
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997;
997;
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Caim 13; Columns 7-10; 21pp; English.

XX

This sequence represents DNA encoding Streptococcus pneumoniae valy1 tRNA synthetase (vals, NCIMB Deposit No. 40794). Streptococci are the cause of several types of human diseases, including othism encoded, conjunctivitis, pneumonia, bacteraemia, sinusitis, pleural empyema, endocarditis and sepecially meningitis. The frequency of S. pneumoniae infections has risen dramatically over the past 20 years, probably due to the emergence of multiply antiblotic resistant strains and an increasing population of immunocompromised people. Vals represents a target for new antibacterial companies. Inhibition of tRNA synthetases such as vals leads to a reduction in the levels of charged tRNA, which triggers a cacade of responses (known as the stringent response) resulting in a state or dormancy in the bacterium. Vals, its variants and fragments, anti-vals antibodies, vals inhibitors and nucleotides encoding vals may be used in the diagnosis, prevention and treatment of bacterial infections such as meningitis. Wals can be used to screen compounds for inhibitory activity. Vals can be used to screen compounds for inhibitory activity. Vals can be used to screen compounds for inhibitory activity. Vals can be used to screen compounds for inhibitory activity. Vals can be used to screen compounds for inhibitory activity. Vals can actibodies which protect against bacterial invasion into damaged tissues. Such antibodies could, for example, prevent the adherence of bacteria to wounds. Nucleotides encoding vals may be used as diagnostic reagents and therapeutic or prophylactic agents, particularly axis sequence 2652 BP, 733 A, 612 C, 621 G, 686 T, 0 other;
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 SQ Sequence 2652 BP; 733 A; 612 C; 621 G; 686 T; 0 other;

 Alignment Scores:
 0.0223
 Length:
 2652

 Pred. No.:
 130.00
 Matches:
 106

 Percent Similarity:
 32.81%
 Conservative:
 62

 Best Local Similarity:
 20.70%
 Mismatches:
 166

 Ouery Match:
 3.50%
 Indels:
 178

 DB:
 21
 Gaps:
 25

US-10-008-355-2 (1-712) x AAA14369 (1-2652)

δy	192	AspvalPhe	203
qq	92	GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTAAGCCTTATTCAATCGTTATTCCACCA	135
Óλ	204	yGlyAspThrAspAsnTrpMetTrpProArgHisThr	223
QQ	136	CCAAACGTTACAGGTAAACTT	162
Qγ	224	GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer	243
qq	163	GGT	171
Qγ	244	LysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLys	263
QQ	172		228
Òγ	264	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr	282
qq	229		270
QY	283	283 SerTrpGlyValGluAspArglleGluAsnGluAsnAsnProArglleGluValArgGly 3	302
QQ	271		330
Qy	303	303IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr 3	318
qq	331		378
Qy	319		337
qq	379	379 ACTATCAAGGAACAATGGGGCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC 4	438
Qγ	338	338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 3	357
Dp	439		474

358 AlaPheAlaAspTrpIleArgLys------AsnGlyLysSerAlaValTyrGly 373

δλ

ф	
Qy	374 Asp
Qy	389 AlaasnargGluMetThrTyrLeu396
Qy	397SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414
Qy Db	415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
Qy Dp	435 LysaspTyrLeuProSerLeuAspArgLysValLeuProala 448
Qy Db	449 MetLeuAsp
Qy	456 ArgileProAlaAspLysLeuProAspIlePheLysAsnValileAspLysLysPheLys 475 1
da Dp	476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495 1
Oy Db	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515 ::
Qy	516 AspProAlaValGluLeuSerLySSerValIleAlaAlaAlaArgAla 531
Qy	532IleGlnAla 534
qa oʻ	1051 GTTGTGGTTGAACCTGGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110 535 ASDALAMELALAASDALATVAAJAIJEGJULVSGJVLVSATGLEUPHEPHEAJAGJVLEU 554
g qa	op neprimedatonsinataryinitarieorunysoryinyoniybourgieerieoriaoryied op :: :: AACGCCATTGCCAACCAAGACACAGAGACAAG
Qy Db	555 ArgGluMetTyrProGlyArgAlaLeuProSer
Oy Dp	566 AspalaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585
Qy	586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
Oy.	606 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 617
RESU ABK5 ID XX AC XX	JLT 9 52414 ABK5; ABK5;

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271 CAGGCTAAGGTAGAGGAGCGCTTGCGTGAGGGCATTTCCCGCTATGACCTTGGTCGT 330
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                                                                                                                                                                                                                                                                                                                     The invention describes an isolated vals polynucleotide encoding a mature polypeptide the same as that expressed by a vals gene contained in a deposited strain of Streptococcus pneumoniae, a complementary sequence or a polynucleotide containing at least 15 continuous bases of the polynucleotide. The antibody to the encoded protein is used for the treatment of microbial infection. This sequence encodes Vals derived from
                                                                                                                                                                                                                                                                     for producing a valS polypeptide, used disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----CACCTT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LysAspValArgMetValPheAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGATACA---ACTTTGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                       621 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2652
106
62
1166
178
25
                                         gg
                                      ValS; microbial infection; antibacterial; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                    pneumoniae Vals
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                                                                               Location/Qualifiers
1..2651
/*tag= a
/product= "ValS"
                                                                                                                                                                                                                                                                    vel vals polynucleotide useful
the treatment of vals-related
                                                                                                                                                                                                                                                                                                   Claim 4; Fig 1-3; 24pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2652 BP; 733 A; 612 C;
                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                              97JP-0321886
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                    Streptococcus
(first entry)
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130.00
32.81%
20.70%
3.50%
                                                            Streptococcus pneumoniae
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P-PSDB; AAU97883.
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Best Local Similarity:
Query Match:
                                                                                                                                  JP2002119292-A
                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae
                   DNA encoding
                                                                                                                                                                         17-OCT-1997;
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14-AUG-2002
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1051 GTTGTGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lysasp-----TyrLeuProSerLeuAspArgLysValLeuProAla 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----IleGlnAla 534
                                                                                                                                                                                                                                             379 ACTATCAAGGAACAATGGGGCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC 438
                                                                                                                                                                                                                                                                                                                                                                             AlaPheAlaAspTrpIleArgLys-----AsnGlyLysSerAlaValTyrGly 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGACTTGATTGGTAAAAATGTCATCCTTTCCA---ATCGCTAATAAACTCATCCCAATC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            835 CACGATCCAAATGACTTCTTGGTTGGTTGGTCAACGTCATAACTTGCCACAAGTCAAGGTCATG 894
                                                                                                                                                        ArglleLysTyrAla---SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle 337
                                                                            331 GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGAC------GAATATGCCACT
                                                                                                                                                                                                                                                                                                                          GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAlaGluGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTTTGTGGACCTTTACAAGAAAGGCTGGATCTACCGTGGTGTTTTATCATCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asp------ValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLys
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775 GTTGGAGATGAGCACGCAGATCCTGAGTTTGGTACTGGTGTCGTGAAAATCACACCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 CGTTTTGAAGCTCGT------AAGGCAGTCGTTGCTAAGTTGGAAGATC
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|GCGGTTGCGGTCAACCCAGAA-----
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Matches:

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Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybriddise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying
                                        1246 CCTGCCTGGTACAAT ----GCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCCAGAA 1299
586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6004 BP; 1733 A; 1296 C; 1115 G; 1860 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fannon
                                                                                                                                                                                                                                                                                                                                              **Streptococcus pneumoniae genome fragment SEQ ID NO:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BA,
                                                                                                                          1300 GGTGACGGATGGACTCAGGACGAAGACGTCTTGGAT 1335
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                                                                                  SerAspGluPheAlaValGlnGluAsnIleLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 305-309; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                             AAV52160 standard; DNA; 6004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US19588.
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae;
computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
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Kunsch CA,
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                                                                                                                                                                                                                                                          AAV52160;
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6004

Length:

0.0831

Alignment Scores:

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TAAGGTCTTTGTGAACCTTTACAAGAAGGCTGGATCTATCGTGGTGAGTTTATCATCAA 3701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITCACTCTTGATGAAGGTTTGTCA--------AAAGCTGTTCG 3761
                                                                                                                                                                                                 4315 AAAATAAATAATACGAATTTGTCTGCAGAAGAAGCTGCTAAGCAAATTCAAAATAAAATA 4256
                                                                                                                                                                                                                                                                                 4255 AACAAAATAGAGAAAGGACACACACATGTCTAAAGAACTTTCACCTAAATACAATCCAGC 4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1063 CGCTTGGGATACG---ACTTTGCAGGATATCATCCATCCGTCAAAAACGCATGCAAGGCTT 4007
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                                                                                                                                                            131 LysileValLysValThrAspLysValGluGlyGlnLeuLysGlyIleThrAspGluMet 150
                                                                                                                                                                                                                                         151 GluArgLeu-ArgLysAlaGlnGluValCysGlnGluLeuAlaLysLysGluAsnAlaAs 170
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                                          sTyrLysAsp------TyrLeuProSerLeuAspArgLysValLeuPr
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antibiotic; antibacterial; drug design.
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
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                                                                                                                                                       Trawick JD,
                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                           Claim 27; Seq ID No 9586; 511pp; English.
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2000US-242578P.
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P-PSDB; AAU38090
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                                                                  22-DEC-2000;
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Yamamoto RT,
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		- du	1204 GA	
QQ	271 CAGGCTAAGGTTGAGGAGCGCTTACGTGAGGGTATTACGCGTTATGACCTAGGTCGT 330	G O	, d	5 7
οy	303IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr 31	qq	1246	1 2
<u>a</u> ,	331 GAGICITICITGACGAAGGICITGGGAATGGAAGACGAATATGCCACT	ζŎ	e06 se	, e
δ S	319 ArglielystyralaSerlystyralaginSeralaaantyTrpLysAsnSerile 337	q a .	1300 GC	9
Qy Dp	338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg ::::::	RES ABN	RESULT 12 ABN68148 ID ABN6814	4
3 2	4.5. NOTOLI LONGONIO CITTO CONTROL INTOCONTROL INTOCON	AC AC	ABN6814	14
S Q	475 GTCTTTGTGGACCTTTACAAGAAAGGCTGGATCTATCGTGGTGAGTTTATCATCATCAGG	C C C C C C C C C C C C C C C C C C C	01-JUL	.h
οy	374 AspValLeuSerSerLeuGluLysAlaTyrLys	DE	Strepto	S.
Dp	 535 GACCCAGCAGCTCGC	KW		U 4, 4
Qy Dp	385	MY X X X X X X X X X X X X X X X X X X X	Strepto	= 2
οy	395 TyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn	NG XX		(5)
QQ	655 ACTCGTCCTGAGACTATGTTTGGGGACGTT	Od XX		<u>.</u>
ογ Op	415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434	XX XX PR	29-0CT- 27-0CT- 24-NOV-	
1 8	4.55 Treating Texton Taylor Taylor Carlo Taylor Tay			· óc
g G			(CHIR-) (GENO-)	- 77
Qγ	449 MetLeuAspIleValArgArg 455	XX PI	Telfor	2 7
qq	775 GTTGGAGATGAGCACGCAGATCCTGAGTTTGGTACTGGTGGTGGTGAAAATCACACCTGCC 834	XX		7 2
٥y	456	A D D	WPI; ZOP-PSDB;	2 8
Dp	835 CACGATCCAAATGACTTCTTGGTTGGCCAACGTCATAACTTGCCACAAGTCAACGTCATG 894	Ld a	New Str	- I 8
Qy Dp	476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495	T D D T X X X X X X X X X X X X X X X X		1 (0 0
οy	496 L			~
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٥y	516 AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla 531		the spe activit	i i
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Dp	1051 GICGIAGITGAGCCACGCITGICIACTCAATGGTICGICAAGATGGACCAATTGGCTAAG 1110		(I). A	n ≪ 6
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δý	<pre>566 AspalaasnPheThrMetargMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585 </pre>		Alignment So Pred. No.:	Š

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e invention relates to a protein (ABP25413-ABP30895) from group B reptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS treptococcus progenes). Comprising one of 5481 sequences (S1), given in e specification. The proteins have antibacterial and antiinflammatory tivity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and tibodies that bind (I) are used in the manufacture of medicaments for threatment or prevention of infection or disease caused by cleic acids encoding (I) are used to detect Streptococcus in a closical sample. (I) is used to detect Streptococcus in a closical sample. (I) is used to determine whether a compound binds to i. A composition comprising (I) or a nucleic acid encoding (I), may be as a vaccine or diagnostic composition. The disease caused by reptococcus that is prevented or treated may be meningitis. Nucleic definite mencading (I) may be used to recombinantly produce (I) and may be romatography, immunoassays, and distinguishing/identifying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; A streptococcus; Streptococcus pyogenes; antibacterial; gene; flammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reptococcus protein for the treatment or prevention of infection ease caused by Streptococcus bacteria, such as meningitis, and tecting a compound that binds to the protein -
                                                                                                                                          TGCCTGGTACAAT ----GCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCCAGAA 1299
CTGGGTTATCTCTCGTCAGCTTTGGTGGGGTCAC---------CAAATC 1245
                                                                       -yalaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      se 4110 BP; 1462 A; 620 C; 791 G; 1237 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    8 standard; DNA; 4110 BP.
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.2000; 2000GB-0028727.
.2001; 2001GB-0005640.
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163 : 111 260 289 43	TLEUPTOLEUASPSETLEU TCTAACATTATTGAAGAC BPheGlyGlyGlyCysThr	AATGATTAAGAAGCUTCTIGAAAACTATAAAGATCTTTTT	GlnSerGlnSerThrValAspHis ::: :: GAGAGTCAAAAACAATCTTGGAC	uGluLeuProIleProGly :-:: GTTGATAAATGATGATGGT	Thrasp TCATTCAGATAATCTAAAA	GGGAATTCTACAAAGTTTG	sAlaGlnGluValCysGlnGlu : :::::: ACCTGAACAATTGTGGTTGAG	GTCGTAACTCTCGACAACGCTAT	IleValGlu ::::: GAATGGCAATATTTTGAAA	TyrPhe :: TTCCTTTACTACTTACAA	LeulleValTyrAsp CAATTTAAGTCAATATGAT	erValGlyLysPheGlyGly ::: CTATT	eServalPheArgValTyr ::: TTGGTA	ProAlaGluTyrSerLysAsp 	erMetGln	pTyrAlaMetThrIleGly
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126.50 Similarity: 33.29% sal Similarity: 19.81% itch: 3.40% 24 8-355-2 (1-712) x ABN6814	snGlnGluAsnLe ::: arccaGaraarga yrSerPheAspLy	Addodaritanidadadcoror GlylleThrValSerAspGlnGl 	IleGinserthrvalasphis ::: TIGTCTGCTAAGTTAATCAATGGTATTCGAGATAAAGAGAGTCAAAAAAAA	ASPTYrLeuargaspGlyPheValSerArgThrMetGlyGluGluLeuProIleProGly :::	LeuSerValLysTyrLeuArgLysIleValLysValThrAsp 	LysValGluGlyGlnLeuLysGly	IleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl 	LeuAlaLysLysGluAsnAlaAspGluAsnGln- :::[::: ATGGGCGTGAGAATCAAACAAATCAAG		ProPheTyrSerAsnAsnGlu		ValPheLysaspValArgMetValPheAlaProProSerS :: ATTGACCACATTATTCCTCAAGÇTTTCATAAAAGATGATT	AspThrAspAsnTrpMetTrpProArgHi ::: GATAATCGTGTT	AlaGlyAlaAspAsnArg ::: TCATCTGCTAAAATCGTGGAAA	AsnLysProTyrLysProVa	
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Score Percel Best Query DB: US-10	0 oy	oy do	Qy Db	0y Dp	Qy	Oy Dp	Qy Dp	Qy Dp	Qy Dp	Oy Op	Oy Dp	Qy Dp	Oy Dp	Oy Dp	Qy Dp	δ

2710 AATTTGACTAAGGCAGAGGCGGAGGCCTAACTTCCGATGATAAGGCAAGATTTATCCAA 2769 2770 CGTCAGTTGGTTGAGACACGACAAATTACCAAGCATGTTGCCCGTATCTTGGATGAACGC 2829 2890 AAGTCAAATTTGGTTTCAAATTTCCGAAAGAATTTGGATTCTATAAAATTCGTGAAGTT 2949 2830 TTTAATAATGAGCTTGATAGTAAAGGTAGAAGGATCCGCAAAGTTAAAATTGTAACCTTG 2889 AACAATTATCACCATGCACATGATGCCTATCTTAATGCAGTAGTTGCTAAAGCTATTCTA 3009 3589 ATTATTTGCCCAAGTATAGTCTGTTCGAATTAGAAAATGGGCGTCGATTACTTGCT 3648 3010 ACCAAATATCCTCAGTTA----- 3039 ------CCAAAATATAATAGTTAC 3072 3073 AAAACGCGTAAATCCGCTACAGAAAAGCTATTTTTCTATTCAAATATTATGAACTTCTTT 3132 3133 AAAACTAAGGTAACTTTAGCGGATGGAACCGTTGTTGTAAAA------GAT 3177 3178 GATATTGAAGTTAATAATGATACGGGT------GAAATTGTTTGGGATAAAAG 3225 3379 TTAGATCCTAAGAAATATGGAGGT-----TTTGATAGTCCGATAGTAGCTTACTCTGTT 3432 3433 TTAGTTGTAGCTGATATCAAAAAGGGTAAAGCACAAAAACTAAAAACAGTTACGGAACTT 3492 3493 TTAGGAATTACCATCATGGAGAGGTCCAGATTT-----GAGAAAAATCCATCA 3540 3541 GCTTTCCTTGAATCAAAAGGCTATTTA------AATATTAGGGCTGATAACTA 3588 290 IleGluAsnGluAsnAsnPro-------ArgIleGluValArgGlyIle 303 LysglnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIleLysTyrAla 323 324 SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArgGlyLeu 343 344 AlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIle 363 364 ArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyr 383 384 LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGlu----- 398 LysaspTyrLeuProSerLeuAspArgLysValLeu-----ProAlaMetLeuAspIle 452 AlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGly----- 476 477 ---AspThrLysLysTyrAlaAspPheValPheAspLysSerValValPvoTyrSerAsp 495 -----ThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414 519 ValGluLeu---SerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMet 537 538 Ala------AsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAla 552 415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434 553 GlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThr----- 570 273 PheProGlySerThrAspArgTyrLeuThrSerTrpGly------ValGluAspArg LysPheHisAlaMetLeuLysSer-----453 ValArgArgArgIlePro-----3040 435 304 399 459 496 504 δy qq qq qq δy qq δý qq qq Пb οy Dp QQ ò δ QΛ δ Q δλ Ω οy Οy Op δ QQ QQ ò Dp QΥ pp 5

CTGGTGAATTACAAAAAGGTAATGAGCTAGCCTACCAACACAATTATGAA :::	C 3708 CC - 585 CC G CC C CC	594 3825	601 3885	P 617 Percen 1 9339 Best Lo 1 9339 Dery J	- 625 US-10	642	qa .c	qa	. Οδ	qa	is media; Qy detection; Db	. Oy	q _Q	δō δλ	qa	. Qy	qa ,	Υ;	ga ko	t Db	qa —	sferrin Qy	
Db 3649 M OQY 571 OD 3709 T OQY 586 M OQY 586 M OQY 595 M OQY 602 M OQY 618 M OQY 618 M OQY 618 M OQY 643 M OQY	AGTGC	GlyalarrpTyrAsnTyrHisThrThr ::: ::: AAACAAGAATTTGTAAATCAACATGTCTCTTATTTG	GlyLysGlyVal	GInAspProLysSer			3 31948 standard DNA 2142			catarrhalis strain LES1 tbpB	otit ine;	Moraxella catarrhalis.	WO9952947-A2.	21-OCT-1999.	12-APR-1999; 99WO-CA00307.	14-APR-1998; 98US-0059584.	(CONN-) CONNAUGHT LAB LTD.	Schryvers AB, Harkness RE, Loosmore SM, Du	WPI; 1999-620376/53. P-PSDB; AAY43380.			his sequence encodes the Moraxella catarrhalis strain LES1 tran	binding protein (Tbp2) of the invention. This sequence is also referred to as the TbbB gene. The TbbB gene is used to produce recombinant Tbp2:

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Moraxella infections, e.g. otitis media. The Tbp2 proteins are useful as antigens, either in vaccines (including components of conjugate vaccines that contain antigens from other bacteria or from tumours, in which case they elicit production of antitumour antibodies that may be coupled to chemotherapeutic agents or biologically active agents) or to raise antibodies (for use as diagnostic reagents and for treating Moraxella infections), also for detecting Moraxella antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      985 ACAGACAAAAATAACAAGCCCAGTGATTACAATGGTGCATATGGTCATAGCAGTGAATTT 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 ValCysGlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGlu 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyr 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 ACTCAATTTGCCCAAGAAAAATACAAGGAGCTAATTGAGAACGCCGATGATAAAAAATCT 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAla
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Conservative:
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Local Similarity:
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2065 GGGTCATTTACACACGATACCGAT 2088

1164	385 1197	404 1257	424 1317	444 1377	464 1386	483 1446 ·	502 1506	522 1548	542 1605	560 1665	576 1725	593 1785	613 1824	633 1884	645 1944	652	2004	672 2064	
:::::	6 AsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu 	6 GlyAlaLysAlaAsnargGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThr 	5 GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla :::	5 GlylleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLys ::: ::: 8 GGGGTCTTTGGTGCTAAACGAGATAAAGTAGAAAAAACCGAAGCCATCTTAGATGCCTAT	5 ValLeuProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAsp 	STEEPHELYSASNVALILEASPLYSLYSPHELYSGLYASPTHTLYSLYSTYTALAASP	-	3 SerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer	3 LysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAla 	3 IleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGly	Argala	7 SerileLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr	4 ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGlu 	4 ASDILeLeuaspLeuPheargThrLysAsDTyrGlyargTyrAlaGluasDGlyGlDLeu :::1	4 HisllealaPheLeuSerAsnAsnAspIleThrGly	6GlyAsnSerGlySerProVal	5 ACCACCAAAGGGGAGGCGAGGGTACAAGATAGATTCTAGCAGTACAGGGAAATCCATG	3 PheAspLysasnGlyArgLeulleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSer :::111	3 GlyaspileGluPheGluProAsp 680 :::
110	366 1165	386	405	425	445	465	484	503	523	543	561	577 1726	594 1786	614	634	646	1945	653	673
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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1675 GGCGCAGTTGTATTGCCTGGGGAAAAGGAAAAGGGAAAGTTAAACTTTTCAGCAAAGCT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 ------LysGlyMetTrpLeuLeuAsnGluLeuAsnGlnGluAsnLeuAspArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 MetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysProSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and pathogenicity of Listeria (potential therapeutic agents), als
treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4716 BP; 1750 A; 734 C; 1110 G; 1122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAsp----
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Matches:
Conservative:
Mismatches:
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                                                                                                               Listeria innocua DNA sequence #1034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; SEQ ID 2408; 180pp; French.
               BP.
                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
             ABQ69595 standard; DNA; 4716
                                                                                                                                                                                                                                                                                                   04-OCT-2001; 2001WO-FR03061.
                                                                                                                                                                                                                                                                                                                                    04-OCT-2000; 2000FR-0012697
                                                                              29-AUG-2002 (first entry)
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122.50
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                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F, Glaser P;
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                   Listeria innocua.
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                                                                                                                                                                  infection; ds.
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ABQ69595
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Q	1783	GTAGGTGTTTTAGGTGTAGGATTAAGCGCTACTGAGTTGATTGGTATGAACAAAAATAAT 1842	
>	62		
Q	1843		
>	82	GlyLeuilePhe	
Q	1897		
>-	95	IleGlnSerGinSerThr 100	
q	1957	GCTTTTGCTGGAACTGCATTAGGTAAAGAATTAGGGAAATATGTTCAAAAAGAAGGACCA 2016	
Α.	101		
Q	2017		
×	120		
q	2077	CCGATITITAGGAGCAAATATAAATGTAATAAATAAAACTATCGATGCGGCAAAGAAGGC 2136	
۸.	135	valThr 136	
д	2137	ATTAAAGCAGTTGGAGACACGCATAAAACTGTTTGGAATGCTTCAAAATCAATAGTCGCC 2196	
>-	137		
Q	2197	GACCCGCT	
≻	155		
q	2242	TCTGCTAAAGCAATGAACGAGTATTACGAAATGAGCAGAAAATGCAAGATGCGAGGTGTGGGGGGGG	
^	175		
q	2302	GAAATCATGGTATCTGGTCGTCGTATTACTGAAAAGAACTCGAAAACAAC 2352	
· > ₇	188	LeulleValTyrAspValPheLysAspValArgMetValPheAlaProProSerSerVal 207	
q	2353		
Α.	208	GlyLysPheGlyGlyAspThrAspAsnTr	
Д	2410		
>	228		
q	2455		
>	244		
Q	2515		
×	264	AlaaspaspTyrAlaMetThrIleGLyPheProGlySerThrAspArgTyrLeuThrSer 283	
q	2574	2574	
×	284	TrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGlyIle 303	
q	2575	GGGCAA	
>-	304		
Q	2623		
>	322	: TyralaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArg 341	
q	2682	2682	
Α.	342	GlyLeuAlaArgLeuAspValileGlyArgLysArgAlaGluGluArgAlaPhe 359	
Q	2683		

ΟŊ	09	snGlyLysSerAlaValTyrGlyAspV
qq	2734 0	GAAAAAGAAGTTAGAAAGATTGAA 2757
Qy	380 C	GluLysalaTyrLysGluGlyalaLysAlaAsnArgGluMetThrTyrLeuSerGluThr 399
QY	400 1	LeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThr 418
Dβ	2818	ACTAGGAAACTTAGAAAACTCGAAAGAAAAAT
Qy	419	AsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyrLys 435
QQ	2878 (29
Οy	436 4	ProAlaMetL
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Qy	456 4	ArgileProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLys 475
qq	2980	ť,
δŏ	476 (GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495
qq	3034 #	30
ΟŊ	496 I	LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515
qq	3094	rgaaacattaaataag 31
QY	516 /	AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAsp 535
qq	3151	
QY	536 4	AlaMetAlaAsnAlaTyrAlaTleGluLysGlyLysArgLeuPhePheAlaGlyLeuArg 555
qq	3205	GGCTCGGAAAATGGAACGAGTTGTCCTCTGCGACAGTTAATATTTTCAGTGGAATGAAA 3264
QY	556 (rProGlyArgAl
q	3265 (GCGTTGAGAGTATTTGATAGTTTTAAGACAAACTTGTATAAAGTCATT
QY	576 (GlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr 593
qa	3322 1	GTAATTACCGGAGTCAAT
Qy	594	ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 612
qq	3379 (STGCTTGGGAACGGTAGGTTCAAGT3111
Qy	613 (3]uAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGln 632
qa	3412 (AC
QY	633 1	LeuHisIleAlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSer 648
qq	3472 (ATGGCT
Qy	649	9
QQ	3532 (CTAGG
RESULT ABQ678 ID	r 15 373 \BQ67	873 standard; DNA; 4731 BP.
X Z X	ABQ67	
X D X	89-AU	G-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                anti-Listeria vaccines.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                 New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LysGlyMetTrpLeuLeuAsnGluLeuAsnGlnGluAsnLeuAspArg
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                        food contamination; mutational analysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4731 BP; 1752 A; 735 C; 1117 G; 1127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       present invention relates to nucleic acid sequences
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID 686; 180pp; French.
 Listeria innocua DNA sequence #675
                                                                                                                                                                                           RECH SCI
                                                                                                                              04-OCT-2001; 2001WO-FR03061
                                                                                                                                                       04-OCT-2000; 2000FR-0012697
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122.50
32.84%
18.72%
3.29%
                      Antibacterial; Listeria;
                                                                                                                                                                            (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT
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Best Local Similarity:
                                                          Listeria innocua
                                                                                  WO200228891-A2
                                  infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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2152 ATTAAAGCAGTTGGAGACACGCATAAAACTGTTTGGAATGCTTCAAAATCAATAGTCGCC 2211
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.....IleGInSerGlnSerThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 Asp-----LysValGluGlyGlnLeuLysGlyIleThrAspGluMetGluArgLeuArg 154
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                                                                                         1972 GCTTTTGCTGGAACTGCATTAGGTAAAGAATTAGGGAAATATGTTCAAAAAGAAGGACCA
                                                                                                                                                                                        101 ValAspHisAspTyrLeuArgAspGlyPheValSerArgThr---MetGlyGluGluLeu
                                                                                                                                                                                                                                                         111 ::: ::: 111:::
032 AAAATATTAGATAAATTCCAAGATGGTTGGAAAGGCTTAAGCAAAATTGCTGAAGAGCAT
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T 2892	s 435	A 2952	g 455	Т 2994	s 475	 3048	p 495	A 3108	s 515	G 3165	p 535	A 3219	9 555	A 3279	r 575	т 3336	- 593	Т 3393	n 612	A 3426	n 632	T 3486	r 648	A 3546		
:::	9 AsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyrLys		S ASPTYrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArg					AACGGCGTAGTTAAAGAAGCGGAGAAGATGCACGATAATGTAGTGCGAGAAGCTCAGCAA	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys	CAAGCAAAAGGACATTTAAGAGAAGTAGATTGGGAAACTGGTGAAACATTAAATAA			; AlaMetAlaAsnAlaTyrAlaIleGluLysGlyLySArgLeuPhePheAlaGlyLeuArg		GluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyr	 GATACAGCGTTGAGAGTATTTGATAGTTTTAAGACAAACTTGTATAAAGTCATTAA	5 GlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr	7 AATGTAATTACCGGAGTCAATAAAGTACTATCGTTCTTTAACATTAAGACAATACC	ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln		3 GluasnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGln				GlySerProvalPheAspLysAsnGlyArgLeuIleGly 661	
2833	419	2893	436	2953	456	2995	476	3049	496	3105	516	3166	536	3220	556	3280	576	3337	594	3394	613	3427	633	3487	649	3547
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Search completed: May 23, 2003, 10:05:47 Job time: 379:182 secs

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Page 1

Sequence 1, Appli Sequence 139, App Sequence 2, Appli Sequence 999, App Sequence 79, Appl Sequence 26, Appl Sequence 1, Appli Sequence 20, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 221, Appli Sequence 271, Appli Sequence 271, Appli Sequence 271, Appli Sequence 271, Appli

110 3.0 3279 4 109 2.9 15563 4 109 2.9 4403765 4 107.5 2.9 4851 4 107.5 2 9 4 851 4	106.5 2.9 15213 4 0S-08-961-527-26 Sequence 106 2.9 2472 3 US-08-35-844A-7 Sequence 106 2.9 3358 3 US-08-335-844A-20 Sequence 105 2.9 3698 4 US-09-327-536-1 Sequence 105 5 2.8 1994 3 US-09-600-982-2 Sequence	105.5 2.8 1994 5 PCT-0594-102618-22 104 2.8 3731 4 US-08-811-583-1 102.5 2.8 2571 4 US-09-134-001C-2601 102.5 2.8 6142 4 US-09-134-001C-2601 102.5 2.8 6142 4 US-09-514-302-1	2.7 1415 4 05-09-345-214-12 Sequence 2.7 2408 4 05-09-345-214-12 Sequence 2.7 2401 4 05-09-345-214-5 Sequence 2.7 2401 3 05-09-345-214-5 Sequence 2.7 2401 3 05-09-345-214-5 Sequence 2.7 2410 3 05-09-08-172-1 Sequence 2.7 2410 3 05-08-172-1	102 2.7 4310 4 102 2.7 4310 4 101.5 2.7 2253 1 101.5 2.7 3727 1	101 2.7 3668 4 US-09-302-620B-89 100.5 2.7 2836 4 US-09-157-257-3 100.5 2.7 3278 1 US-08-484-105-13 100.5 2.7 3278 1 US-08-484-105-13	100.5 2.7 52.04 US-08-48-1108-13 100.5 2.7 8501 4 US-08-98-367B-6 100 2.7 4330 3 US-09-398-367B-6 100 2.7 4330 4 US-09-33-1	100 2.7 6744 1 US-08-119-125A-2 S 110 2.7 6744 1 US-08-119-125A-2 S 121-017B-726 ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221017B ence 726, Application US/09221012B ence 726, Application US/09221018 ence 726, Application US/0922101B ence 726, Application US/09/221, US/09/221
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - nucleic search, using frame_plus_p2n model Run on: May 23, 2003, 09:42:03; Search time 60.7132 Seconds (without alignments) 3596.482 Million cell updates/sec	Title: US-10-008-355-2 Perfect score: 3719 Sequence: 1 MQMKLKSILLGASGLFMIDKWGQCPRLIQELKLI 712	Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Searched: 441362 seqs, 153338381 residues	of Hits Satisfying Chosen parameters. eq length: 0 eq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters:

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                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                      US-10-008-355-2 (1-712) x US-09-221-017B-726 (1-1974)
               27340-20021.00
                                                                                                                                                                                                          Gaps:
                                                                                                                       ORGANISM: PORYPHYROMONAS GINGIVALIS
NAME: MODICOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                  726:
                                                                            MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTL SENSE: UNKNOWN
                                                                                                                                                                     1.3e-317
2995.00
99.65%
99.65%
80.53%
                                                INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1...1974
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Best Local Similarity:
Query Match:
DB:
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ArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspValLeu
                                                                                       SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeu
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ArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysPro

4 1

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APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
1317
168
74
172
23
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-DEC-1997
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 10-DEC-1998
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT: INFORMATION:
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                                                                                            Sequence 382, Application US/09221017B Patent No. 644799 GENERAL INFORMATION: APPLICANT: ROSS, Bruce C.
                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,430
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TELEPHONE: 650-813-5600
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19.99%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                        Diskette
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                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Query Match:
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TELEFAX: 6
                                                                                US-09-221-017B-382
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US-10-008-355-2 (1-712) x US-09-221-017B-382 (1-1317)

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16 CAGATGAAAGAGCGCGCCCTTAAGATGAAGGAATACGACCTTTATAATCCCAACGGCACA
                                                                                       SerIleAlaAsnAlaValValIlePheGlyGlyGlyCysThrGlyIleThrValSerAsp
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US-09-221-017B-1045
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                                     1093 ATGATAGAAGAAGCCATCCATCCGTGGGATCGAGTTTGCCCGTTCTCCTATCCCCACCGAA 1152
                                                                                                1204 ATCGATAAGATTCGTACACGCTACAGCAAATTTGCCAACAAGGACTACAGTGCAGAGGTG 1263
                                                                                                                                                       --LysAspTyrLeuProSerLeu 441
     -- PheAla 410
                                                                          411 GlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 1264 GACAAGAAAGTGGCCGTAGCCATGCTGACGGAATACCTCAAGGAAATGCCC 1314
                                                                                                                                                                                                                             442 AspArgLysValLeuProAlaMetLeuAspIleValArgArgArgIlePro 458
395 TyrLeuSerGluThrLeuPheGlyGlyThrGluValValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFERATING SYSTEM: Windows
SOFTWARE: FESTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILLING DATE: 23-DEC-1998
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PP288
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                      US-09-221-017B-1045; Sequence 1045, Application US/09221017B patent No. 6444799; GENERAL INFORMATION:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 1045:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION:
TELEPHONE: 650-813-5600
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E: DNA (genomic)
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EDNESS: double
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MEDIUM TYPE: Diskett
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                                                                                                                                                   431 AspAspLysTyr-
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ZIP: 94304-1018
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507 GluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLysSerValIle 526
                                                                                                                                                                                                                                                                                                       527 AlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGly 546
                                                                                                                                                                                                                                                                                                                                                                                             LysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAsp 566
                                                                                                                                                                                                                                                                                                                                                                                                                                    126 CAACGCACCTACATTGCAGGTCTCTTGGAAATGGATGGCGATCAGGATCAATTCCCGGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 GTTTACTACGACATCAAACCACATTGGATGGTGTGGAAGAAAAAGAAGATCCCGATAAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 TyralaGlu---AsnGlyGlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAsp 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 SerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeu 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 ATTGTGGATATTCGCTACTCCTGCTTGTATAGACAAAGTAGGCGGTTGCCAACGCCTG 605
                                                                                                                                                                                                                                                                                                                                                  66 GACGAATACCGCAAACTCTACAACGAACTTCGTCCCTATGACGATCCTATTCTAAGGGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 AlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSer 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 GGCAACTCAGGCAGTCCGGTCATGAATGCCAACGGCGAACTGATCGGTCTCAACTTCGAT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 GlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle 685
                                                                                                                                                                                                                                            607 AspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDEMESS:
ADDRESSEE: MORRISON & FOERSTER
                  2384
90
38
74
5
                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                     US-10-008-355-2 (1-712) x US-09-221-017B-1045 (1-2384)
                    Length:
Matches:
                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2: MORRISON & FOERSTER
755 PAGE MILL ROAD
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                    2.82e-38
                                      441.50
61.84%
43.48%
11.87%
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COMPUTER READABLE FORM:
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 755 PAG
CITY: Palo Alto
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Alignment Scores:
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Patent No. 5849555
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 ArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysPro 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGlnMetLysLeuLysSerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGly 20
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22
12
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Mismatches:
Indels:
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                                  OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   NAME: MODICOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
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                                                                                                            CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1182

FILING DATE: 31-DEC 1997

PRIOR APPLICATION NUMBER: PP182

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1546

FILING DATE: 30-JAN 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2911

FILING DATE: 09-APR 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                 APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08953492
                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.28e-20
265.50
96.83%
93.65%
. Diskette
IBM Compatible
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LOCATION: 1...561
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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544 TCCATGGCA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-221-017B-12
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US-08-953-492-1
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112 TGGGATACA---ACTTTGCAAGATATTATCATCGTCAAAAAGGCATGCAAGGTTFTGAT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTAAGCCTTATTCAATCGTTATTCCACCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CACCTT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLys 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgFroAlaGluTyrSer
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106
62
166
178
25
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,492
FILING DATE: 17-0CT 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 9867991.8
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9867991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/POCKET NUMBER: 91458-4/1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                   TITLE OF INVENTION: NOVEL valS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SAITHKLING Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                    APPLICANT: Jaworski, Deborah
APPLICANT: Lawlor, Elizabeth
APPLICANT: Wang, Min
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130.00
32.81%
20.70%
3.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
TELEX:
                                                                                                                                                                                          CITY: King of Prussia STATE: PA
APPLICANT: Brown, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similari
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AspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp
                                                                                                                                             586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys
                                                                                              1204 GACTGGGTTATCTCGTCAGCTCTGGTGGGGGTCAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFREENCE/POCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,373
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strepto
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome S
STREET: 9410 Key West Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.00173
129.00
33.628
20.218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                   US-08-961-527-27/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20850
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                                                                                                           CAGGCTAAGGTAGAGGAGCGCTTGCGTGGTGGAGGGCATTTCCCGCTATGACCTTGGTCGT 330
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264 AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu---Thr 282
                                        ----ACCCTTTGGCTTCCTGGGATGGACCACGCAGGGATTGCCACT 270
                                                                               SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly 302
                                                                                                                                                                                                                                                                                         ACTATCAAGGAACAATGGGGCCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC 438
                                                                                                                                                                                                                                                                                                                                                                        ACTCTTGACGAAGGTTTGTCA--------AAAGCTGTTCGTAAG 474
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                                                                                                                                                                                                                                                ArgileLysTyrAla---SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle 337
                                                                                                                                                                                                                                                                                                                                 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTTCTACCACATGAATTACATGCTGGAAGATGGTTCACGCGTCCTTGAAGTTGCTACA 654
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                                                                                                                                                                                                       331 GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGAC------GAATATGCCACT
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Streptococcus pneumoniae Polynucleotides and Sequences $^{\rm 391}$ 1246 CCTGCCTGGTACAAT-----GCTGATGGTGAAATGTAGTCGGCGAAGAAGCTCCAGAA 1299 151 GluArgLeu-ArgLysAlaGlnGluValCysGlnGluLeuAlaLysLysGluAsnAlaAs 170 :::::: ||||||| ||| 131 LyslleValLysValThrAspLysValGluGlyGlnLeuLysGlyIleThrAspGluMet 150 6004 116 77 194 187 26 3.50 inch, 1.4Mb storage Length:
Matches:
Conservative:
Mismatches:
Indels: 1300 GGTGACGGATGGACTCAGGACGACGACGTCTTGGAT 1335 US-10-008-355-2 (1-712) x US-08-961-527-27 (1-6004) 617 606 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 3: Human Genome Sciences, Inc. 9410 Key West Avenue Diskette, 3.50 incn, 1.

HP Vectra 486/33

SYSTEM: MSDOS version 6.2

us-10-008-355-2.p2n.rni

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Db 4255 AACAAAATAGAGAAAAGGACACACACATGTCTAAAGAACTTTCACCTAAATACAATCCAGC 4196	Qy 170 pGluAsnGlnLeuCysIleValGluProPheTyrSerAsnAsnGluTyrPheLeuIleVa 190	Qy 190 ITyrAspValPhe		Oy 222 SThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTy 242 	Oy 242 rSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTy 262 ::: :	Oy 262 rLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu 281	QY 282 -ThrSerTrpGlyValGluAspArg1leGluAsnGluAsnAsnProArg1leGluValAr 301	OY 301 gGlyIleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAl 317	Qy 317 aThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSe 336 	Oy 336 rIleGlyMetAsnargGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGl 356 :::::	Oy 356 uArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTy 372 :::	0y 372 rGlyAsp	Oy 385	Oy 393 tThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAl 413	<pre>Qy 413 aASNAlaLeuAlaThrASNProAspAlaHisAlaGlyIleLeuLySSerLeuAspAspLy 433</pre>	QY 433 STYLLYSASPTOTTYTLGUPROSETLGUASPATGLYSVALLGUPR 447	OY 447 OALAMELLEUASP	Oy 454 gArgArgIleProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysEySPh 474
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3244 AATCGGTGCCCTTGTCAAAATCGAAAAACGTGTCCACACAGTGTTGGTCACTCAGAACGTAC 3185
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474 eLysGlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSe 494
                                            3340 CATGAACGACGGAACTATGAATGAGCTTGCCTTTGAATTTTCAGGCATG-----
                                                                                          494 rAspLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGl
                                                                                                                                                                                     514 uLysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla-----
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Fatent No. 6440701

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Barkness, Robin E
APPLICANT: Lossmore, Sheena M.
APPLICANT: Lossmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Tang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENITON: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sin & McBurney
CORRESPEE: Sin & McBurney
CORRESPEE: Sin & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3031 CCACGACTGGGTTATCTCTCGTCAGCTTTGGTGGGGTCAC-------
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 oLysSerAspGluPheAlaValGlnGluAsnIleLeuAsp 617
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6th Floor, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6th Floor, 330
CITY: Toronto
STATE: Ontario
COUNTR: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                 532 -----
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LeuProlleProGlyLeuSerValLysTyrLeuArgLysIleValLysValThrAspLys 138
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Mismatches:
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                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                          Indels:
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 2142 base pairs
TYPE: nucleic acid
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Best Local Similarity:
Query Match:
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1387 ACATTTAATAATACAAATAAAGCAACCACATTCACCCCATTTACCAAAAAACAACTGGAT 1446 1447 AACTITIGGCAATGCCAAAAAGTTGGTCTTGGGTTCTACCGTCATTAATTTGGTGTCTACC 1506 1549 AAGCCAACTTCTGCCACAAACAAAGGGGGGGGGAGT---TTGATGGTGAATGATGAAGTT 1605 1165 CGTGGCAGTGCC-----GAA 1197 CCAACCACAGGCAAAGCCAAATATCTGGGGAACTGGGTAGGATACATCACAGGAGCGGGC 1785 1045 GATGTTAATTTTGCTGATAAAAAATTAAAGGCAAACTTATCAGTAATCAGTTATCAGGC 1104 1105 ACAGCTGTAACCGCCAAAGAGCGTTATAAAATAGAAGCTGATATCCACGGCAACCGCTTC 1164 TATGGACCAAAAGGCGAGGAGCTGGCAGGTAAATTCTTAACCGATGACAACAACTCTTT 1317 GGGGTCTTTGGTGCTAAACGAGATAAAGTAGAAAAAACCGAAGCCATCTTAGATGCCTAT 1377 1825 TTTGACATTGACTTTGAGAAAATCAGTTAAAGGCAAACTGACCACCCAAGGCCGCACA 1884 GATCCTGTCTTTAACATCAAAGGTGAAATTGCAGGCAATGGCTGGACAGGCAAAGCCAGG 1944 1945 ACCACCAAAGCGGACGCAGGAGGCTACAAGATAGATTCTAGCAGTACAGGCAAATCCATC 2004 2005 GTCATCGAAAATGCCGAAGTTACTGGGGGCTTTTATGGTCCAAATGCAAACGAGATGGGC 2064 GlyAlaLysAlaAsnArgGluMetThrTyr---LeuSerGluThrLeuPheGlyGlyThr 404 405 GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla 424 GlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLys 444 445 ValLeuProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAsp 464 465 IlePheLysAsnValIleAsp---LysLysPheLysGlyAspThrLysLysTyrAlaAsp 483 561 ArgAla------LeuProSerAspAlaAsnPheThrMetArgMetSerTyrGly 576 ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGlu 613 LeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLys AsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu ---PheValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLys SerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer LysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAla 543 IleGluLys-----GlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGly ATCGTCAAAACCTATGGCAAAAACTTTGAATACCTAAAATTTGGTGAGCTTAGTGCGGT AsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeu 653 PheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSer SerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr----GATGCCACCAAAAATGAATTCACCAAAAATTCACCAAAGAC-----634 HisIleAlaPheLeuSerAsnAsnAspIleThrGly--------484 1507 1606 1726 1786 1885 346 386 425 503 523 577 594 g qq qq q QQ δý g g g δ qq g ά QQ δ ò Ω Dρ Ω QQ QQ οχ ŏ g ò g q ò οy οý ò ò ò

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119 uProlleProGly-
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                                                                                                                                              APPLICANT: Giffard, Philip molliace...
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Genetic Manipulation of Plants to
TITLE OF INVENTION: Increase Stored Carbohydrates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Griffith Hack & Co
STREET: Level 8, 168 Walker Street
CITY: No. 5981838th Sydney
STATE: Naw South Wales
COUNTRY: Australia
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161
106
262
257
40
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PatentIn Release #1.0, Version #1.30
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GlyGlyGlyCysThrGlyIleThrValSerAsp-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus salivarius
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,824
                                                                                                                                         Christine Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PM7643
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
                             2065 GGGTCATTTACACACGATACCGAT 2088
                                                                                      Sequence 1, Application US/08793824 Patent No. 5981838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
GlyAspileGluPheGluProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 26547
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4853 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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34.10%
20.56%
3.09%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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                                                                           US-08-793-824-1
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673
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2241 AAAGTACACCCAGTACAATATCCCAGCTGCCTATGCCACAATGTTGACCAACAAGGATAG 2300
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                                                                                                                                                                                                                                            2001 CCGTGGCAGCTTGGAGCGCGGTGATTACTAACTCTCTTAACAATCGITCAAGTGAGCAGAA 2060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LysValGluGlyGlnLeuLysGlyIleThrAspGl 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rPheLeuIleValTyr-----AspValPheLySAspValArgMetValPheAlaProPr 204
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                                                                          1941 GTCTATCGACAATCCACTACGTGAAACGCTTTTGACGACTTTCTTGCGTAAGAGCAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uMetGluArgLeuArgLysAlaGlnGluValCysGln---GluLeuAlaLys----Ly
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-LeuSerValLysTyrLeuArgLys
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ço d	Oy 335 snSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgA 354 1 1 1 1 1 1 1 1 1 1	
Qy Dp	354 laGluGluArgAlaPheAlaAspTrpIleArgLysAsnGly 367	RESULT 9 US-09-103-840A-1/C ; Sequence 1, Applicat : Patent No. 6294328
oy g	368	
δ d	379 euGluLysAlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluT 	APPLICANT: VENTER; TITLE OF INVENTION:
3 & 2	3221	CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NO
	417 laThrAshProAspAlaHisAlaGlyIleLeuLySSFLeuAspAspLySTyrLySA	SEQ ID NO 1 SEQ ID NO 1 LENGTH: 4411529 TYPE: DN A ORGANISM: NA YCODACT
کې و	436 spTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArgA ::::::	, OTHER INFORMATION US-09-103-840A-1
3 6 8		Alignment Scores: Pred. No.: Score: Percent Similarity:
ογ	476 lyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAspL	Query Match: DB:
QQ	Db 3426TTCAAACGGCCGTAAATTGACTACCAATGAG 3456	US-10-008-355-2 (1-712
Oy Dp	Oy 496 yspheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlalleGluLy 515 ::	Qy 75 GlylleThrVal
ò qa	OX 515 SASPProAlaValGluLeuSerLysSerValIleAlaAlaArgAlaIleGlnAlaAs 535	Qy 95 IleGlnSerGln ::: Db 4023665GTCCG
ر ا ا	535 palaMetalaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuAr : :!!! ::::::::::::::::::::::::::::::	115 MetGl
2 d	555 gGluwettyrProGlyArgalaLeuProSerAspAlaAsnPheThrmetArgMe	Oy 135 ValThrAspLys Oy 135 ValThrAspLys Ob 4023578 ATGGAGGACAA
ò	573 tSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAla	Qy 155 LysAlaGlnGlu
ò	588	DD 4023563
qq		402
Oy Dp	29 606 rAspGiuPheAlaValGInGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyAr 626 ::::::	Qy 191 TyrAspvalPhe Db 4023488 TACGACGCTCT
. 40	2y 626 gTyrAlaGluAsnGlyGlnLeuHisIle	Qy 211 GlyGlyAspThr Db 4023452
οy	2y 639 rAsnAsplleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgle 659	Qy 230
QQ		Db 4023419 GAGATGATCGA
οy	ζγ 659 u 659	Qy 240 AlaGluTyrSer

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.uLeuProIleProGlyLeuSerValLysTyrLeuArgLysIleValLys 134
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                                                 Sr, Claire M.
SR, Claire M.
SR, John C.
NN: TUBERCULOSIS
1436-2007.00
ON NUMBER: US/09/103,840A
NOS: 2
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                                                                                                                                                                                                                                                                                                                 4411529
137
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187
286
35
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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N: H37Rv
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HMAN, Robert D.
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111.00
29.45%
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Db 4022669GGGGCCTTGCGAAGCGCTAGCGCGATTCGGGCGATGATGG	Qy 579 sGlyTyrGlubroGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGl	Oy 599 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAs	Qy 619 -PheargThrLysasnTyrGlyargTyrAlaGluasnGlyGlnLeuHisIleal	Qy 638 uSerAsnAspIleThrGlyGlyAsnSerGlySerProValPheAs :::::	Oy 656 nGlyArgLeulleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGl 	Oy 675 eGluPheGluProAspLeuGlnArg 683 ::: Db 4022397 CAAGTAGATGCCCGGTAACTCTCGG 4022373	RESULT 10 US-08-961-527-134 ; Sequence 134, Application US/08961527 ; Patent No. 6420135	; GENERAL INFORMATION: ; APPLICANT: Charles Kunsch ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotid ; NUMBER OF SEQUENCES: 391	CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville	; STATE: Maryland ; COUNTRY: USA	. COMPUTER READABLE FORM: ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage	86/33 OS version 6.2	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/961,527 ; FILING DATE: ; CLASSIFICATION: 424	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: ; FILING DATE:	; ATTORNEY AGEMT INFORMATION: ; NAME: BYCONES, A. ANGELS ; REGISTRATION NUMBER: 36,373	; REFERENCE/DOCKET NUMBER: PB340P1 ; TELECOMMULCATION INFORMATION:	; TELEFRONE: (301) 309-8519 ; TELEFAX: (301) 309-8512 ; INFORMATION FOR SEQ ID NO: 134: ; SEQUENCE CHARACTERISTICS:	: LENGTH: 12665 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double ; TOPOLOGY: linear	8-961-527-134 nment Scores:	Score: 10.578 Length: 12052 Score: 110.50 Matches: 132 Percent Similarity: 35.47% Conservative: 100 Best Local Similarity: 20.18% Mismatches: 246
	4023341 CCGGAGTACGCCAGTTATCCGGTCAAGATCACGTTATCCGGTCACAAGATCAACGATCACGTCACAAGATCAAGATCAACGATCAAGATCAACGATCAAGATCAACGATCAAGATCAACGATCAAGATCAAGATCAACGATCAAGATCAACAACAACAACAACAACAACAACAACAACAACAACA	Oy 274ProGlySerThrAspArgTyrLeuThrSerTrpGlyValGlu-AspArg11eG1 291	291 uAsnGluAsnArnProArgileGluValArgGlyIleLysGlnGlyIleTrpLysGluAl 3 11 11 11 11 11 11 11	311 aMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAs 3	331 nTyrTrpLysasnSerIleGlyMetasnArgG 	345 gLeuAspvallleGlyArgLysArgA ::: :::	Qy 360 aSeralaValTy 372	<pre>Qy 372 rGlyAspValLeuSer</pre>	OY 383 rLysGluGlyalaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGl 403	Qy 403 yThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHi 423	4022877	<pre>Qy 423 sAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspAr 443 ::::: :: Db 4022876</pre>	Qy 443 gLysValLeuProAläMetLeuAspIleValArgArgArgIleProAl 459	Oy 459 aAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLy 479	OY 479 SLYSTYRALAASPPheValPheAspLysSerValValProTyrSerAspLysPheHisAl 499	Db 4022778 4022778	Qy 499 aMetLeuLysSerMetAspLysGluLysPheAlaLysAlalleGluLysAspProAlava 519 bb 4022777	Oy 519 IGluLeuSerLysSerValIleAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAs 539	Oy 539 nAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPr 559	*

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eAspLysAs 656
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|CCGAC---- 4022439
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GTGGTGACAC 4022398
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                                                                         CCAGGCTGA 4022536
                                                                                                               4022490
                                    4022595
-GGCATCCT 4022623
                                                      AspLeu-- 618
                                                                                            AlaPheLe 638
                   Glyvalle 599
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15.978 Indels: 176 Gaps: 30 Safyrteukrglystlleval ANTHORISTANANANAROGGGGGGGGGGGGGAAAATCAACAAAAAAGGGGACATACA InleuLysGly11EThrAspGluMetGluargleuarglysalaGlnGluvyalCysGlu TTACTGTAGCTCTAACTTAACGACTGACAAAATCAACTAACAAAAAAAA	Qy 423 HisAlaGlyIleLeuLysSerLeuAspAspLys		Oy 463 ProAspilePheLysAsnValileAspLysLys ::: Db 1816GAAAAA	Qy 483 AspPheValPheAspLysSerValValProTyr :: Db 1849 GAA	Qy 503 SerMetAspLysGluLysPhealaLysAlaile	Qy 523 LysSerVallleAla		Oy 555 ArgGluMetTyrProGlyArg Db 2059 ACTCAACAGCAACGCCAAAAACTGAAAAACCA	Oy 571 MetArgMetSerTyrGlySerIleLysGlyTyr	Qy 591 TyrHisThrThrGlyLysGlyVal 	Qy 608 GluPheAlaValGlnGluAsnIleLeuAspLeu Db 2188	Qy 628AlaGluAsnGlyClnLeuHisIle	Oy 643IleThr 111 Db 2263 TACTATCTAAACGCTAATGGTTCAATGGCAACA	Qy 652 ValPheAspLysAsnGlyArgLeulle ::: ::: Db 2323 TACTACCTAAACGCTAATGGTTCAATGGCGACA	Qy 669 GluAlaMetSerGlyAsp-IleGluPheGluPr ::::::::::::::::::::::::::::::::::::	Oy 688 pileargTyrValLeuPheMetileAspLysTr	RESULT 11 US-09-134-078-14 ; Sequence 14, Application US/09134078 ; Patent No. 6368844	; GENERAL INFORMATION: ; APPLICANT: Bylina, Edward J. ; TITLE OF INVENTION: GLYCOSIDASE ENZYW
9. Match: 127 LysTyrLeuArglyslleVal	Indels: . Gaps:						SAAGCT			p E								411 GlnPheAlaAsnAlaLeuAlaThr
		10-008-355-2 (1-712) x US-08-9 127 LySTyrLeuArgLySIleVal ::: :::: 808 GAATATGTAAAAAAAAATAGTGGG	142 GInLeuLysGlyIleThrAspGl ::: ::: 868 ATTACTGTAGCTCTAGTTAACGAC	162 GluLeualarystysGluasnala 11::::::::::::::::::::::::::::::::::	182 SerasnasndluTyrPheLeull	202 AlaProProSerSerValGlyLy:	222 HisthrGlyAspPheservalPh. :::	240 AlaGluTyrSerLysAspAsnLy: :::::: 1063 TCAGATACAGCGAAGCCAAACAA	252ValTyrPheAlaAlaVa. 1123 aagaaggmgaaggaaggmaaggaaa	270 ThrileGlyPheProGlySerTh.	290 11eGlu	299 GluValArgGly1leLysGlnGl: 1294 GAGCAAAAATTAAGCAAGCA	319 ArglleLys	332 TyrTrpLysAsnSerlleGlyMe 1411 CATCTTAAACACAACGTAA	352 LysArgAlaGluGluArgAlaPh 352 LysArgAlaGluGluArgAlaPh 1468 CHACCAACACACATAAAAAAAAAAAA	372 TyrGlyAspValLeuSerSerLeu 1522 GGTGAAGAAACTTTCCAGCCC	391 ArgGluMetThrTyrLeuSerGli::::::::::::::::::::::::::::::::::::	411 GlnPheAlaAsnAlaLeuAlaThr

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leAlaPheLeuSerAsnAsnAsp----- 642 :::111 | 11111 | CAGGATGGCTCCAAAACAATGGTTCATGG 2262
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                                                        alargargileProAlaAspLysLeu 462
                                                                                                                       ysPheLysGlyAspThrLysLysTyrAla 482
                                                                                                                                                                                                                                                                                                                                                                    rgLeuPhe------PheAlaGlyLeu 554
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ysTyrLysAspTyrLeuProSerLeuAsp 442
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-TGGCGACAG 2476
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182 rAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPheAl
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-----ATCCTGGACGACTACTATTA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 GlyalaIleGlnSer---GlnSer-ThrValAspHisAspTyrLeuArgAspGlyPheVa 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 ThrGly---IleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyr 92
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155
105
268
258
42
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Mismatches:
Indels:
Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
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COMPUTER: IBM COMPATIBLE
ODERATURG SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELEPHONE: 858/677-1456
TELEPEAX: 858/677-1456
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding Sequence 1...2316
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2319 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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110.00
33.128
19.758
2.968
                                                                                                                                                                                                                                                                                NAME: Haile, Lisa A.
REGISTRATION NUMBER:
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                        San Diego
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Best Local Similarity:
Query Match:
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                      CITY: Sar
STATE: CA
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US-09-134-078-14
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1043 GTTACGATCCTTACCTGTTCTGGTTCCGGAGGGCAGATACTCAACCGATCCCAAAAACC 1102 1103 CACACACGAGAATCAGAGAAGTCAAAGAAATGGTCAAAGCCCTTCACAAACACGGTATAG 1162 |||| | 1223 ATCAGACGGTGCCGTACTTCTACAGAATCGACAAGACAGGTGCCTATTTGAACGAAA 1282 283 GCGGATGTGGTAACGTCATCGCAAGCGAAAGACCCATGATGAGAAAATTCATAGTCGATA 1342 1163 GTGTGATTATGGACATGGTGTTCCCTCACACCTACGGTATAGGCGAACTCTCTGCGTTCG 1222 672 GATCAGAACAACCGTCGATCCT---TATTCGAAAGCGGTT-------TACGCAAA 716 eLysTyrAlaSerLysTyr---AlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMe 339 tAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAlaPh 359 924 GACAACAGGCCTTTGGCACCTTGTGGAACTCGGTGTTACACACGGTTCATATACTTCCTTT 983 eAlaAspTrp-----37z 382 aTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGl 402 -----TyrLysAspTyrLeuProSerLeuAs 442 pargLysValLeuProAlaMetLeuAspIleValArgArgArgIleProAla-AspLysL 462 euProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyr- 481 -----AlaA 483 304 sGlnGlyIleTrpLysGluAlaMetSerAlaAsp------GlnAlaThrArgIl 320 864 AAAAAACAAAGGCCTCTATCTCGGGCTCACCGAAGAAAACACGAAAAGGACCGGGCGGTGT 923 ------CAGCTGGAAACTACGGAAA 671 244 sAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAl 264 264 aAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSerTr 284 717 CAACCAAGAGAGCGCCGTTGTGATCTTGCCAGGACAAACCCAGAA------GGATG 767 pGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGlyIleLy 304 507 CCCCGTTTCTAAGTGGGTAAAGGTGCTTCTCTTCAAAAACGGAGAAGACACAGAACGTA -----AsnTrpMetTrpProArgHisThr---GlyAs 567 CCAGGTTGTGAACATGGAATACAAGGGAAACGGGGTCTGGGAAGCGGTTGTTGAAGGCGA pPhe---SerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLy AGACGCGATAATCTATGAAATACACATAGCGGACATCACAGGACTCGAAAAACTCCGGGGT -----SerLeuGluLysAl y------GlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAs 150 CGATGGAGAG --- CTCGGAGCCGTATATTCTCCAGAGAGACGATATTCAGAGTCTGGTC --ValGlyLysPheGlyGlyAspThrAsp----419 nProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLys------482 ò

; CURRENT FILING DATE: 1998-08-13 ; PRIOR APPLICATION NUMBER: US 60/064,964 ; PRIOR FILING DATE: 1997-11-08 ; PRIOR FILING DATE: 1997-11-08 ; NUMBER OF SEQ 1D NOS: 5674 ; SEQ ID NO 195 ; LENGTH: 2667 ; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-195	Alignment Scores: 0.059 Length: 2667 Score: 110.00 Matches: 112 Score: 34.72\$ Conservative: 89 Best Local Similarity: 3.43\$ Mismatches: 178 Query Match: 2.96\$ Indels: 201 BB: 4 Gaps: 28 US-10-008-355-2 (1-712) x US-09-134-001C-195 (1-2667)		0y 243 SerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyr 262 Db 205GATACTACTATACAAGATATAATAATAATGAAAGAAAGCAATAC 255 Qy 263 LysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr 282	Db 325 AATGAACAGGTATATCTAGACCGACTTAGGAAGAGAA	QY 348 ValileGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLys 365	Oy 379 LeuGluLysalaTyrLysGluGlyalaLysalaAsnArgGluMetThrTyr 395 :::
Db 1442 TTCATAAAATCGATCCAACTATCATTCTAGGGGGAACCGTGGGGTGGAGCAC 1501 Qy 483 spPheValPheAspLysSer	Qy 503 erMetAspLysGlu	Oy 532 leGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheA 552	589TyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnA 603 589TyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnA 603 1979 TCATAGACGTGTTCAATTACCACAGGGTCTCATAAAACTGAGAAAGAAC 202 603 SPPTOLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysA 623 1970 ACCT	2099 GAATAGTTGCGTTCATGCTTAAAGACCACGCAGGTGGTGATCCCTGGAAAGACATCGTGG 2 653 heAspLysAsnGlyargLeulleGlyLeualaPheAspGlyAsnTrp 6 111	DD 2219 TGGTTGTGAACAGCCGGAACAGAAGTGATAGAAACCGTCGAAGGAACAATAG 2278 Qy 676 luPheGluPro 679 Db 2279 AACTCGATCCG 2289 RESULT 12 US-09-134-001C-195	; Sequence 195, Application US/09134001C ; Betent No. 6380370 ; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS ; TITLE OF INVENTION: BPIDERAIDIS FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: GTC-007 ; CURRENT APPLICATION NUMBER: US/09/134,001C

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IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR USES
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63
206
186
29
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OTHER INFORMATION: /product= "immature protein L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OD: experimental / codon.start= 280 / product= "mature protein L" /evidence= EXPERIMENTAL
                                                                                              AUDKESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Peptostreptococcus asaccharolyticus
STRAIN: 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 280..3183
LOCATION: 280..3183
OTHER INFORMATION: /codon_start= 280
OTHER INFORMATION: /product= "mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
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Matches:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3279 base pairs
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Laurence, Oliver S. APPLICANT: Daggleby, Clive J. TITLE OF INVENTION: FROM L PROTITLE OF INVENTION: FROM L PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: double
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
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OTHER INFORMATION:
                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                 STATE: Washington
COUNTRY: USA
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OTHER INFORMATION:
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LOCATION:
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US-08-446-137B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958 AAATACAAAGGGATGGATAGATTTGATTGTAGAAATCAGCTTGTTAAAGACTTAAAAGAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1018 CAAGAICTIGITATAAAAAITGAAGAACATACACAITCAGIAGGACAITCIGAACGIICI 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1078 GGTGCAATAGTAGAACCTTATTTGTCTACAATGGTTTGTAAAAATGAAACCTTTGGCA 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1198 GAAAATACATTCAATCGCTGGATGGAAGAAATTAGAGATTGGACGATTTCGCGTCAACTA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1258 TGGTGGGGCCACCAAATACCT------GCTTGGTAT---CATAAAGATACAGG 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1302 TGAAGTCTTTGTTGGTGAAGAAGCACCTGAAGACATCGAGAATTGGATACAAGATGAGA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1422 TACAAATGCTGATGATTTTAAACGTTATTATCCGACAAATGCATTAGTTACTGGTTATGA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 rGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGl 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 yLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln---GluAs 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 nIleLeuAspLeuPheArgThrLys-AsnTyrGlyArgTyrAlaGlu---AsnGlyGlnL 633
                                                                                                       425 GlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLys 444
                                                                                                                                                                                               445 ValLeuProAlaMetLeuAspIleValArgArgArgIlePro-----AlaAspLysLeu 462
                                                                                                                                                                                                                        465
                                                                                                                                                                                                                                                                                                                                                                          466 -----AspLysLysPheLysAsnVallle-----AspLysLysPheLys 475
                                                                                                                                                                                                                                                                                                                                                                                                                   880 TITGAAATIGGTCAAAGACATCAATIAGAAAATATIATAGTCAIGGAIGAATAIGGTAAG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           940 ATGAACGATAAA-----GCTGAT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIle---Glu 514
                    405 GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla 424
                                                                                                                                                                                                                                                                                                                              820 GITGATATTGAATTTGGTTCAGGAGCAATGAAAGTTACTCCGGCACATGATCCTAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 LysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            556 GluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMet-ArgMetSerTy
                                                                                                                                                   ----GACGAAAGGTATAAAGATGTGATTGGTAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 -----AlaIleGlu------LysGlyLysArgLeuPhePheAlaGlyLeuArg
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                                                                -----GCTATTGTTAAATCCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 AspalaMetalaAsnalaTyr-----
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Patent No. 6162903
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Atkinson, Anthony
Murphy, Jonathan P.
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                                                                                                                                                                                                                                                                                    463 ProAspile
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APPLICANT:
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ą	1861	TGGTTATTAAAGAATGCTAAAGAAGAAGCAATCAAAGAATTAAAAGAAGCAGGAATCACT 1920	
<u>ک</u> ۾	1921	LeuProLeuAspSerLeuTyrSerPheAspLysProSerIleAlaAsnAlaValValIle 68	
á	69	PheGlyGlyGlyCy	
Q	1963		
<u>ک</u> ج	89	HisCysGlyTyrGlyAlaIleGlnSerGlnSerThrValAspHisAspTyrLeuArgAsp 108 	
ζ	109	GlyPheValSerArgThrMetGlyGluGluLeuProIleProGlyLeuSerValLysTyr	
. ფ	2035	::: ::: GGATATGCAACATATGAAGAAGCAGAGCAGCTAAAAGAAGCTTTGAAAAATGATGAT 2094	
≿ 4	129	LeuArgLysIleValLysValThrAspLysValGluGlyGln	•
2 2	145	GlylleThrAspGluMetGluArgLeuArgLysAlaGluGluValCysGlu	
g q	2155	ATTGAAGTTGCAGACGAAGAAGAACCAGGTGAAGACTCCAGAAGTTCAAGAAGGTTAC	
λ	162		
ď	2215	GCAACTTACGAAGA	
ý	176	IleValGluProPheTyrSerAsnAsnGluTyrPheLeuIle	
ð	2272		
λ	190	ValTyraspvalPheLysAspValArgMetValPheAlaProProSerSerValGly 208	
q	2311		
. Y.	209	LysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSer :::	
ð	2371		
ά	228	ValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLys	
g	2425		
č	248	ProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyr 267	
g	2464		
à :	268	AlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGlu	
<u>a</u>	2482	AACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
à :	288	AspargileGluAsnGluAsnAsnBroArg 297	
g G	2512	GCGTTAAAGAACGAAATCTTAAAAGCACGCTGAAAAACCAGGCGAAAACCCAGGA 2568	
ž	298	IleGluVal 310	
ą	2569	ATCACAATTGATGAATGGTTATTAAAGAATGCTAAAGAAGCTGCAATCAAAGAATTAAAA 2628	
χ̈́	311	AlaMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGln 328	
q	2629		
λ̈́	329	SerAlaAsnTyrTrpLysAsnSerIle	
g	2689	GGCGTAGAATCATTAAAGAACGAAATCTTAAAAGCACACGCTGAAAAACCAGGCGAAAAC 2748	

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RESULT 14
US-08-961-527-139/C
Squence 139 Application US/08961527
Squence 139 Application US/08961527
Squence 139 Application US/08961527
GENERAL INFORMATION:
TATLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                --ACAATTGAT 2766
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                                                                                                                                                                                       361 AspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGlu 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 ArgArgIleProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPhe 474
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341 ArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAlaGluGluArgAlaPheAla 360
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2962 GAAGATAAAAAACCAGGTGAAGATAAAAAA------
                                                                                                                                                                                                                                                 :::|||:::
2767 GAATGGTTATTAAAGAACGCTAAA-------
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                                                                                           2749 CCAGGAATC----
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COUNTRY: USA
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Alignm Pred. Score: Percen Best L Query DB:	#2 2 3	nt Scores: No.: Similarity: cal Similarity: latch:	1.14 109.00 17.03 17.93 2.93%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	15363 124 124 222 284 30		
ns-	10-008-	355-2 (1-712)	x US-08-961-527	-139 (1-15363)			
ογ	210 10583	PheGlyGlyAsp-::: 	PheGlyGlyAsp	ThrAspAsn' :: AACAGCAACCGCTTCA'	ThrAspAsnTrpMetTrpProArg ::: ::: ACCGCTTCATGGACTTTTGACCGT	221 10524	
Qy	222 10523	HisThrGlyAspPl : GACAACGCTGGCTI	HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgPro 	ITyrAlaGlyAlaAs; :::: ctggaCaGGTACGGA	pAsnArgPro CTATATTGGTGAACCT	239	
٥y	240	AlaGluTyrSerLy	uTyrSerLysAspAsnLysPr	-ProTyrLysProValTy	alTyrPheAlaAlaValSer	258	
Dp	10463	ACACCATGGCACA		 TGTTAAGAGCTCTTA	 CTTTGGTATCGTAGAT	10404	
Qy Db	259	MetGlnGlyTyrLysAlaAspA ACAGCCGGCATTCCAAAACATG	GlyTyriysalaAspaspTyralaMetThrileGlyPheProGlySerThrasp 	<pre>spTyralametThrileGlyPhebroGly ll::: ::: ACTTCTATCTCTACCAAAGCCAATGGGTT</pre>	eProGlySerThrAsp ATGGGTTTCTGTTAAG	278 10344	
Qy Db	279	Arg	ArgTyrLeuThrSerTrpGlyValGluAspArg ::: 	-TyrLeuThrSerTrpGlyValGluAspArg 	parg	289 10284	
δy	290			II	eGluAsnGluAsnAsnPro	296	
Dp	10283	AAAGTAGCTGACT	AAAGTAGCTGAGATCAAGATTCCAGTTCGTGCTTATTCGAATGCTTCTAGTGT	AGTTCGTGCTTATTC	<	10224	
oy P	297	ArgileGluValA: ::: :::	ArgileGluValArgGlyIleLysGlnGlyIleGarmmers :::	.yIle		307	
λ	30				TrpLys)	
Dp	10163	GATGGGCGGACTT		NTGCTAATGAACTĪTA	 TCTTGAATGGAAAGTT	0	
Óγ	310		GluAlaMe	tSerAlaAspGlnA		317	
Dp	10103	GCCTATCAACCAG	::::: GCCTATCAACCAGTACCTTGGAAGCAATTGCTCGTGATGAATCTGGCAAGGAAATTGCT	TGCTCGTGATGAATC		10044	
Qy	318	ThrArgileL	ThrargileLysTyralaSerLys			325	
Dp	10043	CGAGATAAGATTA	CGAGATAAGATTACGACTGCTAGTAAGCCAGCGGCAGTTCGTCTTATTAAGGAAGACCAT	AGCGCCAGTTCGTCT	TATTAAGGAAGACCAT	9984	
Οy	326	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		TyrAlagl	aGlnSerAlaAsnTyrTrp	333	
qq	9983	GCGATTGCAGCAG	GCGATTGCAGCAGATGGAAAAGACTTGACTTACATCTACTATGAAATTGTTGACAGCCAG	TTACATCTACTATGA	AATTGTTGACAGCCAG	9924	
οy	334	LysAsnSerIleG	SASnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGly	uAlaArgLeuAspVa	lilegly	350	
Op	9923	GGGAATGTGGTTC		GGTTCGCTTCCAATT	: GCATGGCCAAGGTCAA	9864	
ογ	351		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ArgLysArgAl.	-ArgLysArgAlaGluGluArgAlaPhe	359	

qa	9863	AGCCGTGAACGCTATAAGGCGCAAGCAGAT 9	9804
Qy	360	AlaAspTrp1leArgLysAsnGlyLysSer3	369
qa	9803		9744
Qy	370		382
qa	9743	AATTCACCCTGACTGCCCACTGATCTCTTGAAATCGAACCAGTCACT	9684
Qy	383	ThrLe	402
qq	9683	LTTTG	9642
Qy	403	GlyThrGluVal	406
qa	9641	ACAGACCATTATTGGAGAGGCACCTGAAATGCCTACCACT	9582
QY	407	InPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIle	426
qq	9581	CCGTTTGTATACAGTGATGGTAGCCGTGCAGAACGTCCTGTAACCTGGTCTTCAGTA	9522
Qy	427		437
qq	9521	CGAGAAGTA	9465
Qy.	438	LeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArgArgIle 4	457
qa	9464		9405
ΟŻ	458	ProAlaAspLysLeuProAspIlePheLysAsnVallleAspLysLysPheLysGlyAsp 4	477
Ф	9404	CCAAATACTGACTTGAATTCTGTAGACAAATCTGTTTCCTATGTTTTGATTGA	9345
Qy	478		496
QQ	9344	GTTGAAGAGTATGAAGTGGACAAGTGGGAGATTGCCGÁAGAGATAAAGCT 9	9294
QY	497		497
QQ	9293	AATT	9234
QY	498	pPro	517
QQ	9233		9183
Qy	518		526
QQ	9182	ACTAGTCAAAACCAATGCAATAC	9123
Qy	527		528
qq	9122	ACAGCAAGTGCTAAAAATGCAGCT	69063
ΟŸ	529		539
qa	9062	GTTCTTCAAGCAAGCGCAGCAAACGGCATGCGTGCGAGCATCTTTATTCAG	9006
QY	540	GluLysGlyLysArg 5	548
QQ	9005	ATTCCTTGAAGAAGCGCCAAAA	8946
QY	549	LeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAsp 5	266
QQ	8945	SCTCACTTGAGCTTGCAAGTGGAAAAGCTGACAGTCTCAAAGAAGACCAAACT	8889
Qy	267	AlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGly 5	286
qq	8888		8853
Qy	587	AlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeu 5	599
5	9852		9700

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spLeuPhe 619 :: AGTTGCAT 8763 euHisIle 635		.yAspile 675 ::: :AGATTTG 8634		IN MYCOBACTERIUM	it the sequence			94 - 40157	rArgThr 114 : :CGCGT 4015696	134	
spGluPheAlaValGlnGluAsnIleLeuAspLeuPhe 		<pre>slualaMetSerGlyAspIle ::: :::AATGTAGTGACAGATTTG</pre>	688 8595		ons throughout	4403765 136 60 189 284 34	1765)	nHisHisCysGlyTyrGl :: CCGCATATCGGGCAT-	spGlyPheValSe ::::: :cGATGGTTGCTCG	eProGlyLeuSerValLysTyrLeuArgLysIleValLys	
uPhealavalGlnG :::::: AGTCGCAATTCGTA	rGAATATGAGGGAC GlyGlyAsnSerG H SATTGCGCAATCCA	eAspGlyAsnTrpC	:lleServalAsp :::::: ::: \GTAACAGTTGAG	0A FOR STRAIN ANALYSIS /103,840A	osis various positions t, c or g	Length: Matches: Conservative Mismatches: Indels:	x US-09-103-840A-2 (1-4403765	IlePheThrAsnH	AspTyrLeuArgA CGACATCCTGCGC	LeuSerValLysT :	
ProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPhe		leGlyLeuAlaPhe	spLeuGlnArgThr stCTTCCAGCAACA	cation US/09103840 1001: CCHMAN, Robert D. E. Owen R. ER, Claire M. ER, John C. CON: TUBERCULOSIS 24366-2007.00 ION NUMBER: US/09/ 110N NUMBER: US/09/ ATE: 1998-06-24 IN Ver. 2.1	tubercul 1551 pases at esent a,	7.14e+03 109.00 29.34% 20.36% 4	x US-09-103-8	rAspGlnGlyLeuIleP CAGGGCCTA	<pre>InSerGinSerThrValAspHisAspTyrLeuArgAspGlyPheValSerArgTh</pre>	uProlleProGly	
GluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPhe	::: AAGCCAGGAGCAGTCACTCTGAACGCTGAATATGAGGGAGCTAAAGACCAAGTTGAACTC AlaPheLeuSerAsnAsp11eThrGlyGlyAsnSerGlySerProvalPheAspLys :::	AsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIle : : :	GluPheGluProAspLeuGlnArgThrIleSerValAsp 	A-2/C APPLI 629432 ORMATI ORMATI WHIT WHIT WHIT NVENTI NVENTI ENCE: PLICAT	765 cobacte ATION: ATION:	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match:	355-2 (1-712)	GlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyrGlyAla 	<pre>1leGlnSerThrValAspHisAspTyrLeuArgAspGlyPheValSerArgThr</pre>	MetGlyGluGluLeuProIleProGlyLeuSerValLysTyrLeuArgLysIleValLys 	
Oy 600 Db 8798 Oy 620	Db 8762 Qy 636 Db 8702	Qy 656 . Db 8651	9 6	RESULT 15 US-09-103-840 Sequence 2, Sequence 2, Settle No. GENERAL INER APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: AURIENT APPLICANT: CURRENT APPLICANT APPLICANT APPLICANTENT APPLICANT APPLICANTENT APPLICANT APPLICANTENT APPLICANT APPLICANTENT APPLICANTENT APPLICANTENT APPLICANTENT APPLICANTEN	LENGTH: 4403 TYPE: DNA ORGANISM: My FEATURE: OTHER INFORM OTHER INFORM COTHER INFORM US-09-103-840A-2	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	US-10-008-355-2	Oy 75 (Oy 95 Db 4015746	Oy 115 P	

οy	155 LysAlaGlnGluValCysGlnGlu
qq	4015644
Q 4	175 CysileValGluProPheTyrSerAsnAsnGluTyrPheLeuileVal 190
VO do	191 TyrAspValPheLysAspValArgMetValPheAlaProProSerSerValGlyLysPhe 210
δδ	211 GlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPhe 229
qa	4015533
9. 0.0	230 239 1 1 1 1 1 1 1 1 1
οy	240 AlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSer 258
qq	
oy 4	259
2 2	4010422
g G	4015362 GCTGCCGGCAAGCGGCGCGCGCTTCATTTGTGGAAGGCGGAAAAGCCGGGTG
δŷ	291 uAsnGluAsnAsnProArglleGluValArgGlylleLysGlnGlylleTrpLysGluAl 311
Dp	4015304
δy	311 aMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAs 331 :::
QΩ	4015253
Qy	331 nTyrTrp
qq	4015245
Qy Db	345 gLeu
· 0y	
qq	4015126
οy	372 rGlyAspValLeuSer
qq	4015066 GGCCAACGTGTTGTCCATGCCGGCGATGTTGCAGCGGGTGCGGCTGGGCTGAGCTGCGTTA
QQ Op	383 rLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGl 403 4015006 TTACCTGGCARGGGGGGAGAGTAGAGAGTGGAGTTGTCGAGAGAGC 4014958
Qy	403 yThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHi 423
· Db	4014958 4014958
δý	423 sAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspAr 443
qa	4014957
οy	443 gLysValLeuProAlaMetLeuAspIleValArgArgArgIle
qq	4014924CTAGAGGACTTCCTGCACCGCGTTCGCACCGGGTGGGCGCCGTCTGCCCCGG 4
ΟŅ	459 aAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLy 479

Search completed: May 23, 2003, 13:33:17 Job time: 4891.71 secs

v th.∰

Sequence 1925, Ap Sequence 171, App

App Appli

14, Appl 14, Appl 61, Appl 61, Appl 61, Appl 1, Appli 1, Appli 1, Appli

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Sequence 79, April Sequence 79, April Sequence 26, Appl Sequence 20, Appl Sequence 20, Appl Sequence 862, Appl Sequence 444, Appl Sequence 470, Appl Sequence 1, Appl Sequence 3, Appl Sequence 3, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl S
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Sequence 138, App
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Sequence 78, Appl
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Sequence 221, App
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Sequence 197, App
Sequence 1, Appl
Sequence 1, Appl
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Sequence 209,
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APPLICANT: Banbula, Agniesaka
TITLE OF INVENTION: Dipeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11-08
LENGTH: 2139
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US-10-100-049-7
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
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Query Match:
  Score:
Percent Similarity:
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-MODEL=frame+_p2n.model -DEV=x1h
-O=/cgn2_1/USPPO_spool_/US10008355/runat_16052003_110406_2649/app_guery.fasta_1.1230
-DB=Published_Applications_NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62
-TRR.NN=0 - ALIGN=15 -MODE=LOCAL_COTFMT=pto - NORM=ext -HEAPSIZE=500 -MINLEN=0
-THR_NNN=0 - ALIGN=15 -MODE=LOCAL_COTFMT=pto - NORM=ext -HEAPSIZE=500 -MINLEN=0
-WAXLEN=200000000 -USER=US10008355_eCGN_1_1_132_etunat_16052003_110406_2649
-NCPU=6 -ICPU=3 -NO_XLDXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIGG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 9284, Ap
Sequence 9586, Ap
Sequence 1, Appli
                                                                                                                                                                                                (without alignments)
5031.128 Million cell updates/sec
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                                                                                                                                                                                                                                                                 US-10-008-355-2
3719
1 MQMKLKSILLGAALLLGASG......LFMIDKWGQCPRLIQELKLI 712
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/cgn2_6/ptcdate/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptcdate/2/pubpna/NSO6_PUBM_PUB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO6_PUBM_PUB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO9_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seg:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*
                                                                                                                                                                    May 23, 2003, 10:12:58; Search time 186.87
                       5.1.4_p5_4578
Compugen Ltd.
                                                                                                                       nucleic search, using frame_plus_p2n model
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US-09-81E
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, Ygapext
, Fgapext
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Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su
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DB seq length: 200000000
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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133 127 116.5

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Fotal number

Minimum Maximum

Searched:

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Sequence 137, App Sequence 643, App

15:40:30

25

May

Sun

1320 1440 1620 1380 1680 1800 1860 1920 2100 440 460 480 540 580 009 640 LysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArg AAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC GlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAsp LeuAspArgLysValLeuProAlaMetLeuAspIleValArgArgArgIleProAlaAsp LeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGlu LeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAla ArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGly ThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsn AsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIle LysAlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeu 712 GlnCysProArgLeuIleGlnGluLeuLysLeuIle 1261 1441 1681 1741 2041 1081 1141 1321 1381 1621 1801 1861 1921 1021 381 1201 1501 1561 541 561 1981 401 421 441 461 481 501 521 581 601 621 641 661 681 701 361 qq ò QQ οy Db Q Db οy QΩ οy Db οy Db δ Db Qγ dd οy Db Qγ Db οy qq οy Db οy QQ ò qq οy ΩQ ò q Qy q ò

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991 GGTGCCCTTGTCAAAATCGAAAACGTGTCCACAGTGTTGGTCACTCAGAACGTACAGGT 1050
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                                                                                                                                                                                331 GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGAC------GAATATGCCACT 378
                                                                                                                                                                                                                                                             ----TyrLeuProSerLeuAspArgLysValLeuProAla 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||| aaggacttgattggtaaaaaggtcatccttcca---atcgctaataaactcatcccaatc 774
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GTTGGAGATGAGCACGCAGATCCTGAGTTTGGTACTGGTGTGAAAAATCACACCTGCC 834
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--ACCCTTTGGCTTCCTGGGATGGACCACGCAGGGATTGCCACT 270
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                                             283 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly
                                                                                                                                     -----IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr
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106
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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Matches:
Conservative:
Mismatches:
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2101 CAGTGCCCCGTCTCATCCAAGAGCTGAAGTTGATC 2136
                                                                                                                                                                                                                                                                                                                                                                             TILLE OF LIVENILON: PICKATYOLES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-62
PRIOR FILING DATE: 2000-12-62
SOFTWARE: PRIOR PRIOR DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESEQ FOR WINGOWS VERSION 4.0
SERIOTH: 2652
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                                                                                        Sequence 9284, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                 APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W
                                                                                                                                                           APPLICANT: Haselbeck, Robert
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1).
US-09-815-242-9284
                                                                -09-815-242-9284
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APPLICANT:
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ò g δy Qγ g δ

QY	224	lyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 24
qq	163	
Qy	244	spAsnLys
QQ	172	TGGGATACGACTTTGCAGGATATCATCATCGTCGTCAAAAACGCATGCAGGGCTTTGAT 228
. Qy	264	laAspAspTyrA
qq	229	ATGGACCACGCTC
QY	283	SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnAsnProArgIleGluValArgGly 302
QO	271	GGCTAAG
Qy	303	aMetSerAla
qq	331	GAGTCTTTCTTGACGAAGGTCTGGGAATGGAAAGACGAATATGCCACT 378
Οy	319	
qa	379	
ογ	338	lyLeuAlaArgLeuAspValIleGlyArgL
qa	439	A SAAGCTGTTCGTAAG 4
Qy	358	heAlaAspTrpIleArgLysAsnG
Db	475	
Οy	374	δVds
qo	535	CCAGCAGCTCGCACAGCCCTTTTCT
QY	385	,
qo	595	TACATGCTGGAAGATGGTTCACGCGCCCTTGAAGTT
QY	395	luValValArgPl
Оb	655	ACTCGTCCTGAGACTATGTTTGGGGACGTT
οy	415	aHisAlaGlyIleLeuLysS
Db	685	
Οy	435	LysaspTyrLeuProSerLeuAspArgLysValLeuProAla 448
qq	718	ATCGCTAATAAACT
Oy	449	MetLeuAsp1leValArgArg 455
qq	775	rggagatgagcacgcagatcctgagtttggtactggtgtcgtgaaaai
Οy	456	ArglleProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLys 475
qq	835	CACGATCCAAATGACTTCTTGGTTGGCCAACGTCATAACTTGCCACAAGTCAACGTCATG 894
Οy	476	GlyaspThrLysLysTyrAlaAspPheValPheAspLysSerValValValProTyrSerAsp 495
qa	895	
QY	496	sSerMetAspLysGluLysPheAlaLysAlaIleG
qq	946	
Qy	516	AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaAlaArgAla 531
Db	991	GGTGCCCTTGTCAAAATCGAAAAACGTGTCCATTCAGTCGGTCACTCAGAACGGACAGGT 1050

Qy 532IleGlnAla 534	ò
Db 1051 GTCGTAGTTGAGCCACGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110	:
Oy 535 AspalaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeu 554 ::: Db 1111 AACGCCATTGCCAACCAACAACACAGAAAG	o v
555 ArgGluMetTyrProGlyArgAlaLeuProSer	Db 1
	oy 4
Oy 566 AspalaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585	od o
GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys	Db 1
1246 CCTGCCTGGTACAATGCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCCAGAA	Ολ
Qy 606 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 617	Dp 7
Db 1300 GGTGACGGATGGACTCAGGACGTCTTGGAT 1335	. d
RESULT 4 US-10-143-186-1	δλ
; Sequence 1, Application US/10143186 ; Publication No. US20030072771A1 ; CRUMDAN TANGORMATION.	r qa .
; APPLICANT: MENGELING, WILLIAMS L. ; APPLICANT: NORMERLY ANN	QY
	Db 1
; APPLICANT: BURKHER KELLY ; APPLICANT: GORCYCA. DAVID F.	Qy
TITLE OF INVENTION: BORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VACCINE,	Dp
; FILE REFERENCE: 27093a ; CURRENT APPLICATION NUMBER: US/10/143.186	Qy
CURRENT FILING DATE: 2002-05-09; PRIOR APPLICATION NUMBER: US/09/461,879	Db 1
; PRIOR FILING DATE: 1999-12-15 ; PRIOR APPLICATION NUMBER: 09/298.110	Qy
PRIOR FILING DATE: 1999-04-22 HUMBER OF SEO ID NOS: 2	. da
SOFTWARE: Patentin Ver. 2.1	Qy
; LENGTH: 15424 ; LENGTH: 15424 : TYPE: DAR	[qa
; ORGANISM: Porcine reproductive and respiratory syndrome virus IIS-10-143-186-1	Qy
Alignment Scores:	C qa
0.155 Length: 116.50 Matches:	Qy
larity: 33.12% imilarity: 20.43%	qa
Indels: Gaps:	Qy
US-10-008-355-2 (1-712) x US-10-143-186-1 (1-15424)	ପୁପ ,
Qy 7 SerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAspLys 26	δλ
Db 10035 TCTAATGTGTTGGGAGGAGGTTCATCGGCCCGGCTGGTGCTGGGAAA 10085	ପୁପ (
uAsnGluLeu	ζ, i
Db 10086 ACATACTGGCTCCTTCAACAGGTCCAGGATGGTGATGCCATTTACACGCCAACTCACCAG 10145	00 :
37	ν. do
Db 10146 ACCATGCTCGATATGATTAGGGCTTTGGGGACGTGCCGGTTCAACGTCCCAGCAGGTACG 10205	!

Οy	54	AspLysProSerIleAlaAsnAlaValValI	71
qq	10206	acgcrecaarreccreccccrecceraccesccrreserrescarecreserreser	10265
Qy	72	GlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis	88
Dp	10266	TGGTGTCCTGGCAAGAATTCCTTGGATGAAGCAGCGTATTGTAATCACCTTGATGTC	10325
QY	88		88
QQ	10326	TTGAGGCTTCTTAGCAAAACTACCCTCACCTGTCTGGGAGATTTCAAACAACTCCACCCA	10385
δy	89	HisCysGlyTyrGlyAlalleGlnSerGlnSer	66
qq	10386	GTGGGTTTTGATTCTCATTGCTATGTTTTTGACATCCATGCCTCAGACTCAACTGAAGACC	10445
οy	100	ThrValAspHisAspTyrLeuArgAspGly	109
QΩ	10446	ATCTGGAGATTTGGACAGAATATCTGTGAGGCCATTCAGCCAGATACAGGGACAAA	10502
Qy	110	PheValSerArgThrMetGlyGluGluLeuProIleProGlyLeuSerValLySTyrLeu	129
qq	10503		10541
Qy	130	ArgLysIleValLysValThrAspLysValGluGly	141
QQ .	10542	GAAAAACCTGTCAAGTATGGGCAAGTCCTCACCCCTTACCACAGGGACCGAGAGGGCCGC	10601
QY	142	GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln	161
QQ	10602	GCCATCACAATTGACTCCAGTCAAGGCGCCACATTTGATGTGGTTACACTG	10652
ΟŸ	162	GluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr	181
QQ	10653	CATITGCCCACTAAAGATTCACTCAACAGGCAAAGAGCCCTTGTTGCTATT	10703
Qy	182	SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe	201
QQ	10704	ACCAGGGCAAGACATGCTGTTTTTTTTTTTTTTTTTTTT	10763
Qy	202	AlaProProSerSerValGlyLysFheGlyGlyAspThr	214
qq	10764	- 0	10814
Οy	215	AspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGly	234
qq	10815	CAGCTGATCGTGCTAGATAGAAATAACAAAGAATGCACGGTTGCTCAGGCTCTAGGCAAT	10874
Qγ	235	AlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPhe	254
qq	10875	GGGGATAAATTCAGGGCCACAGACAAGGGGGTTGTAGATTCTCTCCGCGCC	10925
Οy	255	AlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGly	272
QQ	10926	ATTTGTGCAGATCTGGAAGGGTCGAGCTCCCCGCTCCCCAAGGTCGCACACATGGGGA	10985
٥y	273	PheProGlySerThrAspArgTyrLeuThrSer	283
QQ	10986	TTTTATTTCTCGCCTGATTTGACACAGTTTGCTAAACTCCCGGTAGAACTTGCA	11039
Ωy	284	TrpGlyValGluAspArgIleGluAsnGluAsnAsnAsnProArgIleGluValArg	301
QQ	11040	CCCCACTGGCCCGTGGTGACAACCCAC	11078
Qγ	302	rpLysGluAlaMetSerAlaAspGln-AlaThrArgIl	321
QQ	11079		11120
ΟY	321	sTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLys	334
QQ	11121	TATAGCCGCGCGCGTCCGTCCCGCCTACATCGTCGCCTCACTTCTCGCCACC	11180

Db 12116 CCAACTTTTCGTGGATGCTTTC 12137

ογ	335		350	-
qq	11181	CCTGGGGTTGTGTCATACTATCTCACAAATTTGTCAGGGGGGGG	11240	1 1
S S	350	yargLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl	367 11300	
oy O	367	yLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl	387 11347	
Oy Dp	387 11348	aLysalaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa 	407	
oy Ob	407	1ArgPheAlaGlnPheAlaAsnAlaLeuAlaTh	418	
Oy Db	418	rAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr	434	
Oy Db	435	-LysaspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleVa ::: CGAAGACCAGTCCAAGTGCTGGAAAATGATGTTGGACTTCAA	453	
Oy Dp	453 11561	largargileProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLy	473	
Oy Dp	473	SPheLysGlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValPr 	11668	47 LT (2) LT
o o	492	OTyrSerAspLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAl ::: GOTTAAC	512	шог
2 A	512	alleGluLysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaAr	530 .	ъ o
O.Y	530	galalleGinAlaAspAlaMetAlaAsnAlaTyrAlaTleGluLysGlyLysArgLeuPh	550	ο ο
Q Q	550 11795	ePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAs :::	568 . 11854	Δ Ο
P Q	568 11855	nPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGl	586 11911	Δ Ο
Oy Dp	586	yalarrprasantyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSe	606 11962	Δ α
Oy Dp	606	rAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyAr:	626 12004	Δ Φ
Oy Dp	626 12005	gTyralaGluAsnGlyGlnLeuHisIleAlaPh :: :: CACTGCCACCAGCATGAGGTTTCATTTTCCCCGGGCCCTGTCATTGAACCAACTTAGG	637 12064	<u> </u>
Qy Dp	637 12065	eLeuSerAsnAsplleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGl 65	657 12115	Δ Ο Ι
٥y	657	yArgLeuIleGlyLeuAlaPhe 664		a

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APPLICANT: USERALLY
APPLICANT: LAGER, KELLY
APPLICANT: LAGER, KELLY
APPLICANT: BURKHART, KELLY
APPLICANT: BURKHART, KELLY
APPLICANT: GORCYCA, DAVID E
TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VACCINE,
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION NUMBER: US/10/143,186
CURRENT APPLICATION NUMBER: US/09/461,879
PRIOR FILING DATE: 1999-12-15
PRIOR PELING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTI VET: 2.1
SED ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10035 TCTAATGTGTTGGGCAGCAGCAGCTTCATCATCGGCCCGCCTGGT------GCTGGAAA 10085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10086 ACATACTGGCTCCTTCAACAGGTCGTGGTGTGTGTTTTACACGCCAACTCACCAG 10145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10146 ACCATGCTCGATATGATTAGGGCTTTTGGGGACGTGCCGGTTCAACGTCCCAGCAGGTACG 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10206 ACGCTGCAATTCCCTGCCCTCCCGTACCGCCCTTGGGTTCGCATCCTAGCGGGGGT 10265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10386 GIGGGTTTTGATTCTCATTGCTATGTTTTTGACATGCCTCAGACTCAACTGAAGACC 10445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10266 TGGTGTCCTGGCAAGAATTCCTTCCTGGATGAAGCAGCGTATTGTAATCACCTTGATGTC 10325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10326 TTGAGGCTTCTTAGCAAAACTACCCTCACCTGTCTGGGAGATTTCAAACAACTCCACCCA 10385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GluAsnLeuAspArgMetArgGluLeuGly-----PheThrLeuProLeuAspSer 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAspLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AsnGln 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 LeuTyrSerPheAspLysProSerIleAlaAsn-----AlaValValIlePheGlyGly 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis------ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 -------HisCysGlyTyrGlyAlaIleGlnSerGlnSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA CRGANISM: Porcine reproductive and respiratory syndrome virus US-10-143-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-008-355-2 (1-712) x US-10-143-186-2 (1-15424)
                          ; Sequence 2, Application US/10143186
; Publication No. US20030072771A1
; GENERAL INFORMATION:
                                                                                                     APPLICANT: MENGELING, WILLIAMS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GlyMetTrpLeuLeuAsnGluLeu--
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116.50
33.128
20.438
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
US-10-143-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
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11441	11501 CGAGCTTACCTC	453	473	11669	512 11681	530	11795 CCTGTCTAGTG	568 11855	586	11963	12005		Qy 657 yargLeulleGlyLeuA.	EIΩ	9	CURRENT FILING DATE: 2000-4 PRIOR APPLICATION UNMER PRIOR APPLICATION UNMER	O)
110 PheValSerArgThrMetGlyGluGluLeuProIleProGlyLeuSerValLysTyrLeu 129	130 ArgLysllevalLysVal	142 GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln 161	162 GluLeualaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 181	182 SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe 201 ::: ::: ::: ::: :::: :::	202 AlaProProSerSerValGlyLysPheGlyGlyAspThr 214	215 ASPASNTIPMECTIPPROARGHISTHIGLYASPPHESEIVALPHEARGVALTYRALAGLY 234 ::: ::: ::: ::: 10815 CAGCTGATGGTAGAAATAACAAGAATGCACGGTTGCTCAGGCTCTAGGCAAT 10874	235 AlaaspasnargProalaGluTyrSerLysaspasnLysProTyrLysProValTyrPhe 254	255 AlaalavalSerMetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGly 272 :::: ::: ::: ::: 10926 ATTGTGCAGATCTGGAAGGGTCGCGCTCCCGAAGGTCGCACACACA	273 PheProGlySerThrAspArgTyrLeuThrSer	284TrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArg 301		321 STyralaSerLysTyralaGlnSeralaAsnTyrTrpLys	335	350 yargLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl 367	367 yLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl 387	387 aLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa 407	407 1
Qy Db	Qy Db	Qy	Qy	Qy	Qy	Oy oq	Oy Db	QY	QY Db	Qy Db	QQ Op	QY Db	Qy	QQ QD	Qy Db	Qy Db	QY Db

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JICTGGAAGGACAAGACGCCTATTTTCAACTTGAAGGCCGCCA 11620
                                                                                                                                                                                                                                                                                                                                                  recargescerecertrecaacagaagrigressgreat 11740
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGTICACCGGAAACGGI-----GAGGACTGGGAGGATTACAA 11962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCCAG------AAAGGGAAAATTTATAAGGC 12004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: ||||
AGGTTTCATTTTCCCCCGGGCCCTGTCATTGAACCAACTTTAGG 12064
                                                                                                                                                                                                      TCGCAGTCACCCCTTAT-----GATTACGGTGCCAAAATCAT 11794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSe 606
                                                                                                                                                                                                                                                                                                                    AlaVal-----GluLeuSerLysSerValIleAlaAlaAlaAr 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGl 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyAr 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGl 657
                                              roSerLeuAspArgLysValLeuProAlaMetLeuAspIleVa 453
                                                                                                                 laAspLysLeuProAspIlePheLysAsnValIleAspLysLy 473
                                                                                                                                                                                   hrLysLysTyrAlaAspPheValPheAspLysSerValValPr 492
                                                                                                                                                                                                                                                    HisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAl 512
                                                                                                                                                                                                                                                                                                                                                                                       AlaMetAlaAsnAlaTyrAlaIleGluLysGlyŁysArgLeuPh 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AlaPh 637
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2001-08-10
BER: PCT/US00/05882
00-03-08
BER: 60/124,270
19-03-12
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quals a, t, quals a, t, quals a, t, quals a, t, quals a, t, 0.06% 12% 12% 12% 12% 12% 12% 12% 12% 12% 12
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TIGCGCTIGGTAGAAAGTGACGCAGAAGCTGAA------1156
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------TGGAAGCGCTACATTTAT-----1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||||
| AACTATGCACTCTATGAAGAA-----TTGGAGGCAAAGGATCCTGAGAGACA 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgalaileGlnAlaAspAlaMetAlaAsnAlaTyrAlaileGluLysGlyLys 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAla 567
CGCCAAGTCAMCCATGCTCGA------AATATCTGGGACCGGGCCATA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACATC---AACTTTGAGCTGAGATACAAAGAG------GTGGATCGGGCC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....-ThrAsnProAspAlaHisAlaGlyIle---LeuLysSerLeu 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeu 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /alProTyrSerAspLysPheHisAlaMetLeuLysSerMetAspLys---Glu 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAla 587
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                                                               AspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyr 332
                                                                                                                        -----ACAACGCTGCCTCGAGTTAATCAGTTCTGGTACAAGTACACGTAC 586
                                                                                                                                                                                AsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLys 352
                                                                                                                                                                                                                                             -----AACGTTGCCGGTGCCCGG 622
                                                                                                                                                                                                                                                                                                         GluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyr 372
                                                                                                                                                                                                                                                                                                                                                                     TTTGAGCGC-----TGGATGGAGTGGCAGCCTGAGGAGCAAGCCTGG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                 ValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLysAlaAsnArgGlu 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrLeuSerGluThrLeuPheGlyGlyThrGluVal------ValArgPhe 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTATGAGGGAKTTGTCCTCGTGCACCCTGATGTTAAGAACTGGATCAAGTAT 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITGAAGAAAAACATGCTTATTTTGCCCATGCACGGAAAGTGTATGAGAGAGCT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICITIGGAGATGAACATATGGATGAGCACCITTATGTTGCCTTTGCCAAGTTT 898
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Application US/09815242
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                                                                                                                                                                                                                                         SAAATGTTGGGA-----
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; Patent No. US20020061569A1 ; GENERAL INFORMATION:	^o	260 GlnGlyTyrLy
; APPLICANT: Haselbeck, Robert	i 2	
. Zyskind,		TAD ICAGCACATOC
	0y	280 TyrLeuThrSe
	qa	255 TACCCAGATGG
ramamoto, kobert T. Xu, H. Howard	Qy	299 GluValArg
<pre>; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes</pre>	qa	111 315 CGGCCGCGAAG
; FILE REFERENCE: ELITRA.011A : CURRENT APPLICATION NUMBER: US/09/815.242	² C	
T FILING DATE: 2001-03-21		
FRIOR FILING DATE: 2000-03-21	Qri	3/5 TACCCGTCAGE
; PRIOR APPLICATION NUMBER: 60/206,848	QY	331 nTyrTrpLysA
APPLICATION N	qa	411 Crecence
FRIOR APPLICATION NUMBER: 60/242,578	QY	351 gLysArgAlaC
APPLICATION N	qa	111 459 GAAAGAAGTTI
FILING DATE: APPLICATION N	Oy	371 lTyrGlyAsp
<pre>; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/269,308</pre>	qa	
FILING DATE: 2001-02-16 OF SEQ ID NOS: 14110	QY	386
৺	· qa	579 GAAAGGITCGA
	Qy	392 uMetThrTyrI
; ORGANISM: Escherichia coli ; FEATURE:	qa	 639 TAAAGATTATC
; NAME/KEY: CDS ; LOCATION: (1)(2856)	. Oy	406 lValArgPhe
US-09-815-242-6368	qu	
No.: 0.0272 Length:	QY	426 eLeuLysSerI
Matches: Conservative: Wignations	qa	715
3.058 10	Qy	uPr
)-815-242-6368 (1-2856)	qq	
Oy 150 MetGluArqLeuArqLysAlaGluGluValCysGlnGluLeuAlaLys165	Qy	464 pIlePheLys/
	qq	
Oy 166LeuCysIleValGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro 179	Qy	
Db 61 CAGGGCTACTTTAGCCTAATGGCGATGAAAGCCAGGAAAGTTCTGCATCATGATCCG 120	qq	
Qy 180 PheTyrSerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMet 199	δλ	
Db 120	qq	
Qy 200 ValPheAlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrp 219	VO 2	
Db 121126	qq	978 CGAAATCCCTC
Qy. 220 ProArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgPro 239	ŠČ.	1018
ac-ceecagn	^0	531
OY 240 AlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaValSerMet 259 :: ::: ::: ::: ::: ::: :::	qq	1062 GGAAGAAATI
100 GCARACCATCATGGGTTACCATGGCT		

δy	260 GlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArg 279
qq	195 TCAGCGCCATGCAGGGCAAAAACACCCTGTGGCAGGTCGGTACTGACGACGACGGGGATGGC 254
Qy	280 TyrLeuThrSerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIle 298
qq	GTTGAGCGCAAGATTGCCGCAGAAGAAGGTAAAACCCGTCACGACT
Οy	299 GluValArgGlylleLysGlnGlylleTrpLysGluAla 311
Dp	315 CGGCCGCGAAGCTTTCATCGACAAAATCTGGGAATGGAAAGCGGAATTGGCGAATTGGAATTGAAAGCGGAATTGGCAAATTGAAAGCGGAATTGGCAATTGGAAAGCGGAATTGGCAATTGGAAAGCGGAATTGGCAAATTGGAAAGCGGAATTGGCAATTGGAAAGCGGAATTGGCAATTGGAAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGCGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAATTGGAAAGCGGAAATTGGAAAGCGGAAATTGGAAAGCGGAAATTGGAAAGCGGAAATTGGAAAGCGGAAATTGAAATTGAAAATTGAAATTAAATTAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAAAA
Qy	312 MetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGln-SerAlaAs 331
QQ	
Qy	331 nTyrTrpLysAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyAr 351
QQ	411 CTGGGAGCGTGAACGCTTCACCATGGACGAAGGCCTGTCCAATGCGGT 458
Qy	351 gLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaVa 371
QQ	459 GAAGGAAGTTTTCGTTCGTCTGTATAAAGAAGACCTGATTTACCGTGGCAAACGCCTGGT 518
Oy	371 lTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu 385
QQ	CGAAACTGCG
QY	386GlyalaLysAlaAsnArgGl 392
qq	579 GAAAGGTTCGATGTGGCACATCCGCTATCCGCTGGCTGACGGTGCGAAAACCGCAGACGG 638
QY	392 uMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluVa 406
qa .	639 TAAAGATTATCTGGTGGTGGGGACTACCGGTCCAGAAACCCTGGTGGGGGGATACTGGGGT 698
Qy	406 lvalArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIl 426
QQ	
QY	S
qq	715GATCCGCGTTACAAAGATCTGATTGGCAAATAT 747
QY	446 uProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAs 464
qq	\circ
QY	464 pllePheLysAsnVal
qq	804 CATGGAAAAAGGCACCGGCTGCATGAAATCACTCCGGCGCACGACTTTAACGACTATGA 863
Qy	470 -IleAspLysLys
qq	864 AGTGGGTAAACGTCACGCCCTGCCGATGATCAACATCCTGACCTTTGACGGGGATATCCG 923
Qy	479 sLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAs 495
qq	924 TGAAAGCGCCCAGGTGTTCGATACCAAAGGTAACGAATCTGACGTTTATTCCAG 977
Qy	AspLysGluLysPheAlaLysAla
qq	978 CGAAATCCCTGCAGAGTTCCAGAAACTGGAGCGTTTTGCT 1017
οχ	spProAlaVal
qq	1018GCACGTAAAGCAGTCGTTGCCGCAGTTGACGCGCTTGGCCTGCT 1061
Qy	531
qq	1062 GGAAGAAATTAAACCGCACGACCTGACCGTTCCTTACGGCGACCGTGGCGGCGTAGTTAT 1121

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Percent Similarity: 35.394 Conservative: 78 Best Local Similarity: 19.884 Missacches: 168 Best Local Similarity: 19.884 Missacches: 168 Discol Similarity: 19.034 Ansacches: 168 Discol Similarity: 19.034 Ansaches: 168 Discol Similarity: 19.034 Ansaches: 168 Discol Missacches: 168 Ansaches: 168 Discol Missacches: 168 Ansaches: 168 Us-10-008-155-2 (1-712) x Us-09-781-9864-221 I. II. II. Discol Missacches: 168 II. II. II. Discol Missacches: 168 II. II. II. Discol Missacches: 168 II. II. Discol Missacches: 168 II. III. III. Discol Missacches: 168 III. III. III. Discol Missacches: III. III. III. III. III. Discol Missacches: III. III. III. III. III. III. Discol Missacches: III. III. III. III. III. III. III. III. III. Discol Missacches: III. II	Oy 516 ASPProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAla 534
0y 532	Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: double Standbless: doubless:

148 148 148 148 148 148 148 148 148 148	CCTAAGGACCTAAATGATTACAAATATGATCCTGAAAAAGCTAAAAAAATCTTAGATAAG 1107	 583	GAGATTAACTTTAAACATAATTCAGGTTCTAATCCTACTTTTGAACCA 1215 GlnAspGlyAlaTtpTyrAssnTyrHisThrThrGlyLvsGlyValLeuGluLysGlnAsp 603	ProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsn 623	TTAGTAGAA 1281	TyrGlyArgTyrAlaGluAsnGlyGlnLeuHis		::::::::::::::::::::::::::::::::::::::	AsnGlyArgLeulleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIle 675 ::: :::	695	 		plication US/09769787 US20030091577A1 US20030091577A1 US20030091577A1 US2011001 US20110240 US20110250 US201102
					255 TTGAAACAA	624	636	342	656		459	IleaspLys ::: ATAGATCGT	uence 197, Ap Lication No. Elication No. PLICANT: Micz PLICANT: Gil PLICANT: Han TLE OF INVENT LE REFERENCE: RRENT APPLICATI IOR FILLING DA MBER OF SEQ I IOR FILLING DA MBER OF SEQ I TWARE: Pate: ID NO 197 ENGTH: 2082 YPPE: DNA RYPE: DNA RYPE: DNA RGANISM: STIE 769-787-197 ment SCOFES:

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1132 AAAAAAGCGGAGCTTGAACTAGTAAAAGAGGAAGCTAAGGAA-----CCTCGAAACGAG 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 HisAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAsp 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 TyrGlyAspValLeuSerSerLeuGlu---LysAlaTyrLysGluGlyAlaLysAlaAsn 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 ArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAla 410
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298 ATTACTGTAGCTCTAGTTAACGAGTTGAACAACATTAAG-----AACGAGTATTTGAAT 351
                                                                                                                                        162 GluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 181
                                                                                                                                                                      352 AAAATAGTTGAATCAACCTCAGAAAGCCAACTACAGATACTGATGGAGGAGGTCGATCA 411
                                                                                                                                                                                                                                                                                                        202 AlabroProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArg 221
                                                                                                                                                                                                                                                                                                                                              ------GCTGTGTCTAAGTTTGAAAAGGACTCATCTTCT------TCG 459
                                                                                                                                                                                                                                                                                                                                                                                    222 HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgPro---- 239
                                                                                                                                                                                                                                                                                                                                                                                                                         460 TCAAGTTCAGACTCTTCC------AGTAAACCGGAAGCT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 AAGAAGGTTGAAGAAGCTGAGAAAAAGCCAAGGATCAAAAAGAAGAAGATCGTCGT--- 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AACTACCCAACCATTACTTACAAAACGCTTGAACTTGAAATTGCTGAGTCCGAT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------AsnGluAsnAsnProArglle 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluValArgGlyIleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 AGGTTAAAAAAAATCAAGACAGATCGTGAAGAAGCAGAAGAAGAAGCTAAACGAAGAGCA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 GATGCTAAAGAGCAA---GGTAAACCAAAGGGGCGGGCGGAAAACGAGGAGTTCCTGGAGAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 LysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaVal 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMet 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 GTGGAAGTTAAAAAAGCGGAGCTTGAACTAGTAAAAGTGAAAGCTAACGAACCTCGAGAC 723
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                                                                                                                                                                                                                           182 SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe 201
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Patent No. US20020172690A1
GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.
TITLE OF INVENTION: AN INFECTIOUS CDNA CLONE OF NORTH AMERICAN PORCINE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC10278A
CURRENT APPLICATION NUMBER: US/10/127,391
CURRENT FILING DATE: 1202-04-22
PRIOR APPLICATION NUMBER: US/09/470,661A
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1617
1186 GAAAAAGTTAAGCAAGCAAAAGCGGAAGTTGAGAGTAAAAAAGCTGAGGCTACAAGGTTA 1245
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                                                                                                                                                                                GATAAAGTTAAAGAAAAACCAGCTGAACAACCACAACCAGCGCCGCCTCCAAAAGCAGAA 1368
                                                                                                                                                                                                                                           AAACCAGCTCCAACCACAAAACCAGAGAATCCAGCTGAACAACCAAAAGCAGAAAACCA 1428
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                                                                                                                                                                                                              LysSerValIleAla-----AlaAlaArgAlaIleGlnAlaAspAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyr
                             ProAspIlePheLysAsnVallleAspLysLysPheLysGlyAspThrLysLysTyrAla
                                                                                         AspPheValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLys
                                                                                                                                                                                                                                                                                                                                  555 ArgGluMetTyrProGlyArg-----AlaLeuProSerAspAlaAsnPheThr
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                                                           -----GAAAAATCAAGACAGATCGTAAAAAGCAGAA
                                                                                                                                                  SerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer
                                                                                                                                                                                                                                                                         AlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhe-----PheAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                      -----AlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsnAsnAsp----
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INFORMATION: Description of Artificial Sequence: cDNA INFORMATION: corresponding to No. US20020172690Alth American Porcine INFORMATION: Reproductive And Respiratory Syndrome (PRRS) Virus INFORMATION: Genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10016 TCTAATGTGTTGCGCAGCAGGTTCATCATCGGTCGCCCGGT------GCTGGGAAA 10006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10067 ACATACTGGCTCCTTCAGCAGGTCCAGGATGGTGATGTCATTTACACACCGACTCACCG 10126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10247 TGGTGTCCTGGTAAGAATTCCTTCCTGGATGAAGCAGCGTATTGTAATCACCTTGATGTC 10306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAspLys 26
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Matches:
Conservative:
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                                                  LENGTH: 15450
TYPE: DNA
ORCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Corresponding
2.1.
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  SOFTWARE: Patentin
SEQ ID NO 1
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QQ QD	2)y 202 AlaproProSerSerValGlyLysPheGlyGlyAspThr 214	Db 11671 GGACCCTG
Oy .	215 AspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGly	Oy 533 nAlaAspAl
o o	Db. 10796 CAGCTGATCGTACTGGATAGAATAATAAAGAATGCACAGTTGCTCAGGCTATAGGCAAC 10855)v. 235 AlaaspasnarqProAlaGluTvrSerLvsAspasnLvsProTvrLvsProValTvrPhe 254	Qy 553 yLeu
QQ	10856 GGAGATAAATTCAGGGCCACCGACAAGGCGCTTGTAGATTCTCTCCGCGCC	1.1785 CGCTT
Qy dy	255 AlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGly	QY 5/1 tAr Bb 11845 CGACGACCC
S S	DD 1990/ MITIGIOCTICALCTICGAAGGGTCGCTCCCCCAGGGTCGCACACATGGGA 19966 DV 273 Phebrodiage-maracaration-margaritan-margaritan	Qy 58.9 rAsnTyrHi
G G	10967 TITIATITCICACCIGATTIGACAGITICCIAAACTCCCGGTAGACCTTGCA	11899
ÓΫ	284TrpGlyValGlu	Oy 609 eAlaValGI Db 11930TG
අ	11021 CCCCACTGGCCCGTGGTGACAACCCAGAACAATGAAAAG	Qy 629 uAsnGlyGl
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ò	321 sTyralaSerLysTyrAlaGlnSerAlaAsnTyrTrpLys	Oy 638LeuSe
q	11102 TATAGCCGTGCGTGCGTGCTGCGCTATATGGTGGGCCCCTCGGTGTTTCTAGGCACC	Db 12043 AGGCCTGAA
Qγ	335AsnSerlleGlyMetAsnArgGlyLeuA	Oy 656 nGlyArgLe
qq	DD 11162 CCTGGGGTCGTCTCATACTACCTCACAAAATTTGTCAAGGGCGAGGCTCAAGTGCTTC 11219	Db 12094 TGGCCAGCT
δλ	2y 350 yArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAl 370	RESULT 11 US-10-121-032-14
Op	Db 11220 -CGGAGACAGTCTTCAGCACCGGCGAATTGAGGTGGATTGC-CGGGAGTATCTTGATGA 11277	; Sequence 14, Appl ; Patent No. US2002
οy	370	, APPLICANT:
g	Db 11278 CAGGGAGCGAGAAGTTGCTGAGTCCCTCCCACATGCCTTCATTGGCGACGTCAAAGGC 11335	NUMBER OF
δλ	390 nArgGluMetThrTyrLeuSerG	ADDRE
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Οy	408	COUNT
QQ	11371 ATACCTTCCGCGCTTCCTTCCCAAGGAATCAGTCGCGGTAGTCGGGGTT	COMPUTER H
QY Db	29 421 palaHisAlaGlyileLeuLysSerLeuAspaspLysTyrLysAspTy 437	COMPU
ολ.	. 437 rLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArgAr	CURRENT AP
qq		FILIN
Οy	2y 456 glleProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGl 476	, ; PRIOR APPL
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δλ	476 yAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAs :::::	APPLI
අ	11611 GTATCAGCTTGCAAGCTACGCTCGTACATCCGTGTTCCTGTCAAC	; ATTORNEY/A
ò á	495 pLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLy	REGIS
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TTGAAATGAAATG------GGGTCTATACAAAGCCTCTTCGACAAAT 12093
                                                                                                    CATGGGCCCTGCCCTTTGCAACAGAGTTGTCGGGTCCACCCATTGGGG 11730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTGAAATGCCTCCTGGATACAAGATTCTGGCGTGCGCGGGAGTTCTCGCT 11844
                                                                                                                                                                                                                                                                                                                          CGCAGTCACCCCTTAT----GATTACGGTGCTAAAATCATCTTGTCTAG 11784
                                                                                                                                                                                                                                                                                                                                                                                                                                                -ArgGluMetTyrProGlyArgAlaLeuProSerAspÀlaAsnPheThrMe 571 '
|||||| |||||| ::: :: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTy 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPh 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGl 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAs 656
sAspProAlaVal-----GluLeuSerLysSerValIleAlaAlaAlaAlaIleGl 533
                                                                                                                                                                                                               aMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgieuPhePheAlaGl 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nLeuHisIleAlaPhe------637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WT: Bylina, Edward J.
FINVENTION: GLYCOSIDASE ENZYMES
DF SEQUENCES: 72
NNUENCE ADDRESS:
RESSEE: Gray Cary Ware & Freidenrich LLP
REET: 4865 Executive Drive, Suite 1600
TY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNTRY: USA
P: 92121
P: 92121
MEDABLE FORM:
DIUM TYPE: Diskette
MPUTER: IBM Compatible
MATTING SYSTEM: Mindows95
FFWARE: FastSEQ for Windows Version 2.0
APPLICATION NUMBER: US/10/121,032
ASSIFICATION NUMBER: US/10/121,032
ASSIFICATION NUMBER: US/09/134,078
LING DATE: 13-AUG-1998
LING DATE: 10-OCT-1997
LING DATE: 10-OCT-1997
LING DATE: 10-OCT-1997
LING DATE: 10-OCT-1997
LING DATE: 10-OCT-1996
LING DATE: 10-OCT-1996
LING DATE: 10-OCT-1996
LING DATE: 10-OCT-1996
LING DATE: 10-OCT-1996
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STRATION NUMBER: 38,347
STRATION NUMBER: 09010/024002
STRATION INFORMATION:
PHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ulleGlyLeuAlaPhe 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ication US/10121032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENT INFORMATION:
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QQ	768	
Qy	304	sGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThrArg11 320
QQ	804	GACCCGATAATCTATGAAATACACATAGCGGACATCACAGGGCTCGAAAACTCCGGGGT 863
. Qy	320	eLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMe 339
} ;		1 (
중 점	924	CASIALY SECULATION OF THE CASIAL SECURATION OF
Qy	359	eAlaAspTrp 372
q _Q	984	ACACAGGC
QY	373	GlyAspValLeuSerSerLeuGluLysAl 382
qo	1043	GTTACGATCCTTACCTGTTCATGGTTCCGGAGGCAGATACTCAACCGATCCCAAAAACC 1102
ογ	382	aTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheG1 402
qq	1103	CACACACGAGAAATCAGAAAATGGTCAAAGCCCTTCACAAACACGGTATAG 1162
Οy	402	yGlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAs 419
qa	1163	GTGTGATTATGGACATGGTGTTCCCTCACACCTACGGTATAGGCGAACTCTCTGCGTTCG 1222
Qy	419	nProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLys433
qa	1223	ATCAGACGGTGCCGTACTACTACTACAGAATCGACAAGACAGGTGCCTATTTGAACGAAA 1282
Qγ	434	TyrLysAspTyrLeuProSerLeuAs 442
qq	1283	GCGGATGTGGTAACGTCATCGCAAGGCGAAAGACCCATGATGATGAAAAATTCATAGTCGATA 1342
Qy	442	PArgLysValLeuProAlaMetLeuAspIleValArgArgArgIleProAla-AspLysL 462
qq	1343	CTACTGGGTAÀ
Οy	462	euProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyr- 481
qa	1397	GG
Qy	482	483
q	1442	TTCATAAAATCGATCCAACTATCATTCTTCTACGCCGAACCGTGGGGTGGATGGGGGGCAC 1501
Οy	483	spPheValPheAspLysSer
qq	1502	CGATCAGGTTTGGAAAGAGCGATGTCGCCGCACACACGTGGCAGCTTTCAACGATGAGT 1561
Qy	497	heHisAlaMetLeuLysS 503
qq	1562	TCAGAGACGCAATAAGGGGTTCCGTGTTCAACCCGAGCGTCAAGGGATTCGTCATGGGAG 1621
Οy	503	erMetAspLysGlu
QQ	1622	GATACGGAAAGGAAACCAAGATCAAAAGGGGTGTTGTTGGAAGCATAAAACTACGACGGAA 1681
Qy	508	ysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer522
QQ	1682	CATCAAAAGTTTCGCCCTTG
Qy	523	AlaArgAlaI 532
QQ	1742	ACAACCACACACTGTGGGACAAGAACTACCTTGCCGCCAAAGCTGATAAGAAAAAGGAAT 1801
οy	532	leGlnAlaAspAlaMetAlaAsnAlaTyrAla1leGluLysGlyLysArgLeuPhePheA 552 :::

Query Match: 2.96% Indels: 258 DB: 9 Gaps: 42	US-10-008-355-2 (1-712) x US-10-093-037-14 (1-2319) Oy 74 ThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyr 92 Oy 74 ThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyr 92 Oy 74 ThrGly	93 GlyAlaIleGlnSerGlnSer-ThrValAspHisAspTyrLeuArgAspGlyPheVa ::::::	OY 111 ISerArgThrMetGlyGluGluLeuProlleProGlyLeuSer	Qy 126valLysTyrLeuArgLysIleValLysValThrAspLysValGluGLyGl 142 142 143 144 145	142 nLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl ::: ::: :::	Oy 162 uLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyrSe 182	Qy 182 rAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPheAl 202 :::	Qy 202 aproproSerSerValGlyLysPheQlyGlyAspThrAsp 215 ::: ::: Db 507 CCCCGTTTCTAAGTGGTTAAAGGTGCTTCTTCTTCTAAAACGGAGAAGACACACAA 566	QY 216Glyas 225 LI CAGGTTGTGAACATGAAACGGAAACGGGTCTGGAAACGGTTGTTGAAGGCGA 626 Db 567 CCAGGTTGTGAACATGGAATACAAGGGAAACGGGTCTGGGAAGCGGTTGTTGAAGGCGA 626	Qy 225 pPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProÀlaGluTyr\$erLy 244	OY 244 SASPASDLYSPrOTYrLySProValTyrPheAlaAlaValSerMetGlnGlyTyrLySAl 264	Oy 264 aAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgfyrLeuThrSerTr 284 11 11 Db 717 CAACCAAGAGGCGCGTTGTGAATCTTGCCAGGACAACCCAGAAGGATG 767	OY 284 pGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluYalArgGlyIleLy 304	Qy 304 sGlnGlyIleTrpLysGlualaMetSerAlaAspGlnAlaThrArgil 320 1 1 1 1 1 1 1 1 1	Qy 320 eLysTyrAlaSerLysTyrAlaGinSerAlaAsnTyrTrpLysAsnSerIleĠlyMe 339 :::	Oy 339 tASNArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAlaGluGluArgAlaPh 359	Oy 359 eAlaAspTrp372 111:::
GGACCGAAGAAGAACTGAAAAAGGCCCAGAAACTGGCTGG	Oy 552 ladlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAssPheThrMetA 572	Db 1922 ACTCCTACAACGCCCCTATCTCGATAACGGCTTCGATTACGAAAGAAA	57.9 ICHIROMOGISILCHARITACCAC 603 spProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysA 1 1 1 1 2030 ACCT	623 snTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsn		Oy 653 heAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrp 668	669GlualaMetSerGlyAspileG	676 luPheGluPro 679 ::: 2279 aarmccampec 2289	RESULT 12 US-10-093-037-14	രമയ	۸.	TITLE OF INVENTION: ENZYMES HAVING GLY FILE REFERENCE: 09010-024006 CURRENT APPLICATION NUMBER: US/10/093, CURRENT FILLING DATE: 2002-03-06	7-20 7-20 .us 09/134 8-13	PRIOR APPLICATION NUMBER: US 08/949,026 PRIOR FILING DATE: 1997-10-10 PRIOR APPLICATION NUMBER: US 60/056,916 PRIOR FILING DATE: 1996-12-06	NUMBER OF SEQ 1D NOS: /Z SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 2319		Alignment Scores: O.0486 Length: 2319 Pred. No.: 110.00 Matches: 155 Score: 110.00 Conservative: 105 Best Local Similarity: 19.75% Mismatches: 268

Db 2051 AC	Alignment Scores:
373	908 ysphealaLysalaileGluLysaspProalaValGluLeuSer

D	Db 2051	 AC		AAAAACACCTGGAATT	 GCTGAAGAGATCAAAAAAAAAAAAAAATTCTCCCGGGGGGGAGAA	2098
J	Oy 641	* * * * * * * * * * * * * * * * * * * *	AsnAspIl	-AsnAspIleThrGlyGlyAsnSerGlySerPro	cGlySerProValP	653
ū	Db 2099		CATGCTTAAAGACCA	ACGCAGGTGGTGATCC	GAATAGTTGCGTTCATGCTTAAAGACCACGCAGGTGGTGGTGATCCCTGGAAAGACATCGTGG	2158
O	Qy 653		heAspLysAsnGlyArgLeuIleGlyLeuAlaPhe	suAlaPhe	-AspGlyAsnTrp	899
ם	Db 2159		AAACTTAGAGAAGAC	CAACATACAAACTGCC	TGATTTACAATGGAAACTTAGAGAAGACAACATACAAACTGCCAGAAGGAAAATGAATG	2218
O	оу 669			GluAla	-GluAlaMetSerGlyAspIleG	929
Ц	Db 2219		CCAGAAAGCCGGAAC	CAGAAGTGATAGAAAC	TCGAAGGAACA	2278
	0у 676	luPheGluPro	619			
L	Db 2279	AACTCGATCCG	2289			
ız. ;	ULT 13	0				
	; Sequence 61,	e 61, Applicat	1, Application US/10027806	10		
		GENERAL INFORMATION:	Robald V			
	APPLICANT	Feldman,	Robert A.			
• ••	TITLE	Σi	C ACIDS	AND PROTEINS FROM	CENARCHAEUM	SYMBIOSUM
•• ••		EFERENCE: DCOR T APPLICATION	FILE REFERENCE: DCORP.002A CURRENT APPLICATION NUMBER: US/10/027	327,806		
•• ••		T FILING DATE: APPLICATION NU	ZUU1-12-ZI IMBER: EARLIER A	CURRENT FILING DATE: 2001-12-21 STOR APPLICATION NUMBER: DRIVE ATTACK DAME: DATE: APPLICATION NUMBER:	SR: 09/408,020	
•• ••		OF SEQ ID NOS:	ARLIER FILING L	OATE: 1999-09-29		
	SOFTWARE:		r Windows Version	on 3.0		
	60	n: 2338 DNA ISM: Cenarchaeum	nn symbiosum			
		RE: KEY: CDS	•			
D	S	LOCATION: (1)(2538 10-027-806-61				
هر ت	Alignment Scores	Scores:	20.00	7 0 1 1 1	200	
. 0, 0	Score:	Score:	110.00 37.069	Matches:	2336 121 88	
a m Ori	Best Local S Query Match:	imitarity: 1 Similarity: ch:	27.00% 21.45% 2.96%	atches: ls:	233 123	
, D	us: us-10-008	-355-2 (1-712)		caps:)6-61 (1-2538)	07	
	Qy 20		laAspLysGlyMet1	GlyValAlaLysAlaAspLySGlyMetTrpLeuLeuAsnGlu-	LeuAsn	35
ы	- ab 901		::III ccgacataccccrg1	::::::::::::::::::::::::::::::::::::::		096
J	Qy 36		spargMetargGluI	euGlyPheThrLeuP	GlnGluAsnLeuAspArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyr	55
L	Db 961		 acctgtacaggacc		::: GCCGTCCATCTGCACCTGTACAGGACCTTCTCGAACAGGTCGTTCCAGCTGTAT	1014
J	0y 56		d	AspLysProSerIleA	-AspLysProSerIleAlaAsnAlaValIle	89
1	Db 1015		AGTATACAGATTACT	:::: I I I I I I I I I I	::: GCATTTGCGGCAAAGTATACAGCTTCCCTGAACAGCGTGTCCAAGGCGATGCTCGGC	1074
J	Qy 69		ysThrGlyIleThrV	/alSerAspGlnGlyLo	PheGlyGlyGlyGlyGlyThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis	88
	Db 1075		ATTATGGCGTGTCTC	TCGGGGATCTCACTC	GAGGGCAAGGTCGATTATGGCGTGTCTCTGGGGATCTCACTCTATACCAGACTGCAAAC	1134
O.	0y 89		lyAlaIleG	lnSerGlnSerThrV	IleGlnSerGlnSerThrValAspHisAspTyrLeu	106
ы	Db 1135		ACGCGCCTGACGC	TEGAGCTTAGCACCT	TATTGCTATCATGACGCGCGCCTGACGCTGGGAGCTTAGCACTTTGGGAACGAGATACTG	1194

δy	107 ArgAspGlyPheValSerArgThrMetGlyGluGluLeuProIleProGlyLeuSer 		
Dp	1195 ATGGACCTCCTGGTGGTGACCAGCAGGATTGCCCGGATGCCCATGATGTTGTCCCGC	CCGC 1254	
οy	126ValLysTyrLeuArgLysIleVálLysValThrAspLysValGluGlyGln	yGln 142	
Dp	1255 ATGGGCGTCTCGCAGTGGATAAGGAGCCTGCTGTACTATGAGCACAGGCAGCGCAACGCG	CGCG 1314	
Qy	143 LeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGluValCysGlnGlu	nGlu 162	
QQ	1315 CTGATACCCCGCAGGGACGACTGGAAAAGAGGTCTCAACGAGGTAGCAACGAC	.cgAC 1368	
δy	163 LeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro	179	
QQ	1369 GCCGTAATCAAGGACAAAAGTTCCGCGGTGGTCTCGTAGTCGAGCCTGAAGAGGGC	.GGGC 1425	
٥ý	180	eVal 190	
QQ	 1426 ATACACTTTGATGTTACAGTTATGGATTTTGCAAGCCTGTATCCTAGCATAATAAAGGTG	GGTG 1485	
٥y	191 TyraspvalPheLysaspvalargMetValPheAlaProProSerSerValGlyLys	yLys 209	
Dp	1486 CGAAACCTCTCGTACGAGACCGTCAGGTGCGTTCATCCCGAATGCAGAAAC	GAAC 1539	
οy	210 PheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPhe	1Phe 229	
pp	1540 ACCATCCCCGATACCACTGGGTATGCACGAAAAACAACGGGCTTACATGATATA	: GATA 1599	
δy	230 ArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyr	OTyr 249	
Dp	1600ATAGGATCGCT-CCGCGACCTGCGCGTCAACTATTACAAGAGCCTCTCAAA	CAAA 1649	
٥y	250 LysProValTyrPheAlaAlaValSerWetGlnGlyTyrLysAlaAspAspTyrAlaMet	aMet 269	
qq	1650 GAGCCAGTCTATAACGGAGGAGCAGCGGCAGCAGCAGTATACTGTGAT	TGAT 1694	
٥y	270 ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg	pArg 289	
Db	1695 CAGCCAGGCCCTCAAGGTGGTGCTAAACGCAAGCTACGGGGGTGATGGGCGCCGAGAT	T 1751	
ΟŊ	290 IleGluAsnGluAsnAsnProArgIleGluValArgGlyIleLysGlnGlyIleTrpLys	pLys 309	
qq	1752ATTCCCGCTGTACTTCT	TTCT 1769	
δ	310 GluAlaMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAla	rAla 327	
qq		 CGCA 1829	
ΟŊ	328 GlnSerAlaAsnTyrTrpLysAsnSerIle-GlyMetAsnArgGlyLeuAlaArgLeuAs	euAs 347	
Dp		 CCGA 1871	
Qγ	347 pValileGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl	snG1 367	
qq	1872 TTCGCTGTTCATAAGAATCCAGAGGGGCGCAGATCCATGATATAGTCGAGCACGCCAA	CCAA 1931	
Qy	367 yLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl	11yA1 387	
qq	1932 AAAGGAGCACGGCGTCGAGCTCGAGGTGGACAAAGAGTACAGGTATGTCGT	TCGT 1982	
Qγ	387 aLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa	alva 407	
qq	1983 GCTATCTAACAGGAAGAAAACTATTTCGGGGTGACAAAGTCCGGCAAGGACGCCGCCC	 TC 2040	
ΟŊ	407 lArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLe	leLe 427	
QQ	2040	2040	
ογ δ	427 uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 	Jeupr 447	
3	2041 ANGGOGCC16ACGGGGGAAN - ANGICGCACACCCCCCC11CAIAAAGGAGC1G11CIA	TOTA 2030	

```
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NOCLEIC ACIDS AND PROTEINS FROM CENARCHABUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                  2250 GGGGCCCTCTGAA---TACGTAAAGACCGTCCCGCAGCAC------- 2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2194 ----CTGGAGGAGGGGGGGGCTCCCGCTGGCGGTTCTGATGTGATGATGATAGCAA 2249
                                                                                                                                                                                                                                                                                                                                     2287 ------ATACGGGCGGCGGCAGACTGCAGG------AACGCAAGGGAGGT 2324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        961 GCGTCCATCTGGACCTGTACAGGACC----TTCTCGAACAGGTCGTTCCAGCTGTAT 1014
                                                                                                                                                                                                                                   503 rMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLy 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 sSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaI1 543
447 oAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAspIlePheLy 467
                                                                             467 sAsnVal------IleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPh 484
                                                                                                                                                          484 eValPheAspLysSerValValProTyrSerAsp---LysPheHisAlaMetLeuLysSe 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LeuAsn 35
                                                                                                       ::::
2145 ATCGGCAAAGCTAAAAGATCTCAAAGGCCATAGCGGCATCCGGGAAGAGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyValAlaLysAlaAspLysGlyMetTrpLeuLeuAsnGlu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2538
121
121
88
233
123
26
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-008-355-2 (1-712) x US-10-034-623-61 (1-2538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-10-034-623-61
Sequence 61, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110.00
37.06%
21.45%
2.96%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)...(2538)
US-10-034-623-61
                                                                                                                                                                                                                                                                                                                                                                                                                    ::::|||||||
2325 CAAAAAAGGC 2334
                                                                                                                                                                                                                                                                                                                                                                                          543 eGluLysGly 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
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88 1134 106 1194 125	142 1314 162 1368 179	1425 190 1485 209 1539	229 1599 249	269 1694 289 1751 309 1769	327 1829 347 1871 367	387 1982 407 2040 427
69 PheGlyGlyGlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis	126ValLysTyrLeuArgLysIleValLysValThrAspLysValGluGlyGln 1255 ATGGGCGTCTCGCAGTGGATAAGGAGCCTGCTGTACTATGAGCACAGGCACAGGCGAACGCG 143 LeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGlu 111	1369 GCCGTAATCAAGGACAAAAGTTCCGCGGTGGTCTGTAGTCGAGCTGAAGAGGGC 180		250 LysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMet :::	310 GlualametSeralaaspGlnalaThrargIleLysTyrAlaSerLysTyrAla 1770 GCCTGCCGCGGGCCCCCGCGGTCGGCGCTCTATATCATCATGCAGACCATATCGCA 328 GlnSeralaasnTyrTrpLysAsnSerIle-GlyMetAsnArgGlyLeualaargLeuAs 1830 GTGCGAGCAGGGGTGGGGTGGGGTGGGGTGGGGTGGGGGTGGGGGTGGGG	367 yLysSeralaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	oy oy oy	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Oy Oy Oy	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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Sequence 61, Application US/10027801

Sequence 61, Application US/20030054364A1

Sequence 1 NPORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TILLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT PILIG DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 2538
-- 2040
                                                  2097 TTGGCTGGTGATA------CTGTGGGCTGTACAGACCGAGGACGAGTTTGA 2144
                                                                                                                                                                                          2287 ------ATACGGCGGCGAGACTGCTCGAG------AACGCAAGGGAGGT 2324
                                                                                                                                                                                                                                                                                                           503 rMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLy 523
                              427 uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 447
                                                                                                                                                                                                                                       484 eValPheAspLysSerValValProTyrSerAsp---LysPheHisAlaMetLeuLysSe 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 oAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAspIlePheLy 467
                                                                                                                                                                   467 sAsnVal-----IleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPh 484
                                                                                                                                                                                                                                                                                                                                                                               523 sSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIl 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 GlnGluAsnLeuAspArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0555
110.00
37.06%
21.45%
2.96%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1)...(2538)
US-10-027-801-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2325 CAAAAAAGGC 2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 eGluLysGly 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-027-801-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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2040
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λ q	56 S : 1015 G	SerPhe	
7. q	69 P	PheGlyGlyGlyGlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis 88 	
2y Ob	89 H : 1135 T	HisCysGlyTyrGlyAlaIleGlnSerGlnSerThrValaspHisAspTyrLeu 106 ::: ::: TATTGCTATCATGACGCGCGCCTGACGTGGAGCTTAGCACCTTTGGGAACGAGATACTG 1194	
2y 3b	107 A 1195 A	ArgaspGlyPheValSerargThrMetGlyGluGluLeuProIleProGlyLeuSer 125 	
7. 2.	126 - 1255 A	ValLysTyrLeuArgLysIleValLysValThrAspLysValGluGlyGln 142 ::::::: ::::: ATGGGCGTCTCGCAGTGGATAAGGAGCTGCTGTACTATGAGCACGCGAGCGCAACGCG 1314	
2¥	143 L 1315 C	LeuLysGlyIleThraspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGlu 162 	
λ 2	163 L 1369 G	LeuAlaLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro 179 ::: GCGTAATCAAGGACAAAAAGTTCCGCGGTGGTCTCGTAGTCGAGCCTGAAGAGGGC 1425	
λ 2	180 - 1426 A		
7. 9.	191 T 1486 C	TyraspvalPheLysaspvalargMetValPheAlaProProSerSerValGlyLys 209 ::::: :::: CGAAACCTCTCGTACGAGACGTCAGGTGCGTTCATCCCGAATGCAGAAAGAAC 1539	
2 <u>Y</u>	210 P 1540 A	PheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPhe 229 ::::: ::: ACCATCCCGATACCACTGGGTATGCACGAAAACAACGGGCTTACATCGATGATA 1599	
ž g	230 A 1600 -	ArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyr 249 ATAGGATCGCT-CCGCGACCTGCGCGTCAACTATTACAAGAGCCTCTCAAA 1649	
ζζ	250 L	LysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMet 269 	
දු දු	270 T	ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg 289	
2 6	290 I	IleGluAsnGluAsnAsnProArgIleGluValArgGlyIleLysGlnGlyIleTrpLys 309	
3 2		327	
g	1770 G	GCCIGCCGCGAGGCCACCACGGCGGTGGGCCTATATCATGCAGGCCATATCGCA 1829	
Sy Ob	328 G 1830 C	GInSeralaAsnTyrTrpLysAsnSerIle-GlyMetAsnArgGlyLeuAlaArgLeuAs 347 :: ::	
2y 2b	347 p	pvalileglyargLysargAlaGludluargAlaPheAlaAspTrpIleArgLysAsnGl 367 1	
λ S	367 y 1932 A	YLYSSerAlaValTyrGlyAspValLeuSerSerLeuGluLySAlaTyrLySGluGlyAl 387 	

ΟŻ	387		7
Db	1983	GCTATCTAACAGGAAGAAAAACTATTTCGGGTGACAAAGTCCGGCAAGGTCGACGTC- 2040	4 0
ΟŊ	407	lArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLe 427	7:
QQ	2040	2040	040
QY	427	uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 447	7
qq	2041	- AAGGGCCTGACGGGGAAAAAGTCGCACACGCCCCGTTCATAAAGAGGCCTTCTA 2096	960
Qy	447	oAlaMetLeuAspIleValArgAr	7:
Dp	2097		44
òy	467	sAsnValIleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPh 484	34
Op	2145		193
Qy	484	eValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLysSe 503	33
Op	2194		648
ΟY	503	rMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLy 523	83
q _Q	2250	GGCGCCCTCTGAATACGTAAAGACCGTCCCGCAGCAC	988
QY	523	sSerValIleAlaAlaAlaAlaAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIl 543	23
qq	2287		324
Qγ	543	eGluLysGly 546	
qq	2325	CAAAAAGGC 2334	
Sea	rch co	Search completed: May 23, 2003, 13:41:19	